

Assesment of divergence among soybean [*Glycine max* (L.) Merrill] genotypes based on phenological and physiological traits.

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ARTICLE INFO	ABSTRACT
<p>Received : 07 August 2021 Revised : 15 November 2021 Accepted : 28 November 2021</p> <p>Available online: 11 February 2022</p> <p>Key Words: D²-statistic Randomized complete block design PCA Variability</p>	<p>A study was conducted to understand genetic divergence in Randomized complete block design accommodating 30 soybean [<i>Glycine max</i> (L.) Merrill] genotypes randomly in three replications. These genotypes were evaluated for twenty-seven traits: five phenological, nine agro-morphological, eight physiological traits (from field-trial) and five physiological traits (from laboratory experiment) recorded and subjected to PCA (Principal Component Analysis) and cluster analysis. Among all the studied cultivars, significant diversity, as well as analysis of dispersion, was recorded for different agro-morphological characters. D²-statistic (Tocher method) framed (generalized distance-based) nine clusters: largest with eight and five were oligo-genotypic. Harvest index>seed yield per plant>germination relative index>seedling dry weight contributed maximum towards total divergence. From the most divergent clusters, 21 crosses involving cluster v genotypes (PS-1347, RKS-18, PS-1092, NRC-142, VLS-94, NRC-136, and Shalimar Soybean-1) with monogenotypic cluster VII (AMS-2014), VIII (RSC-11-15) and III (RSC-10-71) suggested for future hybridization. Out of eighteen, only eight principal components revealed more than 1.00 eigen value and exhibited about 85.03% variability among the traits studied. The highest variability (25.41%) by PC1 followed by PC2 (15.60%), PC3 (12.35%), PC4 (10.13%), PC5 (7.20%), PC6 (5.43%), PC7 (4.80%) and PC8 (4.11%) for characters under study.</p>

Introduction

Soybean is the globally oldest cultured plant. Historical shreds of evidence indicate its use for over 5000 yrs by human. It dates back to 1000 AD when soybean was introduced from China to India. Soybean development programme of India was initiated in the 1960s and the expansion was exceptionally rapid between 1972 and 1984. Now, it has centers all across the country. This crop has a fairly wide range of adaptation involving a wide array of climatic, soil and growth conditions and is known for its highly valued protein and oil owing

to its use in food, feed and industrial applications (Kumar *et al.*, 2015). At present, soybean has acquired global importance, first ranked oilseed contributing 25% and 40% share in global and national level, respectively in oilseed production. Brazil, U.S.A and Argentina contribute 80% of the world's soybean production. India is the fourth largest country in the world following the United States of America, Brazil and Argentina regarding area but fifth regarding total production after China. In India, major soybean-producing states are

Madhya Pradesh, Maharashtra and Rajasthan whereas, Bihar is an emerging state for soybean cultivation. It recorded 15-20% annual growth in India. Since the early eighty's it has emerged very fast and in agriculture, edible oil economy, foreign exchange and upliftment of the social status of farmers, soybean played a vital role. According to the first advance estimate in 2019-20, India has an 11.398 million-hectare area, 13.505 million tonnes production and 1.190 tonnes per ha average yield at the national level. D²-Statistic using tocher method was extensively used by several breeders in many crops but more critically, Principal Component Analysis method for factor extraction using statistical analysis system (SAS,2011) using scree plot and rotated component matrix can help to identify and classify maximum variability into total variability and genotype grouping considering between their several trait and relationship. Genetic variability, as this provides a wider scope for selection, is the basic need for every crop improvement(Chandra *et al.*, 2018). To incorporate useful diversity in breeding programme breeders required a better understanding of evolutionary relationships among accessions, to sample germplasm in a more systematic fashion and to develop strategies to incorporate useful diversity in their breeding programs (Yadav and Pandey, 2018).

Material and Methods

The experiment was carried out during *Kharif*, 2019 at the farm of Tirhut College of Agriculture, Dholi (25.5°N, 35.4°S and 52.2m MSL) in Muzaffarpur District (North Bihar) located in the eco-geographical region I Sub-region IV of Bihar. Thirty entries (including 3 checks) were sown in Randomized Complete Block Design. Each plot consisted of three rows of 3-meter length. The row to row and plant to plant distance was 45 cm and 5 cm, respectively. Trial laid out for 27 (22 field and 5 laboratory screening) morpho-physiological traits *viz.*, germination relative index seedling length (cm), seedling dry weight (g), vigour index I, vigour index II, formation of flower tubercles (days), flower budding (days), first flowering (days), cessation of flower (days), physiological maturity (days), plant height (cm), main shoot length (cm), primary branches plant⁻¹, secondary branches plant⁻¹, no of clusters plant⁻¹, no of pods

cluster⁻¹, no of pods plant⁻¹, pod length (cm), no of seeds pod⁻¹, growing degree days (°c), specific leaf weight (g/cm²), leaf area index, 100-seed weight (g), harvest-index (%), dry matter efficiency, effective rainfall use efficiency, seed yield plant⁻¹ (g). Data for individual characters were observed replication-wise and mean data was used for statistical analyses.

