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CHARACTER ASSOCIATIONS AND PRINCIPAL COMPONENT ANALYSIS FOR SEED YIELD AND COMPONENT TRAITS IN SOYBEAN (*GLYCINE MAX* L. MERRILL)

Jayaluxmi Devi Khumukcham[1]*, K. Tandekar[1] and S. K. Nag[1]
Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya,
Raipur, Chhattisgarh-492012, India
*Corresponding author E-mail: jayakhumd@gmail.com
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ABSTRACT

Soybean [*Glycine max* (L.) Merrill], a self-pollinating legume being grown globally as a rich source of protein and oil. There are various contributing elements that affect the seed yield. So, in order to improve the efficacy of the selection standard, a field experiment was conducted to ascertain the relationship between the seed and its components. Based on principal component analysis (PCA), the first five PC1 (eigenvalue = 4.32), PC2 (eigenvalue = 2.36), PC3 (eigenvalue = 1.52), PC4 (eigenvalue = 1.22), and PC5(eigenvalue = 1.16) attributed for the majority of the variability associated with yield and its component traits. The five principal component PCI through PCV with eigenvalues greater than one contributed 75% of total variance among 50 genotypes. Seed yield per plant was found to be highly significant and positive correlation with number of seeds per plant, biological yield, number of pods per plant, days to maturity, and harvest index. Path analysis showed that pod bearing length, harvest index, biological yield and number of seeds per plant had high positive direct effect on seed yield. Traits *viz*., days to 50% flowering, days to maturity, plant height, number of pods per plant and number of seeds per pod showed negative direct effect on yield per plant. These comprehensive studies shed light into the complex relationships among soybean traits, emphasizing that genotype selection based on multi-trait index can effectively steer future breeding and cultivation strategies.

Keywords : Soybean, Correlation, Path analysis, Seed yield, PCA.

Introduction

Soybean crop is regarded as the most prominent edible oilseed crop worldwide. In India, soybean is still in the top among the oilseed crop, succeeded by rapeseed and mustard, groundnut and sunflower. In India, soybean production is estimated to reach 12.6 million tonnes, with a cultivated area of 13.5 million hectare (USDA, India Ministry of Agriculture). It is being cultivated as one of the key oilseed crop during the *Kharif* season in Madhya Pradesh, Rajasthan, Andhra Pradesh, Karnataka and Chhattisgarh. It contain high proteins (38-42%) and edible oil (18-22%) rich in major essential amino acid (Kumar and Meena, 2013). Soybean meal is a key protein source in livestock feed. As a leading legume crop, it provides roughly two-third of the global protein concentrates used in animal nutrition and accounts for 25% of the world's edible oil production. Yield improvement is one of the prime objectives of any research program. Since, a quantitative trait is affected by several genetic and environmental factors, it is usually advised to determine how the yield component is related to highly heritable characters, which explains indirect selection. Hence, the current work was undertaken in order to gain a deeper knowledge of the cause-and effect relationships through correlation, and path analysis between various yield components. Path analysis study was obtained by estimating the simple correlation coefficients. If yield and its relative traits showed correlation among them which is due to their direct effect, it may infer an association among them, and such trait can be used for selection to increase yield. The breeder has to opt for the trait indirectly in case if the correlation of the character is mainly due to the indirect effect through another trait. Additionally, we used PCA, an exploratory technique that reveals the patterns of co-variation among traits across individuals. It serves as a valuable tool for evaluating diversity in plant genetic resources by analyzing growth and yield characteristics (Gangadhara *et al.*, 2024). The primary objective of this study was to evaluate the agronomic performance of 50 soybean germplasm accessions, with the goal of generating meaningful insights to support the genetic enhancement of soybean yield. Through the analysis of various genetic parameters and trait interrelationships, the study also aimed to pinpoint the key agronomic traits that could be used as dependable selection indicators for identifying high-yielding genotypes. This strategy is intended to enhance the effectiveness of parent selection and improvement in soybean future breeding programs.

