Evaluation of phenotypic diversity of exotic soybean (*Glycine max* L. Merr.) germsplasm under Sri Lankan conditions

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Abstract

Study of genetic diversity within available genetic resources is a critical factor for breeders to better understand the evolutionary and genetic relationships among accessions, select germplasm in a more systematic and effective way, and develop strategies to incorporate useful traits in their breeding programs. A study was conducted to evaluate 107 exotic soybean (*Glycine max* L. Merr.) genotypes at the Field Crops Research and Development Institute, Mahailluppallama over three seasons during 2016 and 2018. Twelve morphological characteristics including yield and yield related traits were studied. Considerable diversity in the morphological characteristics was observed. The yield per plant was positively and significantly correlated with days to seedling emergence, days to initial blooming, days to 50% blooming, days to full blooming, days to maturity, plant height at maturity, number of branches per plant and number of pods per plant. Principal Component Analysis revealed that the first two components together explained nearly 65% of the total variation among genotypes and identified important morphological characteristics that could effectively be used to classify soybean genotypes. Five different clusters were formed in cluster analysis for the second season. A total of 71% genotypes were grouped into two major clusters (3 and 4). The major traits contributed to separate the genotypes into different clusters were grain yield per plant, number of pods per plant, number of branches per plant and plant height. This grouping of genotypes and the traits identified can be used to make appropriate decisions in soybean breeding.

Keywords: Cluster analysis, Morphological traits, Phenotypic diversity, Principal component, Soybean genotypes

Introduction

Soybean (*Glycine max* L. Merr.) is unique among the other food legumes because, it can be used as a cheap source of protein. It is highly nutritious and beneficial to human health and used in the production of poultry feed as a raw material in supplementing the protein. There is a good potential to promote soybean as a commercial crop in Sri Lanka. It can be cultivated under rain-fed condition in uplands during *Maha* season and in *Yala* season under supplementary irrigation in the paddy fields in the Dry and Intermediate zones of Sri Lanka as it requires relatively less water. In 2019, the cultivated extent, production and national average yield of soybean were 914 ha, 2,197 t and 2.4 t ha^{-1}, respectively and annual imports as soybean oil cake was 213,801 t (Agstat, 2019). However, to cater this high demand, there are three recommended varieties in Sri Lanka. The variety Pb 01 which is the most popular variety introduced by INTSOY (UNDP–FAO International Soybean Project) as a selection in 1975 (Siriwardena, 1994). The variety PM 13 was developed through the locally performed hybridization and selection program in 1989. The variety MISB 01 is a cream seeded variety which is similar in seed size to PB 01, with a maturity period of 90 days and an average yield of over 3.0 t ha^{-1} and released in 2012. However, there is still a high demand for high yielding varieties with tolerance to pests and diseases to make the country self-sufficient in soybean.

Profitable yields can be obtained through genetic improvement for high yield potential. The examination of genetic diversity is important for plant breeders to utilize it for variety development in general. Introgression of diverse germplasm into the current soybean genetic base through hybridization may increase genetic variability in breeding populations and lead to greater gains from selection (Guedira *et al*., 2000; Thompson and Nelson, 1998). Higher the genetic diversity possessed, greater the chance of success for developing new superior varieties. Germplasm improvement and genetic diversity is the key to reliable and sustainable development of new varieties through breeding.

Measuring available genetic diversity is an utmost importance for effective evaluation and utilization of germplasm (Zubair *et al*., 2007). Some scientists emphasize the importance of evaluation of the levels and patterns of genetic diversity in crop breeding (Franco *et al*., 2001; Habtamu and Milion, 2013; Mohammadi and Prasanna, 2003; Thompson *et al*., 1998). Multivariate analysis is the most popular approach for the estimation of genetic variability to study the patterns of variation and the genetic relationships among genotype collections (Ajmal *et al*., 2013; Malik *et al*., 2014). Principal component analysis (PCA) and cluster analysis are preferred tools for morphological characterization of genotypes and their grouping on similarity basis (Mohammadi and Prasanna, 2003; Peeters and Martinelli, 1989).

Present study aimed at studying the genetic diversity of 107 soybean genotypes and to evaluate the performance of different genotypes based on the morphological characteristics through principal component and cluster analyses with the objective of finding better genotypes for the soybean improvement programme in Sri Lanka.