Two methods of genetic divergence with D² statistic following tocher clustering and PCA were performed to assess the diversity. SAS software 2011 utilised to perform multivariate analysis for PCA.

Results and Discussion

Based on D² (Tocher) values (Table 1), the 30 genotypes were grouped into 9 clusters. Cluster I was polygenotypic with 8 genotypes followed by cluster II with 7 genotypes, cluster V with 7 genotypes, cluster IV with 3 genotypes, cluster III with 1 genotype, cluster VI with 1 genotype, cluster VII with 1 genotype, cluster VIII with 1 genotype and clusters IX with 1 genotype. In conformity to the present investigation, Tyagi and Sethi (2011) 6 clusters by evaluating 40 genotypes, Patil *et al.* (2011) 6 clusters by evaluating 36 genotypes, Pawar *et al.* (2013) 7 clusters by evaluating 42 genotypes and Adsul and Monpara (2014) 15 clusters by evaluating 100 genotypes of soybean, Mehbub *et al.* (2016) 5 clusters by evaluating 28 genotypes, Milli *et al.* (2017) 5 clusters by evaluating 27 genotypes.

Divergence analysis exhibited (Table 2, Fig 1) the maximum inter-cluster distance between clusters V and VII, followed by clusters V and VIII. Larger distance showing clusters are desirable for the breeders. The highest intra-cluster divergence was recorded for cluster V followed by IV. Similar findings have been reported by Tyagi and Sethi (2011) among total 6 clusters highest genetic divergence was observed between cluster II and IV, followed by clusters III and IV. Adsul and Monpara (2014) inter-cluster distance was highest between clusters XIII and XIV followed by clusters X and XII, XIII and XIV, III and XIV and XII and XIV, Pawar *et al.* (2013) among total 7 clusters, intra cluster distance is highest in cluster VI and lowest in cluster V whereas highest inter cluster distance was noticed between cluster III and VII and the

Cluster	No. of genotypes	Genotypes included
I	8	SL1074, JS9752(NC), JS9305, MACS1493, Pusa9712, SL688, SL955, JS-20-116
II	7	RSC1052, NRC132, NRC12, NRC137, RSC1103, NRC128, PS1572
III	1	RSC1071
IV	3	SL1028, JS335(NC), RSC11-7
V	7	PS1347, RKS18(NC), PS1092, NRC142, VLS94, NRC136, Shalimar soy1
VI	1	RSC-11-17
VII	1	AMS-2014
VIII	1	RSC-11-15
IX	1	NRCSL-1

lowest was between cluster I and II. Mehbub *et al.* (2016) highest intra cluster distance was found in
Table 1: Distribution in different cluster based on D² statistic (Tocher method)

Table 2: Mean intra and inter-cluster distances (Toucher) for soybean [*Glycine max* (L.) Merrill]

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	12.63	20.25	25.48	17.19	20.59	27.36	28.51	27.1	27.14
II		15.55	19.39	23.51	22.38	18.56	22.38	20.45	18.46
III			0	22.36	32.13	15.29	10.87	12.18	20.6
IV				15.63	28.2	26.57	24.53	23.45	28.51
V					16.65	29.92	35.33	33.75	29.06
VI						0	14.72	17.05	22.84
VII							0	13.58	26.14
VIII								0	19.49
IX									0