Materials and Methods

The study was carried out at the Research cum Instructional farm, AICRP of Soybean, College of Agriculture, IGKV, Raipur, (C.G.) during *Kharif,* 2021-2022. In the current experiment fifty soybean genotypes were evaluated including five checks namely, RSC 10-46, JS 335, JS 97-52, NRC 37 and CG Soya 1 is given in (Table 1). The experiment was laid out in a Randomized Block Design with two replications. Each entry was accommodated with a spacing of 30 cm between rows and 10 cm between plants within the row. All the recommended packages of practices were followed for raising the successful crop. Observations were recorded from five randomly selected plants for fourteen characters such as days to 50% flowering (days), days to maturity (days), plant height (cm), number of primary branches per plant, number of pods per plant, pod bearing length (cm), number of seeds per pod, number of seeds per plant, hundred seed weight (g), biological yield (g), seed yield per plant (g), harvest index (%), oil content (%) and protein content (%). Correlation was calculated for all the characters. Path analysis was performed following the method of Dewey and Lu (1959). Correlation and Path coefficient analysis was carried out using OP Stat (Sheoran *et al.*, 1998). PCA was analyzed using the 'factoextra' package in R Studio (version R-4.4.1) based on the approach outlined by (Panse And Sukhatme, 1961).

Results and Discussion

Characters Association

The phenotypic and genotypic correlations of fourteen characters in fifty soybean genotypes are represented in Table 2. In general, genotypic correlation coefficients were higher than their corresponding phenotypic correlations, indicating a strong inherent association between characters that might be partially suppressed at the phenotypic level due to environmental influence. In the present study, seed yield per plant showed highly significant and positive association with number of seeds per plant (0.875,0.804) followed by biological yield (0.848,0.801), number of pods per plant (0.719,0.653), days to maturity (0.496,0.409), harvest index (0.412,0.333), days to 50% flowering (0.365,0.332), number of primary branches per plant (0.265,0.220) and protein content (0.242,0.216) at both genotypic and phenotypic level. Similar results for positive correlation of seed yield with number of pods per plant and for biological yield were recorded by Parmar *et al.* (2014), Amrita *et al.* (2014), Baraskar e*t al.* (2015), Silva *et al.* (2015), Vijayakumar *et al.* (2017) Ghiday *et al.* (2017), Bhuva *et al.* (2020), For harvest index and days to 50% flowering by Amrita *et al.* (2014), Goonde and Ayana (2021). The positive correlation of seed yield per plant with number of seeds per plant were obtained by Amogne *et al.* (2020), Geetanjali (2020), Uikey *et al.* (2021) and Tigga and Nag (2021).

The analysis indicated interconnectedness among important traits, such as number of seeds per plant had significant positive correlation with number of pods per plant (0.830, 0.797) suggesting that plants bearing more pods tend to produce a higher number of seeds. Similar findings were reported by Dixit *et al.* (2011), Kumar *et al.* (2014), and Patil *et al.* (2017). Among quality parameters, oil content showed a positive association with seed yield (0.164, 0.124) and harvest index (0.278, 0.233), suggesting that improvement in seed yield may not adversely affect oil content. Protein content also exhibited positive correlations with number of seeds per plant (0.183, 0.135) and pod-bearing length (0.079, 0.077). These findings are in agreement with the results of Mishra *et al.* (2020) and Patil *et al.* (2017), who reported similar trends in soybean.

Certain traits exhibited significant negative correlations, suggesting possible trade-offs. Hundred seed weight showed significant negative correlations with plant height (–0.433, –0.416), number of primary branches per plant (–0.304, –0.259), number of pods per plant (–0.361, –0.333), and pod-bearing length (–0.445, –0.425). This indicates that plants producing a larger number of pods or longer pod-bearing zones tend to have smaller seed size, possibly due to resource partitioning among more sink organs. Similar negative associations between seed size and number of pods were reported by Patil *et al.* (2017) and Mishra *et al.* (2020). Harvest index (HI) exhibited significant negative correlations with plant height (–0.418, –0.304), number of primary branches (–0.342, –0.151), and pod-bearing length (–0.407, –0.287). This implies that taller and more branched plants may allocate relatively less assimilate to seeds, lowering harvest efficiency.