Materials and Methods

Hundred and seven soybean germplasm received from United States Department of Agriculture (USDA) were evaluated with three locally recommended varieties (Pb 01, PM 13 and MISB 01) during three seasons (2015/16 *Maha* , 2016 *Yala* and 2018 *Yala*) at the Field Crops Research and Development Institute (FCRDI), Mahailluppallama. The experiment was laid out in a Randomized Complete Block Design with two replications. The trial was maintained according to the recommendations made for soybean cultivation by the Department of Agriculture.

Days to Seedling Emergence (DSE), Hypocotyl Colour (HC), Flower Colour (FC), Days to Initial Blooming (DIB), Days to 50% Blooming (DFB), Days to Full Blooming (DFlB), Days to Maturity (DM), Plant Height at maturity (PH), Number of Branches per plant (NB), number of Pods Per Plant (PPP), number of Seeds Per Pod (SPP) and Grain Yield per Plant (GYP) were measured in ten randomly selected plants in a plot as they are the important characteristics in soybean improvement.

Data analysis

Descriptive statistics of quantitative traits were calculated. Average values of each trait were used in multivariate analysis (cluster analysis and PCA). The statistical package used was MINITAB 17 software. The Pearson's correlation was calculated to find the correlation coefficient for pairs of morphological characters of the genotypes.

Results and Discussion

Analysis of variance

The analysis of variance for grain yield per plant and other yield components of the soybean genotypes tested in three seasons showed that the mean squares of season, genotypes and genotype × season interactions (GS) were highly significant (Table 1). The results indicated that the season effect was the predominant source of variation followed by genotypes and genotype × season interactions. Highly significant mean square (MS) due to season indicated that growing environment had profound influence on the expression of yield of soybean genotypes. Highly significant MS due to genotype suggested the existance of genetic differences among the genotypes. Cravero *et al.* (2010) stated that environmental effect was three times higher than the genotype and genotype × environment interactions. Gedif *et al.* (2014) explained that both genotypes and environments are important in governing the expression of yield while Krisnawati and Muchlish (2018) and Bhartiya *et al.* (2017) showed that genotype × environment interactions were higher than those shown by the genotypic and environmental effects.

Descriptive statistics

Mean, standard error, coefficient of variation and range for 10 quantitative traits were calculated for soybean genotypes during the three seasons and are presented in Table 2. It indicated the genotypes studied were genetically diverse. Comparatively higher coefficient of variation (CV) was observed for grain yield per plant, number of pods per plant, number of branches per plant and plant height at maturity in all seasons. In the first season, days to full blooming showed the lowest variability and in second and third seasons, days to maturity showed the lowest variability. The observed morphological variation was mainly due to genetic factors and between season was mainly due to environmental factors. Variability in quantitative traits could support for the selection of best lines for soybean crop improvement (Iqbal *et al*., 2008: Khan *et al.,* 2014).

Correlation analysis of quantitative traits

The correlation coefficients among the morphological traits for three seasons (Tables 3, 4 and 5) revealed that the grain yield per plant was positively and significantly (p<0.05) correlated with days to seedling emergence, days to initial blooming, days to 50% blooming, days to full blooming, days to maturity, plant height at maturity, number of branches per plant and number of pods per plant. Number of pods per plant and days to 50% blooming were highly correlated with the grain yield of the plant. These traits can be considered as favourable attributes for soybean improvement through effective phenotypic selection. Correlation between grain yield per plant and other yield traits have been reported in many previous studies (Satpute *et al*., 2016; Malik *et al*., 2014; Ojo *et al*., 2012; Varnica *et al*., 2018). Most of the traits showed positive correlations between each other. Pod number per plant, seeds per pod and days to maturity appeared to be the first order traits for higher seed yield in soybean and priority should be given in selection for traits with strong associations as well as high magnitudes of direct effects on seed yield (Malik *et al.,* 2014). However, seeds per pod showed significant correlation with yield per plant only in the second season.