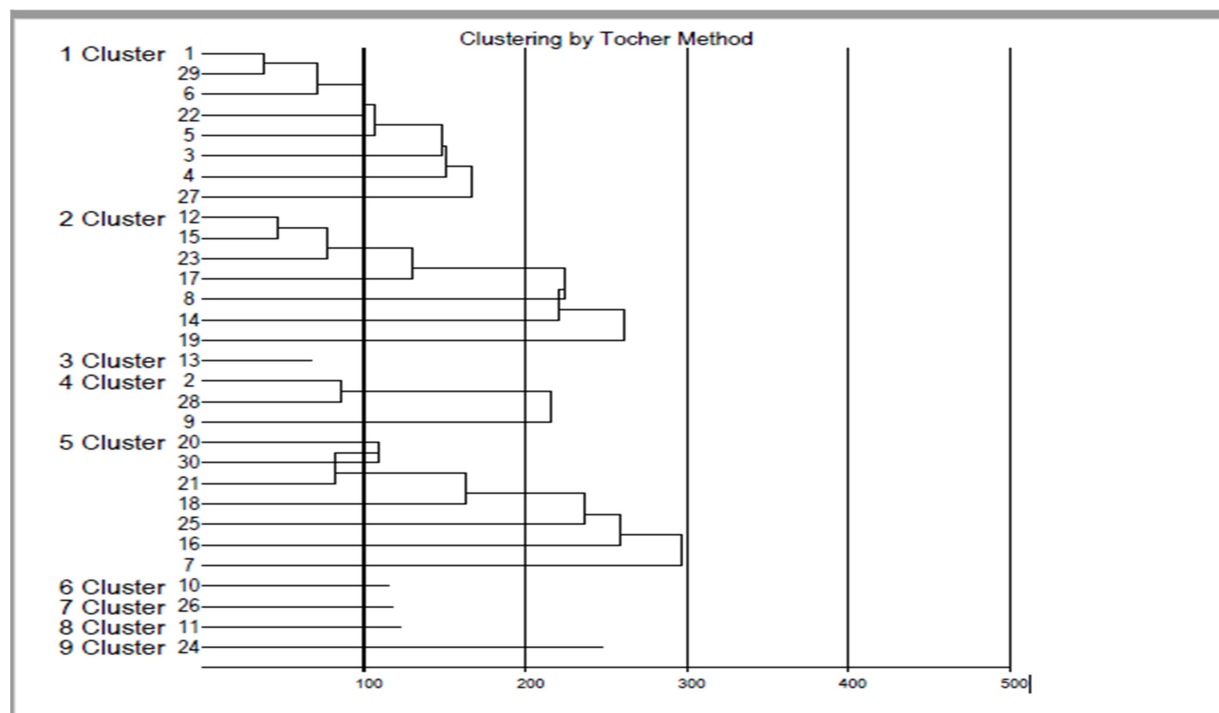


Figure 1: Clustering Pattern of 30 Genotypes of Soybean [*Glycine max* (L.) Merrill] by Toucher method.

cluster V and the lowest in cluster IV whereas highest inter cluster distance was noticed between cluster II and IV followed by II and V, III and IV and the lowest between II and III, and Milli *et al.* (2017) among total 5 clusters highest inter cluster distance was found between cluster I and IV followed by I and V. The independent character contribution percentage (Table 3) was found maximum in 100-seed weight (g), followed by grain yield per plant (g), germination relative index, seedling dry weight, vigour index I, days to cessation, seedling length, harvest- index (%), specific leaf weight, effective rainfall use efficiency, days to physiological maturity, vigour index II, days to flower budding, pod length (cm), and seed per pod. The above results revealed that the highest percentage contribution towards genetic divergence was recorded by yield and yield attributing traits. In conformity to the present investigation Dhapke *et al.* (2011) for no. of branches per plant, Shadakshari *et al* (2011) for seed per pod and seed yield per plant, Adsul and Monpara (2014) for pods per plant revealed highest percentage contribution.

The cluster mean values (Table 4) of all the twenty-seven characters were studied in the present investigation and found high for most of the yield and yield attributing traits in cluster I, cluster V, cluster VI, and cluster III. The overall conclusion of D² analysis revealed that the genotypic distribution into various clusters was at random and sufficient D² values among different clusters suggests that the genetic constitution of the promising entries in one cluster is in close proximity with the promising line in other clusters of the pair. A sufficient intra-cluster distance was also observed among the genotypes of different polygenotypic clusters. The genotypes of cluster V (PS1347, RKS18 (NC), PS1092, NRC142, VLS94, NRC136, Shalimar soy1) showing higher inter-cluster distance with cluster VII (AMS-2014) may be crossed to broaden the genetic base of soybean. Intra cluster distance has been found the highest of cluster V hence, the hybridization among the genotypes of cluster V may also result in transgressive recombinants.

PCA analyses provide superiority over D² statistics following the Tocher method as it offers an opportunity to compute the voluminous data and interpretation thereof. Loading of many traits on

particular PCs reflects their comparative superiority and value thus provide criteria to a researcher for selecting genotype for genetic divergence through such measure axis of differentiation. In this investigation, out of eighteen, only 8 principal components (PCs) revealed more than 1.00 eigen value and exhibited about 85.03% variability among the traits studied (Table 5, Figure 2). A similar result was reported by Li *et al.* (2020) in which 3 principal componants with cumulative contribution of 84.4-87.6 % was found.

Rotated component matrix had shown that the first principal component (PC1) which accounted for the highest variation (25.41%) was mostly related to traits such as effective rainfall use efficiency, grain yield per plant, seedling length and vigour index I. In PC2 (15.60%) the traits *viz.*, days to tubercles formation, days to flower budding, days to first flowering and days to the cessation of flowering, PC3 (12.35%) was consisting of mainly three traits *viz.*, no of pod per cluster, harvest index and dry matter efficiency, PC4 (10.13%) was related with seedling dry weight (g) and vigour index II, PC5 (7.20%) was related with no of primary branches and leaf area index, PC6 (5.43%) with specific leaf weight, while PC7 (4.80%) with no of pod per plant. Whereas, principal component 8 (4.11%) was more related with days to physiological maturity, no of secondary branches, no of cluster per plant and leaf area index (Table 5). Based on PCA, most of the important yield and yield attributing traits were present in PC1, PC2 and PC8. The top principal component scores (PC score) for all the traits and in 30 soybean genotypes, were estimated in these eight components and shown in table 6. To propose precise selection indices, these scores can be utilized whose intensity can be decided by variability explained by each principal component. For a particular genotype, a high PC score in a particular component indicates high values for the variables in that particular genotype. NRC-136 had the highest PC score followed by SL 955, MACS 1493, NRC 137, and NRC-128 in PC1 indicated that these genotypes possess high values of traits *viz.*, effective rainfall use efficiency, grain yield per plant, seedling length and vigour index I. The highest PC score of AMS 2014 followed by NRC 128, RSC 11-17, RSC 11-15, RSC 1071, and NRC 132 in PC2 was mainly related to days to tubercles formation, days to flower budding, days to first