Path coefficient analysis

The analysis showed that biological yield per plant (0.762) exerted the highest positive direct effect on seed yield per plant, followed by harvest index (0.657), number of seeds per plant (0.376), and number of pods per plant (0.326) presented in Table 3. These traits emerged as the most important components directly influencing seed yield, suggesting that genotypes with higher biological productivity and efficient translocation of assimilates towards reproductive parts tend to achieve superior yield. Similar observations were reported by Kumar *et al.* (2014), Patil *et al.* (2017), and Singh *et al.* (2019), who emphasized the significance of biological yield, pods per plant, and harvest index in soybean yield improvement.

The characters pod bearing length, biological yield, harvest index, number of seeds per plant had high positive direct effect on seed yield per plant. Similar findings were reported for the trait pod bearing length by Baraskar *et al.* (2015) and Mahbub *et al.* (2015). Result was accordance with finding of Dubey *et al.* (2015), Baraskar *et al.* (2015), Baig *et al.* (2017), Bhuva *et al* (2020), Parihar *et al.* (2020) and Ghuge *et al.* (2021) for biological yield and days to maturity. The plant height showed high negative direct effect on seed yield followed by number of pods per plant, number of seeds per pod, days to 50% flowering and days to maturity. The result was confirmed with the findings of Chavan *et al.* (2016) and Bhuva *et al.* (2020) for plant height and for number of pods per plant by Baig *et al.* (2017) and Khadka *et al.* (2020) for days to maturity and plant height by Thakur *et al.* (2015).

Considerable positive indirect effects were observed for days to 50% flowering (0.296), days to maturity (0.341), and pod bearing length (0.404) through biological yield and number of pods per plant. This indicates that moderately late flowering and maturing genotypes might utilize longer vegetative phases to accumulate photosynthates, which are subsequently partitioned into reproductive growth, resulting in higher yield potential. These results are in agreement with the findings of Dixit *et al.* (2011) and Kumari *et al.* (2018), who reported that flowering and maturity duration influence yield indirectly via yield-contributing traits. In contrast, plant height (-0.691) exhibited the highest negative direct effect on seed yield per plant, indicating that excessive vegetative growth could lead to competition among plant organs and poor resource partitioning towards pod and seed development. Similar negative effects of plant height on seed yield were also reported by Yadav *et al.* (2015), suggesting that medium-statured genotypes are ideal for yield improvement under dense planting conditions. The hundred seed weight (0.149) exhibited a low positive direct effect, signifying that seed size alone cannot ensure higher yield unless supported by higher pod and seed numbers per plant. The oil content (0.164) and protein content (0.242) exhibited moderate positive direct effects on seed yield, indicating their partial but favourable contribution towards yield. However, their indirect negative effects through other traits such as biological yield and pods per plant reflect complex physiological relationships and trade-offs between yield and quality parameters (Sahoo *et al.*, 2018). The residual effect (0.0277) was low, indicating that the traits included in the analysis explained most of the variability in seed yield per plant, confirming the reliability of the model.

Cluster analysis

The genetic divergence of 50 soybean accessions was estimated by Mahalanobis D^2 statistics as described by Rao (1952). Based on relative magnitude of D^2 estimates 50 genotypes were grouped into 6 clusters. The distribution of genotypes in different clusters is presented in Fig. 4. Among the six clusters, cluster I was the highest cluster with 33 genotypes followed by cluster II consist of 13 genotypes and the remaining clusters III, IV, V and VI consists of one genotype each. Similar results were earlier suggested by Tyagi and Sethi (2011) and Mahbub and Shirazy (2016).

The cluster mean values for 14 characters of 50 genotypes is presented in Table 4. The result revealed that cluster III and IV exhibited highest mean values for days to 50% flowering (46 days), whereas cluster III showed highest mean values for days to maturity (100 days), biological yield (48.67 g), seed yield/plant (19.34) and oil content (21.88%). Cluster IV exhibited high mean values for 100 seed weight (15.34), harvest index (43.34%) and protein content (41.06%). Cluster V exhibited lowest mean values for days to maturity (83.50 days), number of seeds/plant (67.33), biological yield (17.67g) and seed yield (7.00). Cluster VI exhibited highest mean values for plant height (76.17cm), number of primary branches/plant (5.50), number of pods/plant (106.17), pod bearing length (70.33cm), number of seeds/pod (2.55) and number of seeds/plant (195.33). From the present study on cluster mean we can conclude that cluster I, II and V had shown intermediate mean values for the maximum characters.