Table 1. Analysis of variance for yield and other yield components of soybean genotypes evaluated in three seasons at FCRDI, Mahailluppallama

Parameter	**Mean squares**			**CV (%)**
	Season (S)	**Genotype (G)**	**G×S**	
Days to initial blooming	490.52*	191.33*	5.51*	4.01
Days to 50% blooming	323.55*	188.55*	5.66*	3.59
Days to full blooming	2119.89*	69.79*	15.18*	4.33
Days to maturity	8369.23*	232.58*	45.12*	4.19
No. of branches per plant	84.12*	10.11*	2.32*	15.34
No. of pods per plant	95903.45*	2402.43*	467.70*	29.40
Grain yield per plant (g)	11492.88*	185.98*	72.43*	42.60

* *= significantly different at P < 0.0001*

Table 2. Descriptive statistics of quantitative traits of soybean genotypes evaluated in three seasons at FCRDI, Mahailluppallama

Quantitative trait		First season				Second season				Third season			
		Mean	SE*	CV**	Range	Mean	SE	CV	Range	Mean	SE	CV	Range
Days to seedling emergence	DSE	5	0.09	18.49	5-11	6	0.10	15.80	6-13	5	0.05	9.06	5-8
Days to initial blooming	DIB	29	0.53	18.85	23-47	32	0.61	19.98	23-50	28	0.60	20.92	22-48
Days to 50% blooming	DFB	32	0.51	16.34	27-50	35	0.63	18.89	27-55	33	0.57	17.14	26-54
Days to full blooming	DFlB	46	0.16	3.65	43-55	40	0.54	14.03	36-58	40	0.43	10.53	34-56
Days to maturity	DM	98	0.84	8.93	81-151	109	0.77	7.38	98-129	108	0.46	4.19	103-118
Plant height at maturity (cm)	PH	21.13	0.92	45.00	8-60.6	28.58	0.98	35.68	12.6-67.1	30.59	0.87	28.01	13.66-55.5
No. of branches per plant	NB	4	0.19	52.18	1-10	5	0.15	31.28	2-10	5	0.13	27.18	1-8
No. of pods per plant	PPP	25	1.43	59.16	9-86	61	2.75	46.74	20-158	63	2.63	41.18	24-188
No. of seeds per pod	SPP	2	0.04	18.12	2-3	2	0.03	14.4	2-3	2	0.03	15.08	2-3
Grain yield per plant (g)	GYP	4.98	0.29	60.73	0.96-22.5	19.39	1.01	54.66	5-59.69	13.14	0.69	51.98	1.04-42.5

**SE – standard error, **CV – coefficient of variation*

Table 3. Pearson's correlation coefficients among 12 traits of soybean germplasm grown in the first season at FCRDI, Mahailluppallama

	DSE1	HC1	FC1	DIB1	DFB1	DFlB1	DM1	PH1	NB1	PPP1	SPP1
HC1	0.091										
FC1	0.091	1									
DIB1	0.342*	0.061	0.061								
DFB1	0.321*	0.01	0.01	0.951*							
DFlB1	0.051	0.059	0.059	0.487*	0.506*						
DM1	0.248*	0.081	0.081	0.765*	0.706*	0.511*					
PH1	0.139	-0.105	-0.105	0.563*	0.527*	0.256*	0.384*				
NB1	0.141	0.091	0.091	0.617*	0.564*	0.258*	0.535*	0.405*			
PPP1	0.356*	0.094	0.094	0.682*	0.69*	0.277*	0.525*	0.519*	0.543*		
SPP1	-0.139	-0.034	-0.034	0.031	0.032	0.126	-0.03	0.202	0.142	0.11	
GYP1	0.197*	0.046	0.046	0.384*	0.407*	0.193*	0.244*	0.293*	0.43*	0.698*	0.096

DSE – Days to seedling emergence, HC – Hypocotyl colour, FC – Flower colour, DIB – Days to initial blooming,

DFB – Days to 50% blooming, DFlB – Days to full bloom, DM – Days to maturity, PH – Plant height at maturity (cm),

NB – Number of branches per plant, PPP – Number of pods per plant, SPP – Seeds per pod, GYP – Grain yield per plant (g)

** significant at $p<0.05$*

Table 4. Pearson's correlation coefficients among 12 traits of soybean germplasm grown in the second season at FCRDI, Mahailluppallama