Table 3: Cluster mean for 27 morpho-physiological characters in soybean [*Glycine max* (L.) Merrill

	Character	Mean of cluster									Total mean
		I	II	III	IV	V	VI	VII	VIII	IX	
1	DT	29.00	31.19	31.00	28.89	28.86	35.00	30.67	33.00	33.33	31.22
2	DFB	38.17	39.19	41.67	36.56	35.29	40.67	41.33	39.00	37.67	38.84
3	DFE	42.58	44.71	46.33	43.11	41.57	43.67	46.33	46.67	41.67	44.07
4	DC	54.00	56.43	59.00	53.78	52.67	61.67	66.33	57.67	55.00	57.39
5	DPM	112.21	107.48	113.33	107.00	102.33	98.00	108.67	112.33	112.33	108.19
6	PH	66.83	68.05	81.00	59.56	59.05	49.33	74.33	69.00	78.33	67.28
7	MSL	50.42	63.81	81.00	46.44	47.29	57.00	63.33	69.00	50.33	58.74
8	PB	8.61	7.20	6.83	7.71	6.80	7.92	6.97	7.77	4.83	7.18
9	SB	3.87	3.35	3.44	3.37	3.19	3.84	2.74	2.49	3.42	3.30
10	C/P	29.20	25.90	24.72	24.76	24.29	21.15	31.33	28.77	21.69	25.76
11	P/C	3.01	2.90	3.13	3.13	3.42	3.40	3.07	3.13	3.13	3.15
12	P/P	83.09	74.32	82.69	74.95	80.86	62.76	91.15	81.13	69.12	77.79
13	PL	3.25	3.28	3.50	3.08	3.65	2.67	2.40	3.10	4.40	3.26
14	S/P	3.00	2.55	3.44	2.55	2.98	1.77	1.89	2.66	3.77	2.73
15	GDD	18.06	18.25	18.03	18.29	18.45	18.65	18.20	18.07	18.07	18.23
16	SLW	0.01	0.01	0.03	0.02	0.01	0.01	0.02	0.02	0.02	0.02
17	LAI	8.98	6.32	4.97	6.82	5.76	5.30	5.15	6.82	5.50	6.18
18	SW	8.64	6.01	5.97	9.63	6.29	4.86	5.99	7.85	6.64	6.88
19	HI	39.57	36.33	47.93	36.77	43.47	48.67	35.72	48.60	29.27	40.70
20	DME	1.29	1.29	1.36	1.31	1.42	1.52	1.28	1.38	1.18	1.34
21	ERUE	2.15	1.92	1.64	1.53	1.89	1.24	1.90	2.15	1.46	1.76
22	GYPP	13.53	11.39	9.82	9.71	11.74	6.54	11.34	11.43	7.77	10.36
23	GER	91.71	87.10	89.33	84.67	86.19	87.67	81.33	81.33	62.67	83.56
24	SL	29.06	28.59	27.67	30.30	26.94	22.13	25.03	29.83	30.73	27.81
25	SDW	0.61	0.43	0.87	0.59	0.55	0.82	0.89	0.70	0.09	0.62
26	V1	2667.71	2497.47	2474.13	2609.03	2348.29	1955.93	2036.47	2425.40	1919.40	2325.98
27	V2	56.36	37.42	77.68	49.39	47.48	71.75	72.66	56.66	6.06	52.83

Table 4: Independent character contribution towards total divergence of soybean [Glycine max]

SN	Character	Times ranked first	Contribution
1	DT	0	0.00%
2	DFB	3	0.69%
3	DFF	0	0.00%
4	DC	11	2.53%
5	DPM	5	1.15%
6	PH	0	0.00%
7	MSL	0	0.00%
8	PB	0	0.00%
9	SB	0	0.00%
10	C/P	0	0.00%
11	P/C	0	0.00%
12	P/P	0	0.00%
13	PL	2	0.46%
14	S/P	2	0.46%
15	GDD	0	0.00%
16	SLW	6	1.38%
17	LAI	0	0.00%
18	SW	129	29.66%
19	HI	8	1.84%
20	DME	0	0.00%
21	ERUE	6	1.38%
22	GYPP	99	22.76%
23	GER	63	14.48%
24	SL	9	2.07%
25	SDW	53	12.18%
26	V1	35	8.05%
27	V2	4	0.92%