Principal component analysis

A total of 14 principal components were obtained for seed yield and its component traits with eigen-values (Table 5). The first five PCs were found to have eigen value larger than one, indicating that only these PCs may be utilized for further analysis of the data. These components are often utilized by plant breeders for selection purposes. Plant breeder generally select these components for the purpose of plant selection (Gangadhara *et al.*, 2024). It was observed that the combined effect of all twelve principal components had contributed to about 100 percent of the total variation, wherein the individual contributions of PC1, PC2, PC3, PC4, PC5, PC6, PC7, PC8, PC9, PC10, PC11, PC12, PC13 and PC14 are recorded as 31%, 17%, 11%, 9%, 8%, 7%, 5%, 4%, 3%, 2%, 2%, 1%, 1%, 0% (Table 5). Furthermore, the first five PCs (PC1, PC2, PC3, PC4 and PC5) had exhibited more than 55 percent contribution towards the total variability compared to PC6 to PC14. A scree plot graphically shows the variance contribution of each principal component (Vennila *et al.*, 2024) . The scree plot aids in determining the number of principal components to retain (Lever *et al.*, 2017). The graph presents variance contributions in ascending order (Fig. 1). According to this, PC1 is more closely related to PC2 and PC3 (31 %, 17 %, and 11 % respectively). From PC4 to PC10, this relationship begins to decline.

Variables contribution

In PCA, traits such as biological yield, number of seeds per plant and seed yield per plant highly contributed to 12.5% of genetic variability. However, oil content and protein content indicated towards the opposite sides of the biplot origin and contributed to 2.5% towards the genetic divergence (Fig. 2).

The relationship between genotypes and quantitative traits were presented on a biplot (Fig. 3). The genotypes displayed on the left top quadrant were described by high number of seeds per pod and high height of primary branch. The genotypes falling in the bottom of left quadrant had the highest seed yield, number of seeds per plant, early days to 50% flowering and maturity.

Conclusion

The results highlight that yield is a complex trait influenced by multiple interacting components. The dominance of biological yield, number of pods per plant, number of seeds per plant, and harvest index as major contributors signifies their direct role in enhancing seed yield. These traits collectively represent the plant's photosynthetic efficiency, assimilate partitioning, and reproductive potential all vital parameters for yield enhancement.

The negative association of plant height with yield suggests that tall plants tend to invest more in vegetative structures rather than reproductive development, leading to lower yield efficiency. Hence, selection of genotypes with moderate plant height, higher pod-bearing capacity, and superior harvest index should be emphasized for yield improvement in soybean. Moreover, the positive but low contribution of seed weight indicates that improvement in soybean yield could be more effectively achieved through an increase in the number of pods and seeds rather than by enhancing individual seed size. Thus, the present study clearly indicates that biological yield, number of seeds per plant, harvest index, and number of pods per plant are the most crucial traits for direct selection in breeding programs aimed at developing high-yielding soybean cultivars.

Table 1 : List of soybean genotypes under study.

Sl.no	Genotypes	Sl.no	Genotypes	Sl.no	Genotypes	Sl.no	Genotypes
1	IC 15089	14	EC 547464	27	PUNJAB	40	EC 456566
2	JS20-38	15	EC 100778	28	EC 457475	41	AGS 205
3	EC 390977	16	JS 20-72	29	EC 274711	42	EC 343310
4	EC 241756	17	RAUS-5	30	EC 546882	43	MACS 1460
5	TGX854-429	18	PALAM SOYA	31	EC 538807	44	EC 325113
6	AGS142	19	PK 308	32	TGX 825-2D	45	Kaeri 651-6
7	BR15	20	DURGA	33	JSM-288	46	JS 335
8	NRC2	21	PUSA 37	34	JS(SH)2001-64	47	CG-Soya-1
9	EC 457464	22	MAUS 71	35	JS 20-73	48	RSC 10-46
10	TGX311-101F	23	TGX860-11D	36	PK 1284	49	JS 97-52
11	B 160-3	24	TGX855-44G	37	PK566	50	NRC 37
12	NRC 86	25	MAUS 1	38	PS 1029		
13	TGX780-5A	26	MACS 1034	39	PI 283327		