	DSE2	HC2	FC2	DIB2	DFB2	DFlB2	DM2	PH2	NB2	PPP2	SPP2
HC2	0.129										
FC2	0.129	1									
DIB2	0.404*	0.136	0.136								
DFB2	0.372*	0.069	0.069	0.968*							
DFlB2	0.355*	0.025	0.025	0.873*	0.914*						
DM2	0.376*	0.073	0.073	0.768*	0.76*	0.668*					
PH2	-0.121	-0.177	-0.177	0.354*	0.447*	0.599*	0.161				
NB2	-0.102	0.085	0.085	0.613*	0.577*	0.426*	0.341*	0.252			
PPP2	0.213	-0.04	-0.04	0.747*	0.764*	0.671*	0.556*	0.507*	0.612*		
SPP2	0.045	-0.064	-0.064	0.021	0.047	0.097	-0.031	0.278	0.034	0.13	
GYP2	0.254*	-0.054	-0.054	0.647*	0.636*	0.509*	0.46*	0.323*	0.565*	0.762*	0.357*

DSE – Days to seedling emergence, HC – Hypocotyl colour, FC – Flower colour, DIB – Days to initial blooming,
DFB – Days to 50% blooming, DFlB – Days to full bloom, DM – Days to maturity, PH – Plant height at maturity (cm),
NB – Number of branches per plant, PPP – Number of pods per plant, SPP – Seeds per pod, GYP – Grain yield per plant (g)
* *significant at* $p<0.05$

Table 5. Pearson's correlation coefficients among 09 traits of soybean germplasm grown in the third season at FCRDI, Mahailluppallama

	DSE3	HC3	FC3	DIB3	DFB3	DFlB3	DM3	PH3	NB3	PPP3	SPP3
HC3	-0.046										
FC3	-0.054	0.979*									
DIB3	0.086	0.015	0.031								
DFB3	0.1	0.035	0.043	0.977*							
DFlB3	0.135	-0.05	-0.046	0.839*	0.822*						
DM3	0.177	0.041	0.054	0.649*	0.682*	0.44*					
PH3	-0.143	-0.003	0.001	0.592*	0.579*	0.626*	0.212*				
NB3	-0.168	0.112	0.111	0.513*	0.539*	0.458*	0.235*	0.471*			
PPP3	-0.115	0.042	0.056	0.675*	0.636*	0.622*	0.335*	0.563*	0.603*		
SPP3	-0.08	-0.109	-0.116	0.009	-0.028	0.15	-0.146	0.137	0.013	0.014	
GYP3	-0.038	-0.09	-0.087	0.64*	0.622*	0.671*	0.226*	0.535*	0.549*	0.76*	0.036

DSE – Days to seedling emergence, HC – Hypocotyl colour, FC – Flower colour, DIB – Days to initial blooming, DFB – Days to 50% blooming, DFlB – Days to full bloom, DM – Days to maturity, PH – Plant height at maturity (cm), NB – Number of branches per plant, PPP – Number of pods per plant, SPP – Seeds per pod, GYP – Grain yield per plant (g)

** significant at $p<0.05$*

Principal component analysis

The results of PCA (Table 6) revealed that four principal components having greater than one eigen value contributed 76% in the first season and 83% in the second season of the total variability among 110 soybean germplasm. In the third season, three principal components contributed 72% of the total variability. In all three seasons, the first principal component was related to days to initial blooming, days to full blooming, days to 50% blooming, days to maturity, grain yield per plant, number of branches per plant and number of pods per plant indicating that these traits are important in classification of soybean germplasm as they captured the largest variability. The traits, days to maturity and number of seeds per pod contributed for the second principal component. The first two components together captured more than 65% of total variability. The third principal component explained morphological characteristics such as days to full bloom and grain yield per plant. In contrast, Iqbal *et al*. (2008) reported that number of filled pods per plant, grain yield per plant and biological yield per plant contributed to the first principal component. The days to maturity negatively contributed to second principal component in all the three seasons.

Therefore, the contribution of traits to different principal components may vary depending on the season and environment. The PCA of this study revealed that days to initial blooming, days to 50% blooming, days to maturity, number of pods per plant, number of seeds per pod and grain yield per plant were contributed to first two principal components collectively in three seasons. Hence, these traits contributed to the diversity of soybean genotypes and show promise in using breeding programs.

Cluster analysis

Cluster analysis using Ward's methods for nine morphological traits evaluated in the second season could group 110 soybean genotypes into five major groups (Figure 1 and Table 7). A total of 71% of total germplasm was grouped into two clusters, cluster C3 (46 genotypes) and cluster C4 (32 genotypes). Cluster C1 with 20 genotypes, cluster C2 with 5 genotypes and cluster C5 with 6 genotypes.