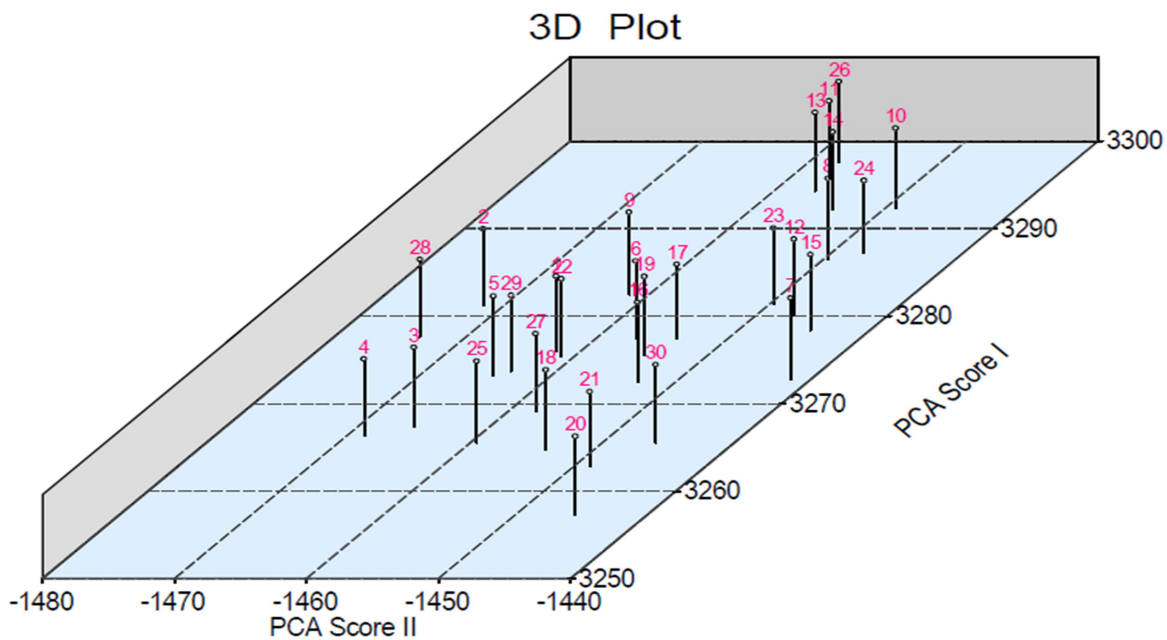


Figure 2: 3D Diagram of 30 Genotype of Soybean [*Glycine max* (L.) Merrill]
 Table 5: Principal components (PCs) for twenty- seven traits of soybean

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
Eigen value	6.86	4.21	3.33	2.74	1.94	1.47	1.29	1.11
Variability (%)	25.41	15.60	12.35	10.13	7.20	5.43	4.80	4.11
Cumulative %	25.41	41.01	53.36	63.49	70.69	76.12	80.91	85.02
Traits	Eigen vectors							
	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
Days to tubercle formation	-0.2661	0.6378	0.2316	-0.3423	-0.2589	-0.1266	-0.3271	0.0905
Days to flower budding	0.0446	0.8842	-0.0541	-0.0046	-0.1481	-0.1038	0.1356	0.2524
Days to first flowering	0.1129	0.8962	-0.0959	-0.0148	-0.0879	0.1722	0.0498	-0.0106
Days to cessation	-0.0053	0.8783	0.0906	-0.0133	0.0473	0.1660	-0.0099	-0.1123
Days to physiological maturity	0.2436	0.1062	-0.1451	-0.0577	-0.0115	0.0671	-0.0672	0.9075
Plant height (cm)	0.3529	0.1329	-0.3680	0.2705	-0.6443	0.0723	0.1901	0.3522
Main shoot length (cm)	0.2138	0.4967	-0.1777	0.2097	-0.7060	-0.0122	-0.0192	0.0621
No. of Primary branches	0.3221	0.0992	0.1938	0.2205	0.6326	-0.0930	0.0889	0.4501
No. of Secondary branches	0.1096	-0.0383	0.1690	-0.0500	0.1265	-0.4173	0.1042	0.6741
No of Cluster per plant	0.4755	0.3682	-0.0176	-0.1320	0.2244	-0.1687	0.2415	0.5237
No of Pod per cluster	0.0220	-0.1781	0.6186	0.0586	0.2071	-0.1515	0.4090	-0.1096
No of Pod per plant	0.4839	0.0955	0.1724	0.0227	0.2176	-0.1321	0.5481	0.2692
Pod length (cm)	-0.0970	-0.5031	0.1026	-0.4294	-0.5061	0.2319	0.1372	-0.1260
No of Seed per pod	0.0664	-0.4523	0.0643	-0.4017	0.0089	0.4023	0.0269	0.4976
Growing degree days(⁰ c)	-0.2647	-0.0981	0.1613	0.0581	0.0240	-0.0628	0.0664	-0.8983
Specific leaf weight(g/cm ²)	-0.0982	0.1227	0.0232	0.1000	-0.0563	0.9214	0.0234	0.0194
Leaf area index	0.2198	-0.1580	-0.1158	0.1071	0.5587	-0.1470	0.0559	0.5746
100-Seed weight(g)	0.2684	-0.3080	-0.1540	0.1322	0.4944	0.2739	-0.0030	0.4847
Harvest index	0.0828	0.0478	0.9526	0.0813	0.0563	0.0569	-0.0567	0.0209
Dry matter efficiency	-0.1142	-0.0370	0.7815	0.1133	0.0600	-0.0100	0.0015	-0.5594
Effective rainfall use efficiency(kg/ha)	0.8629	0.0836	0.2453	0.0795	0.0119	-0.0999	0.0914	0.2140
Grain yield per plant(g)	0.8916	-0.0073	0.1834	0.0957	0.0699	-0.0820	0.1083	0.1881
Germination relative index	0.3527	-0.0987	0.0902	0.2406	0.2242	-0.1166	-0.7138	0.1414
Seedling length(cm)	0.8494	0.0262	-0.2768	0.0061	-0.1197	0.0655	-0.0722	0.1746
Seedling dry weight(g)	0.0550	-0.0121	0.0828	0.9715	-0.0202	0.0594	0.0204	-0.0825
Vigour index I	0.8671	-0.0239	-0.2042	0.1153	-0.0081	0.0045	-0.3109	0.1801
Vigour index II	0.1096	-0.0532	0.0810	0.9629	-0.0151	0.0409	-0.1047	-0.0270