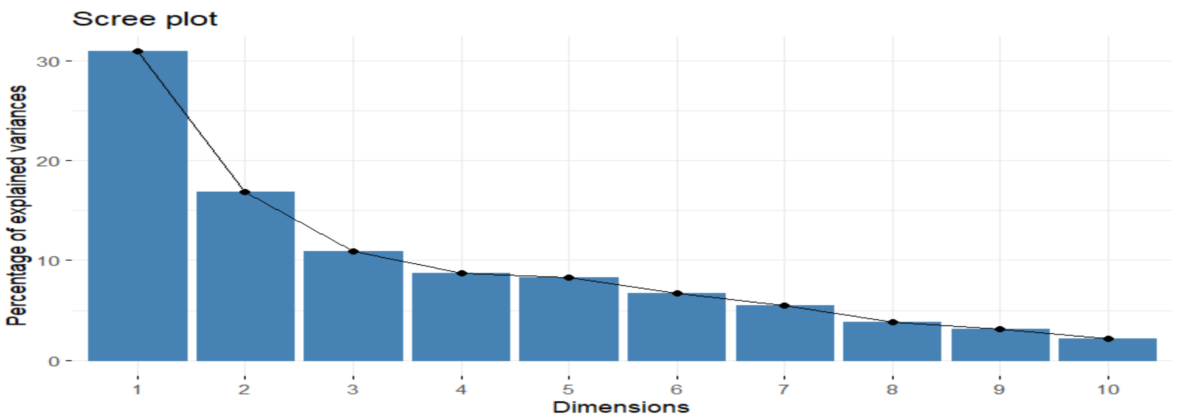

Fig. 1 : Scree plot of percentage of explained variances in ten PC

Table 4 : Cluster mean values for fourteen quantitative characters of 50 soybean genotypes.

Clusters	**I**	**II**	**III**	**IV**	**V**	**VI**
DF	44.20	42.81	46.00	46.00	45.50	45.50
DM	96.82	96.31	100.00	86.50	83.50	88.00
PH	54.12	50.51	62.34	33.83	53.84	76.17
NPB	4.25	4.37	4.84	3.00	4.00	5.50
NPP	72.94	67.01	81.67	29.34	58.00	106.17
NBL	46.07	42.26	54.50	25.34	45.84	70.33
NSP	2.45	2.40	2.45	2.39	2.52	2.55
NSPL	153.48	126.45	188.33	71.00	67.33	195.33
SW	12.80	11.80	9.61	15.34	9.92	5.83
BY	43.34	33.45	48.67	21.17	17.67	48.17
SYP	17.86	14.27	19.34	9.33	7.00	15.67
HI	43.20	42.79	39.86	43.34	39.31	35.02
OC	18.91	19.91	21.88	17.34	19.19	17.88
PC	39.35	35.80	41.04	41.06	39.25	40.68

DF: Days to 50% flowering, **DM:** Days to maturity, **PH:** Plant height**, NPB:** Number of primary branches/plants, **NPP:** Number of pods/plant, **PBL:** Pod bearing length **NSP:** Number of seeds/pod, **NSPL:** Number of seeds/plant, **SW:** 100 Seed weight, **BY:** Biological yield, **SYP:** Seed yield/plant, **HI:** Harvest index, **OC:** Oil content, **PC:** Protein content.

Table 5 : Eigen value, percentage of variance and cumulative proportion of the principal component

Principal component	**Eigen value**	**Percentage of Variance**	**Cumulative of percentage Variance**
PC1	4.32	31%	31%
PC2	2.36	17%	48%
PC3	1.52	11%	59%
PC4	1.22	9%	67%
PC5	1.16	8%	76%
PC6	0.94	7%	82%
PC7	0.77	5%	88%
PC8	0.54	4%	92%
PC9	0.44	3%	95%
PC10	0.30	2%	97%
PC11	0.23	2%	99%
PC12	0.11	1%	99%
PC13	0.07	1%	100%
PC14	0.01	0%	100%