The cluster C5 consisted of higher grain yielding (42.7 g per plant), genotypes with high number of pods per plant (92) and higher number of branches per plant (6). It consisted of the genotypes no. PI628939 (72), PI628919 (89), PI628832 (95), PI628833 (96), PI628929 (103) and PI628933 (104) which gave higher grain yield per plant (Table 8). Cluster C4 comprised of average grain yielding (27.7 g per plant) genotypes with higher number of pods per plant (94), but two seeds per pod. The cluster C3 consisted of average grain yield (14.2 g per plant), average number of pods per plant (44) with shorter plants (20.2 cm). The cluster C1 and C2 comprised genotypes with lower days to maturity compared to other genotypes (medium duration) but varied plant height, number of pods per plant and average grain yield.

Cluster analysis could be considered as a valuable tool for grouping genotypes based on their similarity. Based on the distance levels in cluster analysis, hybridization between the pairs of genotypes that had maximum distance levels may produce outstanding off-springs. The genotypes grouped in to cluster C5 were the suitable genotypes with high yielding, medium duration maturity and comparatively taller plants. Even though, these genotypes required variable days to maturity (100 – 115) all these genotypes belonged to medium duration maturity group.

Iqbal *et al*. (2008) evaluated qualitative and quantitative traits in 139 genotypes and those genotypes were clustered based on grain yield per plant, number of pods per plant, maximum plant height and number of branches per plant. Ghatge and Kadu (1993), Kumar and Nadarajan (1994) and Mehetre *et al*. (1994) have reported similar results. Das *et al*. (2001) revealed that grouping pattern of the accessions suggested no parallelism between genetic divergence and geographical distribution of the accessions. Genetic patterns obtained from the evaluation of soybean germplasm can help soybean breeders to make better choices when selecting among the large numbers of genotypes available for the soybean breeding programme based on their objectives.

Table 6. Principal component coefficients of major principal components for quantitative traits of soybean germplasm in three seasons

Variable#	First season				Second season				Third season			
	*PC-1	PC-2	PC-3	PC-4	PC-1	PC-2	PC-3	PC-4	PC-1	PC-2	PC-3	PC-4
DIB1	0.43	-0.19	0.02	0.14	0.41	-0.19	0.00	0.11	0.41	-0.16	-0.19	0.05
DFB1	0.42	-0.18	0.01	0.07	0.42	-0.15	0.11	0.08	0.41	-0.21	-0.18	0.00
DFlB1	0.26	-0.29	0.48	-0.59	0.39	-0.05	0.39	0.06	0.39	0.07	-0.21	0.26
DM1	0.37	-0.36	0.10	0.01	0.33	-0.33	0.06	0.50	0.26	-0.57	-0.37	-0.30
PH1	0.31	0.20	0.14	0.61	0.24	0.42	0.59	-0.44	0.32	0.28	0.03	0.48
NB1	0.34	0.13	-0.08	0.13	0.29	-0.02	-0.51	-0.51	0.30	0.16	0.39	-0.70
PPP1	0.38	0.25	-0.29	-0.08	0.38	0.09	-0.14	-0.19	0.36	0.14	0.29	-0.08
SPP1	0.06	0.64	0.68	-0.06	0.07	0.76	-0.11	0.48	0.02	0.66	-0.66	-0.31
GYP1	0.27	0.44	-0.45	-0.48	0.34	0.25	-0.44	0.09	0.35	0.21	0.29	0.12
Eigenvalue	4.62	1.14	1.00	0.71	5.28	1.28	0.87	0.71	5.12	1.22	0.93	0.54
Proportion	0.51	0.13	0.11	0.08	0.59	0.14	0.10	0.08	0.57	0.14	0.10	0.06
Cumulative	0.51	0.64	0.75	0.83	0.59	0.73	0.83	0.91	0.57	0.71	0.81	0.87

 # DIB – Days to initial blooming, DFB – Days to 50% blooming, DFlB – Days to full bloom, DM – Days to maturity, PH – Plant height at maturity (cm), NB – Number of branches per plant, PPP – Number of pods per plant, SPP – Seeds per pod, GYP – Grain yield per plant (g)