flowering and days to cessation which are mainly yield attributing traits. The highest PC score was obtained by NRC-136 followed by PS-1092, Shalimar soy 1, RSC 11-17 and RSC 1028 in PC3 for characters namely no of pod per cluster, harvest index and dry matter efficiency. PC scores in PC4 were recorded the highest value for characters viz., seedling dry weight and vigour index II by the genotypes NRC 142, JS 20-116, AMS 2014, RSC 1071, SL 688, NRC 137 and JS 97-52. PC scores in PC5 were recorded the highest value for characters viz., no of primary branches and leaf area index by the genotypes Pusa 9712, SL 955, SL 1028, SL 688 and RSC 1103.

PC scores in PC6 were recorded the highest value for characters viz., specific leaf weight by the genotypes RSC 1071, PS 1572, Pusa 9712, NRCSL 1, VLS-94, NRC-128 and RSC 11-15. PC scores in PC7 were recorded the highest value for characters viz., no of pods per plant by the genotypes VLS-94, Shalimar Soy 1, NRC 12, NRC-136, AMS-2014, NRCSL 1 and SL-688. However, SL 1074, SL 688, Pusa 9712, RSC 1071, and PS 1092 had the highest PC scores in PC8 for Days to physiological maturity, no of secondary branches, cluster per plant and leaf area index. Genotypes were categorized in table 6, based on top PC scores.