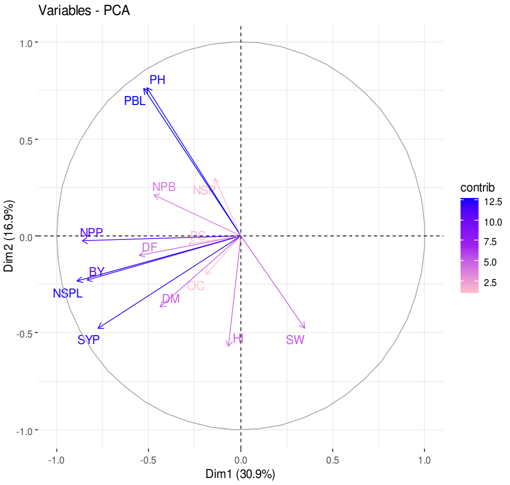

Fig. 2 : Contribution of different traits towards genetic divergence

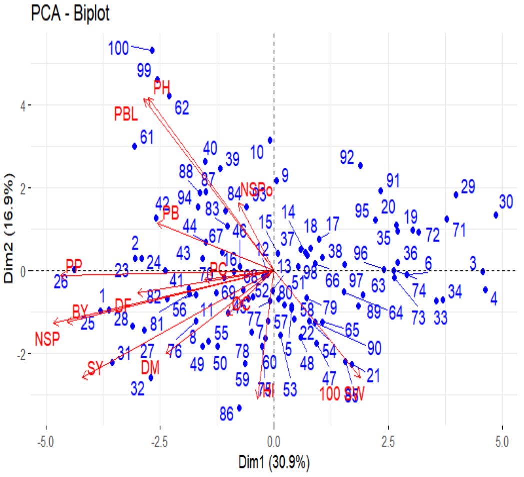

Fig. 3 : Biplot of 14 traits of 50 genotypes of soybean

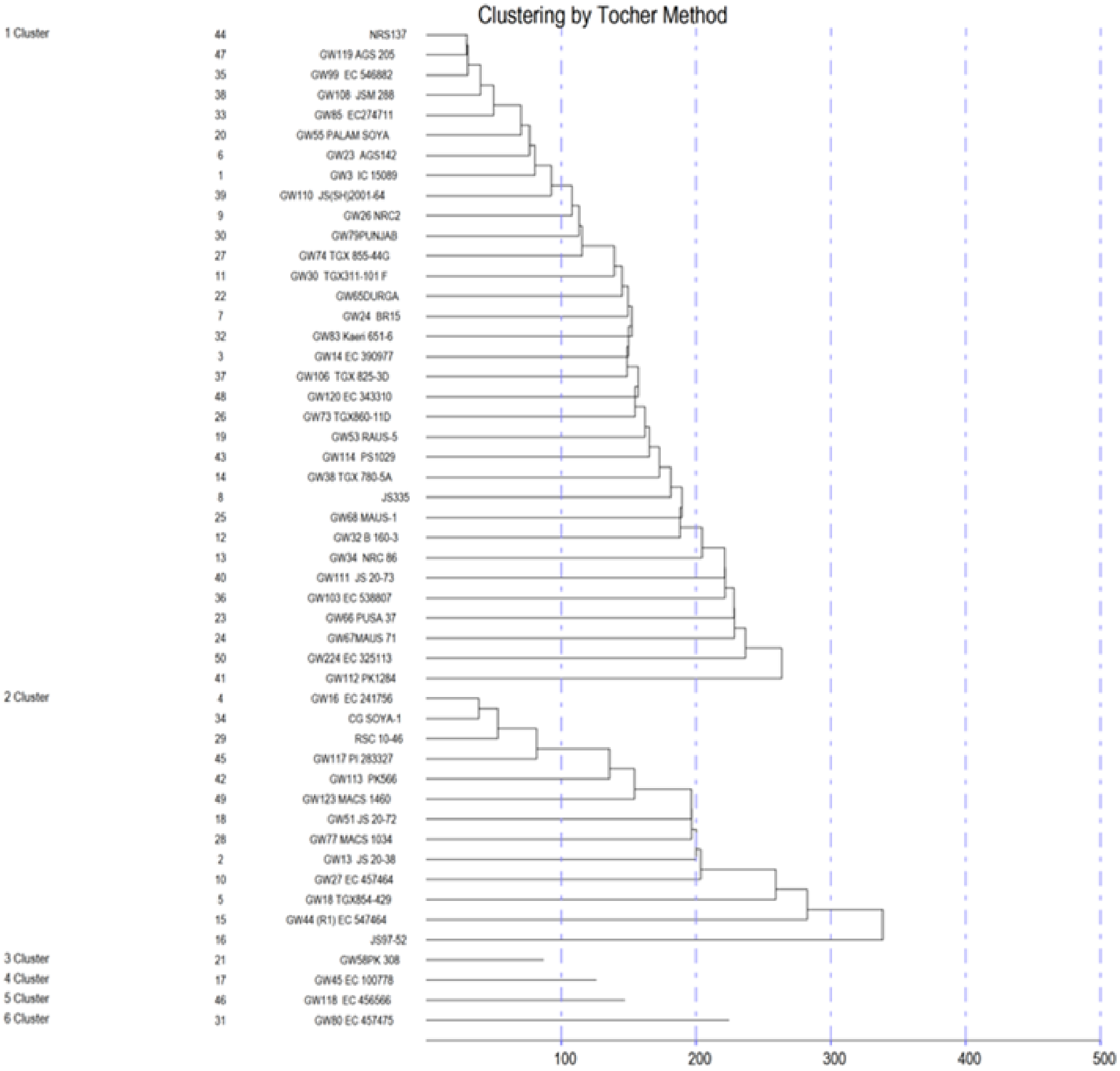

Fig. 4 : Dendrogram representing clustering based on phenotypic data

Table 2: Genotypic and Phenotypic correlation coefficient for seed yield and its components in germplasm of soybean.

S. No	Characters		DF	DM	PH (cm)	NPB	NPP	PBL	NSP	NSPL	SW	BY	HI (%)	OC %)	PC (%)	SYP
1	**DF**	**G**	**1**													
		P	**1**													
2	**DM**	**G**	0.289**	**1**												
		P	0.275**	**1**												
3	**PH (cm)**	**G**	0.232*	0.104	**1**											
		P	0.220*	0.094	**1**											
4	**NPB**	**G**	0.142	0.159	0.302**	**1**										
		P	0.103	0.116	0.230*	**1**										
5	**NPP**	**G**	0.346**	0.285**	0.422**	0.516**	**1**									
		P	0.314**	0.258**	0.370**	0.445**	**1**									
6	**PBL(cm)**	**G**	0.246*	0.103	0.999**	0.304**	0.434**	**1**								
		P	0.235*	0.102	0.988**	0.228*	0.373**	**1**								
7	**NSP**	**G**	-0.003	-0.298**	0.230*	0.196	0.122	0.292**	**1**							
		P	-0.013	-0.255*	0.205*	0.196	0.127	0.250*	**1**							
8	**NSPL**	**G**	0.491**	0.358**	0.278**	0.278**	0.830**	0.298**	0.083	**1**						