**PC – Principal component*

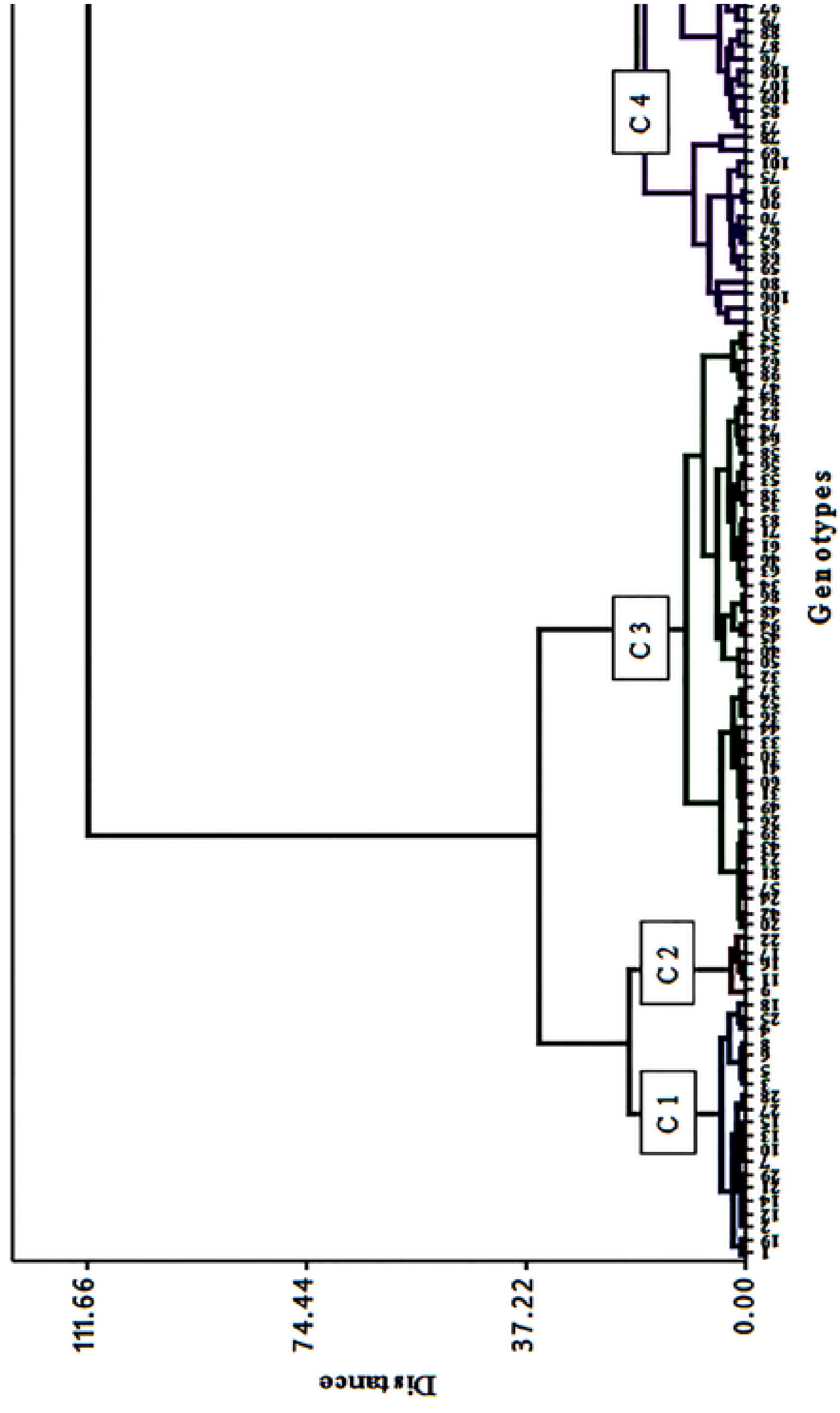

Figure 1. Dendrogram of soybean genotypes based on morphological traits using Ward linkage

Table 7. Mean values of nine qualitative traits of different clusters with number of lines in each cluster of soybean genotypes grown in three seasons at FCRDI, Mahailluppallama