Table 6: Scoring of soybean genotypes in eight principal components

Genotypes	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
SL 1074	-1.0165	-0.1880	0.2491	0.2720	0.6430	-0.4156	-0.2631	1.6818
SL 1028	-0.2779	-0.0701	-1.3125	0.2121	1.5167	0.0003	-0.0241	0.6918
SL 955	2.0295	-0.0299	0.1256	-0.6855	1.5761	-0.1709	-0.0383	0.9771
SL 688	-0.5252	-1.2065	-0.0477	1.1265	1.1750	-0.6176	1.0367	1.6628
Pusa 9712	-0.2577	-0.2231	0.0382	-1.1184	1.7326	1.3082	0.1873	1.1986
JS 9305	-0.4307	0.4301	0.3569	0.7799	0.5665	-0.9888	0.1384	0.9597
Shalimar soy-1	-0.5386	-0.1519	1.6398	-1.6697	0.3798	-0.6765	1.7271	-0.9756
RSC 1103	-1.4011	0.6380	0.4291	-0.6933	1.0267	0.0879	-1.5027	-1.6552
RSC 11-7	-0.6358	-0.1413	0.2214	0.3978	0.4754	0.9444	0.5336	-1.8975
RSC 11-17	-1.5785	1.5325	1.6131	0.9997	0.2313	-1.2243	-1.3299	-0.7703
RSC 11-15	0.1194	1.2644	0.8263	0.3095	-0.3156	1.0033	-0.0106	0.3813
RSC 1052	-0.5068	0.6820	-0.6745	-1.2075	-0.4069	-1.0325	0.3223	0.6122
RSC 1071	-0.4851	1.0761	1.2838	1.2152	-1.7708	2.5826	-0.0302	1.1952
NRC-128	1.0813	1.5515	-0.1055	-0.3493	-0.3447	1.0380	-0.3003	0.0851
NRC-132	0.1173	1.0335	-0.9533	-1.1904	0.5436	-1.6171	-0.8503	0.1501
NRC-136	2.5750	0.0436	1.9839	0.2282	0.4257	-0.7772	1.2502	-1.1396
NRC-137	1.6481	0.1016	-0.1948	1.0500	-1.5055	-1.2734	0.2157	0.4126
NRC-142	-0.3064	-1.8892	-0.7151	1.8299	-0.5170	-0.3892	0.3614	-1.2501
PS-1572	0.6484	-0.2509	-0.7272	-0.4363	0.0364	1.5873	-1.8968	-0.9442
PS-1347	0.3567	-1.1244	0.5780	-0.3904	-0.9138	0.1688	-0.9157	-0.8856
PS-1092	0.0080	-1.5387	1.8551	-0.9565	-1.5747	-0.9565	-1.0929	1.1913
MACS-1493	1.9521	0.5562	-0.8199	-0.7095	-0.5305	0.3415	0.6221	-0.4560
NRC-12	-1.1920	0.6645	-1.3545	-0.1695	-1.7678	-1.2718	1.5325	-0.1963
NRCSL-1	-1.0192	-0.6597	-0.8483	-2.0932	-1.7998	1.1725	1.1339	0.7641
VLS-94	-0.7346	-1.7164	0.4631	0.4497	0.8773	1.1575	1.8447	-1.0094
AMS-2014	-0.2942	2.3342	-0.7455	1.2486	0.3710	0.1373	1.2284	-0.4065
JS-20-116	0.5063	-0.6136	-1.8889	1.6107	-0.5537	-0.2157	-0.7287	-0.4148
JS-335(NC)	0.4171	-0.6028	-1.1446	0.0494	0.8951	0.8210	-0.5476	0.3826
JS-97-52(NC)	0.0372	-0.9071	0.6979	1.0054	-0.2030	-0.0910	-1.4804	0.8840
RKS-18(NC)	-0.2963	-0.5946	-0.8289	-1.1151	-0.2686	-0.6325	-1.1229	-1.2291

Table 7: Genotypes based on overall superiority in divergence and *per se* performance for yield and morpho-physiological traits in soybean [*Glycine max* (L.) Merrill].

SN	Genotype & Pedigree	Desirable <i>per se</i> * for Traits	PCA			Tocher		GYPP <i>per se</i> (g)
			PC	% Variability	Traits	Cluster (O/P)	Traits	
1	NRC-136 (JS 97-52 X NRC-36)	GYPP, DPM, <u>P/C</u> , <u>P/P</u> , <u>HI</u> , <u>DME</u> , <u>ERUE</u>	PC1, PC3, PC7	25.41 12.35 4.80	ERUE, GYPP, SL, V1, <u>P/C</u> , <u>HI</u> , <u>DME</u> , <u>P/P</u>	V (P)	Early DT, DFB(E), DFF(E), DC(E); more P/C	21.00**
2	SL-955 (SL599 X PK1283)	GYPP, PB, SB, C/P, <u>LAI</u> , ERUE, SL, V1	PC1, PC5	25.41 7.20	ERUE, GYPP, SL, V1, <u>PB</u> , <u>LAI</u>	I (P)	More PB, SB, <u>LAI</u> , <u>ERUE</u> , GYPP, GER, V1	20.17**
3	NRC-128 (JS 97-52 X PBM-1-1-9-2-6-1)	PH, MSL	PC1, PC2, PC6	25.41 15.60 5.43	ERUE, GYPP, SL, V1, DT, DFB, DFF, DC, SLW	II (P)	High GER Medium DPM	15.46 (at par)
4	RSC-10-71 (BRAGG X JS 335)	PH, MSL, S/P, <u>SLW</u>	PC2, PC3, PC4, PC6, PC8	15.60 12.35 10.13 5.43 4.11	DT, DFB, DFF, DC, P/C, HI, DME, SDW, <u>V2</u> , SLW, DPM, SB, C/P, <u>LAI</u>	III (O)	PH & MLS (tall) more <u>SLW</u> , high <u>V2</u>	9.82
5	SL-688 (PK 416 X SL 317)	P/C, P/P, <u>LAI</u> , SL, V1	PC4, PC5, PC7, PC8	10.13 7.20 4.80 4.11	SDW, V2, PB, LAI, P/P, DPM, <u>SB</u> , C/P, <u>LAI</u>	I (P)	More PB, SB, <u>LAI</u> , <u>ERUE</u> , GYPP, GER, V1	11.70 (at par)
6	Shalimar Soybean-1 (Selection from local landrace genotype AGR/538)	DPM(E), C/P, <u>P/P</u> , <u>PL</u> , GDD, <u>DME</u>	PC3, PC7	12.35 4.80	<u>P/C</u> , HI, DME, P/P	V (P)	Early DT, DFB(E), DFF(E), DC(E); more P/C	7.19
7	RSC-11-17 (JS 97-52 X JS 93-05)	DPM(E), <u>P/C</u> , GDD, <u>DME</u>	PC2, PC3	15.60 12.35	DT, DFB, DFF, DC, P/C, <u>HI</u> , <u>DME</u>	VI (O)	PH (dwarf), SW (low), <u>high HI</u> , & <u>DME</u>	6.54
8	RSC-11-15 (JS 335 X PS 1024)	MSL	PC2, PC6	15.60 5.43	DT, DFB, <u>DFF</u> , DC, SLW	VIII (O)	<u>Late DFF</u> , High HI	11.43 (at par)
9	AMS-2014 (AMS 99-33 X H6P5)	DPM(E), PH, MSL, C/P	PC2, PC7	15.60 4.80	DT, DFB, DFF, DC, <u>P/P</u>	VII (O)	More C/P & <u>P/P</u> , high SD W	11.34 (at par)
10	Pusa -9712 (Mutant Of DS-74)	<u>C/P</u> , S/P, <u>LAI</u>	PC6, PC8	5.43 4.11	SLW, DPM, <u>SB</u> , C/P, <u>LAI</u>	I (P)	More PB, SB, <u>LAI</u> , <u>ERUE</u> , GYPP, GER, V1	10.32 (at par)
NC	JS-97-52 (NC) (PK327XL129)	GYPP, <u>SDW</u> , <u>V2</u> , PB, LAI, ERUE, GER(High)	PC4	10.13	SDW, V2	I (P)	More PB, SB, LAI, ERUE, GYPP, GER, V1	13.90 ± 3.68 CD (5%)