		P	0.460**	0.341**	0.250*	0.247*	0.797**	0.267**	0.069	**1**						
9	**SW**	**G**	-0.183	0.200*	-0.433**	-0.304**	-0.361**	-0.445**	0.023	-0.258**	**1**					
		P	-0.167	0.188	-0.416**	-0.259**	-0.333**	-0.425**	0.025	-0.247*	**1**					
10	**BY (g)**	**G**	0.389**	0.448**	0.227*	0.477**	0.731**	0.242*	0.058	0.820**	-0.034	**1**				
		P	0.356**	0.423**	0.186	0.392**	0.679**	0.204*	0.069	0.796**	-0.039	**1**				
11	**HI (%)**	**G**	0.175	0.14	-0.418**	-0.342**	0.153	-0.407**	0.066	0.241*	0.072	-0.082	**1**			
		P	0.138	0.1	-0.304**	-0.151	0.146	-0.287**	0.074	0.199*	0.069	-0.11	**1**			
12	**OC (%)**	**G**	0.236*	0.264**	0	0.142	0.158	-0.021	-0.283**	0.122	-0.277**	0.024	0.278**	**1**		
		P	0.220*	0.250*	-0.001	0.108	0.143	-0.025	-0.233*	0.109	-0.268**	0.009	0.233*	**1**		
13	**PC (%)**	**G**	0.318**	-0.015	0.07	-0.063	0.12	0.079	0.183	0.246**	-0.033	0.305**	-0.042	0.125	**1**	
		P	0.298**	-0.011	0.064	-0.043	0.11	0.077	0.135	0.239*	-0.036	0.286**	-0.031	-0.12	**1**	
14	**SYP**	**G**	**0.365****	**0.469****	**0.017**	**0.263****	**0.719****	**0.025**	**0.082**	**0.875****	**0.003**	**0.848****	**0.412****	**0.164**	**0.242***	**1**
		P	**0.332****	**0.409****	**0.04**	**0.220***	**0.653****	**0.062**	**0.076**	**0.804****	**-0.001**	**0.801****	**0.333****	**0.124**	**0.216***	**1**