Trait#	**Cluster no.**	**1**	**2**	**3**	**4**	**5**
	No.of lines	**20**	**5**	**46**	**32**	**6**
DIB	Mean	24.6	24.8	29.6	38.9	38.2
	SD	1.57	0.91	2.08	4.56	3.61
DFB	Mean	28.6	28.4	32.1	42.6	42.1
	SD	1.17	0.55	2.11	5.05	4.91
DFlB	Mean	37.1	37.2	36.7	45.9	45.3
	SD	0.71	0.45	0.89	6.27	5.14
DM	Mean	100.3	100.7	108.5	116.6	115.3
	SD	1.65	2.46	5.24	7.04	6.88
PH	Mean	32.2	36.4	20.2	35.5	37.6
	SD	5.65	8.22	3.75	10.16	11.57
NB	Mean	3.4	3.7	4.8	6.1	6.3
	SD	0.61	0.76	1.02	1.68	0.88
PPP	Mean	43.5	48.7	43.7	94.2	92.3
	SD	7.37	9.04	8.72	26.19	15.40
SPP	Mean	2.0	3.0	2.0	2.0	3.0
	SD	0.00	0.00	0.00	0.00	0.00
GYP	Mean	11.8	16.1	14.2	27.7	42.7
	SD	2.46	4.08	3.83	8.94	13.24

#DIB – Days to initial blooming, DFB – Days to 50% blooming, DFlB – Days to full bloom, DM – Days to maturity, PH – Plant height at maturity (cm), NB – Number of branches per plant, PPP – Number of pods per plant, SPP – Seeds per pod, GYP – Grain yield per plant (g)

Table 8. Genotypes grouped under each cluster at FCRDI, Mahailluppallama

Cluster no.	No. of genotypes	Soybean genotype
C1	20	PI657626 (1), PI614153 (2), PI633608 (3), PI586980 (4), PI593258 (5), PI598124 (6), PI614832 (7), PI597387 (8), PI615555 (10), PI639283 (12), PI639284 (13), PI660989 (14), PI559931 (15), PI595081 (18), PI639740 (19), PI595363 (21), PI593654 (25), PI615556 (27), PI660990 (28), PI664025 (29)
C2	05	PI578057 (9), PI633729 (11), PI560207 (16), PI614155 (17), PI665036 (22)
C3	46	PI559932 (20), PI665035 (23), PI553051 (24), PI639187 (26), PI634193 (30), PI630984 (31), PI618808 (32), PI615582 (33), PI607528 (34), PI613195 (35), PI594922 (36), PI559934 (37), PI633609 (38), PI648270 (39), PI633970 (40), PI635039 (41), PI618809 (42), PI548986 (43), PI553050 (44), PI570668 (45), PI633610 (46), PI592756 (47), PI561702 (48), PI617045 (49), PI564999 (50), PI595645 (52), PI584506 (53), PI615694 (54), PI647085 (55), PI641156 (56), PI617041 (57), PI553045 (58), PI608033 (60), PI568236 (61), PI603953 (62), PI647086 (63), PI612157 (64), PI628937 (71), PI628966 (74), PI561586 (81), PI561712 (82), PI564528 (83), PI628808 (84), PI628834 (86), PI628827 (94), PI628863 (98)
C4	32	PI564261 (51), PI629015 (59), PI628805 (65), PI628810 (66), PI628813 (67), PI628925 (68), PI628927 (69), PI628930 (70), PI628961 (73), PI644103 (75), PI628889 (76), PI628903 (77), PI628943 (78), PI628946 (79), PI628957 (80), PI628811 (85), PI628864 (87), PI628906 (88), PI628935 (90), PI628941 (91), PI628947 (92), PI628797 (93), PI628861 (97), PI628896 (99), PI628904 (100), PI628907 (102), PI628934 (105), PI628942 (106), PI628959 (107), Pb 01 (108), PM 13 (109), MISB 01 (110)
C5	06	PI628939 (72), PI628919 (89), PI628832 (95), PI628833 (96), PI628929 (103), PI628933 (104)

Conclusion

This study has revealed that the considerable phenotypic diversity of the morphological characteristics and yield parameters exists in the exotic soybean genotypes in Sri Lanka. Principal component analysis and cluster analysis showed a similar pattern for 107 soybean genotypes. Principal component analysis revealed that two components contributed over 65% of total variation among genotypes. This clustering pattern can be used for the selection of parents with more genetic distance to increase the genetic gain. Based on distance levels, that the hybridization between the pairs of genotypes that had maximum distance levels may produce good offspring with desirable characteristics.

The genotypes with high yielding and other traits with significant positive correlation with grain yield can be used to select genotypes for further evaluation and finally to be tested with trials at farmer fields.

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