Tochers method resulted in nine clusters; Maximum intra-cluster distance (7genotypes in cluster V) depicting diversity within cluster, which might be attributed to their pedigree. Maximum inter-cluster distance between V-VII followed by V-VIII and V-III; suggested that seven above mentioned genotypes of cluster V were distant and diverse to oligo-genotypic clusters VII, VIII and III with unique genotypes. Genetic divergence and geographical distribution were incomparable mainly due to the free sharing of breeding lines. It was very clear that genotypes from one and different geographic regions are grouped together. Harvest- index (%) > grain yield per plant (g) > germination relative index > seedling dry weight explaining 71 % of the total divergence were most important contributor traits. Genotypes RS-11-17, SL-1074, JS-97-52, JS 93-05, MACS-1493, Pusa-97-12, SL-688, SL-955 and JS-20-116 and AMS-2014 were found desirable for above mentioned traits. Eight Principal Components explaining 85.02 per cent cumulative (Spatial distance-based) variability was obtained in Principal component analysis (PCA). Yield (GYPP) related best genotype was NRC-136 (In PC1, PC3 and PC7) followed by SL-955 (PC1 and PC5); NRC-128 (PC1, PC2 and PC6). For phenol-agro-morpho-physiological traits best source was RSC-10-71(PC2, PC3, PC4, PC6 and PC8) along with SL-688 (PC4, PC5, PC7 and PC8); Shalimar Soybean-1 (PC3, PC7); RSC-11-17 (PC2 and PC3); RSC-11-15 (PC2 and PC6), and AMS-2014 (PC2, PC7). NRC-136, Shalimar Soybean-1(common in PCA and Cluster V: Tocher) RSC-10-71(common in

PCA and Cluster III: Tocher), RSC-11-15(common in PCA and Cluster VIII: Tocher) and AMS-2014 (common in PCA and Cluster VII: Tocher) along with SL-955 (PC1 and PC5), NRC-128 (PC1, PC2 and PC6), Pusa -9712 (PC5, PC6 and PC8) may prove their merit as diverse parents for pheno-agro-morpho-physiological traits (table 7). Their pedigree: NRC-136 (JS-97-52 X NRC-36) and Shalimar soybean-1 (selection from Local Landrace genotype AGR/538)]; RSC-1071(Bragg X JS-335); RSC-11-15(JS-335 X PS-1074); AMS-2014 (AMS-99-33X H6P5); SL-955(SL-599X PK-1283) ; NRC-128 (JS-97-52 X PBM-1-1-9-2-6-1) and Pusa-9712 (Mutant of DS-4) is quite diverse as they involved Local Landrace genotype (AGR/538) / EC: Bragg /Strain: H6P5/ Line: PBM-1-1-9-2-6-1 as parent as well as mutant derivative (table 7).

Conclusion

Crosses may be attempted in future between such diverse parents could through useful transgressive segregants for yield and component traits related to earliness in flowering and maturity, seedling growth and vigour, effective rainfall use efficiency, germination, branching, pod, leaf parameters toward redesigning, for various purposes (for yield, earliness, effective rainfall use efficiency, germination, growth and vigour) the soybean plant types.

Conflict of interest

The authors declare that they have no conflict of interest.

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