***Significant at 5%, ** Significant at 1% levels respectively**

DF: Days to 50% flowering (days), **DM**: Days to maturity (days), **PH**: Plant height (cm), **NPB**: Number of primary branches per plant, **NPP**: Number of pods per plant, **PBL**: Pod bearing length (cm), **NSP**: Number of seeds per pod, **NSPL**: Number of seeds per plant, **SW:** 100 Seed weight, **BY:** Biological yield (g), **HI:** Harvest index (%), **OC:** Oil content (%), **PC:** Protein content (%), **SYP:** Seed yield per plant

Table 3 : Genotypic path coefficient analysis for fourteen yield component traits in germplasm accessions of soybean.

	Days to 50% Flowe-ring	**Days to Maturity**	**Plant height (cm)**	**Number of primary branches /plant**	**Number of Pods/ plant**	**Pod Bearing Length (cm)**	**No. of Seeds/ pod**	**Number of Seeds/ plant**	**Hundred Seed Weight (g)**	**Biological yield (g)**	**Harvest index (%)**	**Oil (%)**	**Protein (%)**	**Seed yield/ plant (g)**
Days to 50% Flowering	**-0.193**	-0.031	-0.160	0.035	-0.113	0.229	0.001	0.185	-0.027	0.296	0.115	0.005	0.025	0.365**
Days to Maturity	-0.056	**-0.107**	-0.072	0.039	-0.093	0.095	0.060	0.135	0.029	0.341	0.092	0.005	-0.001	0.469**
Plant height (cm)	-0.045	-0.011	**-0.691**	0.074	-0.137	0.929	-0.047	0.105	-0.065	0.173	-0.274	-0.000	0.005	0.017
Number of primary branches/ plant	-0.027	-0.017	-0.209	**0.246**	-0.168	0.283	-0.039	0.104	-0.045	0.363	-0.225	0.003	-0.005	0.263**
Number of Pods/ plant	-0.067	-0.031	-0.291	0.127	**-0.326**	0.404	-0.025	0.312	-0.054	0.557	0.101	0.003	0.009	0.719**
Pod Bearing Length (cm)	-0.047	-0.011	-0.689	0.075	-0.141	**0.93**	-0.059	0.112	-0.07	0.185	-0.267	-0.0004	0.006	0.025
No. of Seeds/ pod	0.001	0.032	-0.159	0.048	-0.039	0.272	**-0.203**	0.031	0.003	0.044	0.043	-0.006	0.014	0.082
Number of Seeds/plant	-0.095	-0.038	-0.192	0.068	-0.271	0.278	-0.017	**0.376**	-0.038	0.625	0.159	0.002	0.0192	0.875**
Hundred	0.035	-0.021	0.299	-0.075	0.118	-0.414	-0.005	-0.097	**0.149**	-0.026	0.048	-0.006	-0.002	0.003

Seed Weight (g)														
Biological yield (g)	-0.075	-0.048	-0.157	0.117	-0.238	0.226	-0.012	0.308	-0.005	**0.762**	-0.05	0.001	0.024	0.848**
Harvest index (%)	-0.034	-0.015	0.288	-0.084	-0.050	-0.378	-0.013	0.091	0.011	-0.062	**0.657**	0.006	-0.003	0.412**
Oil (%)	-0.045	-0.028	0.0003	0.035	-0.051	-0.019	0.057	0.046	-0.041	0.018	0.182	**0.019**	-0.009	0.164
Protein (%)	-0.061	0.002	-0.049	-0.015	-0.039	0.074	-0.037	0.093	-0.005	0.232	-0.028	-0.002	**0.078**	0.242*

Residual: 0.0277

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