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Journal homepage: <http://www.plantarchives.org>

DOI Url : <https://doi.org/10.51470/PLANTARCHIVES.2024.v24.no.2.052>

## AGRO-MORPHOLOGICAL CHARACTERIZATION, GENETIC VARIABILITY, ASSOCIATION AND DIVERGENCE ANALYSIS IN RECOMBINANT INBRED LINES (RIL'S) POPULATION IN SOYBEAN [*GLYCINE MAX* (L.) MERRILL]

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(Date of Receiving-19-02-2024; Date of Acceptance-26-04-2024)

### ABSTRACT

A study was conducted to access genetic variability and association analysis among 148 RIL's population excluding checks *viz.*, RILEJ9752-C1 (JS 71-05), RILEJ9752-C2(JS 335) and RILEJ9752-C3(JS 975-2) in Augmented block design in three blocks in year *Kharif* 2019-20. Analysis of variance depicted the presence of sufficient amount of genetic variability and significant for all the traits. High heritability in broad sense was observed in number of pods per plant and pod bearing length. Correlation study revealed that number of pods per plant, number of seeds per pod, number of seeds per plant, 100 seed weight, oil content and protein content were found significant and positively correlated with seed yield. So these traits were used directly in yield improvement programme. Cluster analysis distributed all genotypes into 7 clusters. Cluster II has maximum number of genotypes. Highest inter-cluster distance was observed between clusters III and IV followed by between clusters VI and III and clusters III and I. Cluster II showed the highest number of pods per plant which suggested that the genotype falling in this cluster can be selected directly and used in hybridization programme.

**Key words :** Soybean, RIL's Population, Heritability, Correlation analysis, Analysis of variance, Cluster analysis.

### Introduction

Soybean [*Glycine max* (L.) Merrill], commonly known as "Miracle crop", is a member of the Papilionaceae family. Cultivated soybean is a diploid crop with a chromosome number of  $2n = 40$ . Soybean continues to rank number one oilseed crop of India followed by rapeseed and mustard, groundnut and sunflower. As the best source of protein it truly claims the title "the meat that grows on plant". It is extremely beneficial for the human diet since it provides high-quality protein (40–42%) and oil (18–22%), unsaturated fatty acids (85%), no cholesterol and enough mineral elements (4.5%), salts and vitamins (thiamine and riboflavin) (Rackis *et al.*, 1961). Soybean oil has high amount of minerals like copper, manganese, potassium along with

85% unsaturated fatty acids of zerocholesterol content which is very sensible for human health (Antalina *et al.*, 2000). Recent research revealed that soybean proteins prevent 70% for liver cancer, 73% for colon cancer, and 68% for lung cancer cells using human cell line (Aizawa, 2013). Yield is largely influenced by the qualities that contribute to yield. The most crucial information in a breeding programme is the correlation between character and yield. Focus must be placed on traits of the crop that are strongly positively connected with its seed yield in order to choose high yielding genotypes. Knowledge of genetic diversity within a crop and correlation among the yield contributing characters is essential for the long-term success of a breeding program and maximizes the exploration of germplasm resources (Mahbub *et al.*,

2015). Hence, the current investigation was conducted to study genetic variability, association and diversity with respect to yield and yield contributing traits among the RIL's population

### Materials and Methods

The investigation was carried out in *Kharif* 2019–20 at AICRP on Soybean, Research cum Instructional Farm, Department of Genetics and Plant Breeding, IGKV, Raipur (C.G.), India. The investigation's material included 148 RIL population and three checks, RILEJ9752-C1 (JS 71-05), RILEJ9752-C2 (JS 335), and RILEJ9752-C3 (JS 975-2), all of which were performed using an augmented block design (Federer, 1956) with three blocks. 50 genotypes, excluding three checks, were planted in each block. The 148 RIL population were characterized for their morphological characters on the basis of DUS descriptors anonymous (2009). On five randomly chosen competitive plants, observations were made on twelve different quantitative characteristics, including days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of pods per plant, number of seeds per pod, length of the pod bearing period, number of seeds per plant, 100 seed weight, protein content, oil content and seed yield. The mean values of two replications were averaged, expressed as the mean of the corresponding character and taken into consideration for statistical analysis. For all characters, heritability ( $h^2$ bs) in the broad sense was computed using the method described by Hanson *et al.* (1956). Miller *et al.* (1958) equations are used in correlation coefficients analysis to calculate the link between each feature. Mahalanobis (1936) provided a group distance metric based on numerous characters and the  $D^2$  statistic. To ascertain the genetic divergence between the genotypes, Mahalanobis'  $D^2$  analysis was used to examine the data gathered on various features.

### Results and Discussion

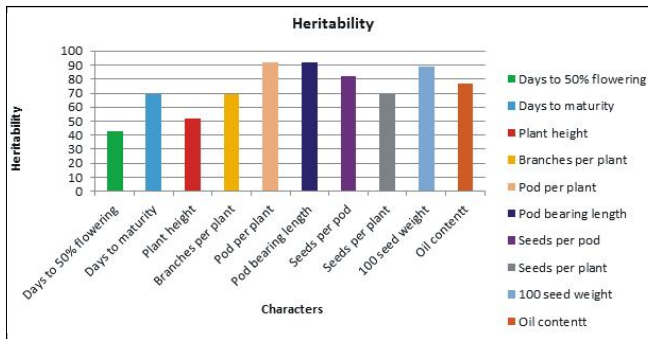
The characterization of soybean genotypes revealed that out of 150 genotypes, 25% genotypes had found green hypocotyl colour, while 75% had purple hypocotyl colour. In terms of plant growth type, 75% of plants were semi-determinate, 21.27% were determinate and 4.72% were indeterminate. Plant growth habits can be divided into three categories: spreading, erect, and semi-erect. Out of 150 genotypes, 62.16% had a semi-erect growth pattern, 28.3% had an erect growth tendency, and 9.45% had a spreading growth habit. 76.35% of pods had pubescence (hairy) genotypes, 23.64% had glabrous (hairless) type and 100% had tawny pubescence, according to hairs on the pods (pod pubescence). In terms

**Table 1 :** Analysis of variance for seed yield and its components in 148 RIL population of soybean.

Sources of Variation	DF	Mean sum of squares											
		1	2	3	4	5	6	7	8	9	10	11	12
<b>Blocks</b>	6	154.87**	465.75**	1712.77**	2.37*	2287.87**	217.38**	14.03**	9395.64**	4.56*	9.47**	20.70**	19.32**
<b>Genotypes</b>	147	37.31**	87.42**	221.99**	0.70	265.41**	32.11**	3.08	817.12**	6.03**	1.94	4.42	6.41
<b>Checks</b>	2	27.69*	2.61	73.24*	0.08	3.92	0.07	0.52	107.10*	0.34	0.24	3.58	5.37
<b>Error</b>	12	6.42	7.26	14.52	0.60	7.33	2.48	1.05	22.51	1.16	0.95	2.38	2.49

**Note:**\* and \*\* Significant and highly Significant at probability levels 0.05 and 0.01, respectively.

1. Days to 50% flowering
2. Days to maturity
3. Plant height (cm)
4. Number of primary branches per plant
5. Number of pods per plant
6. Pod bearing length (cm)
7. Number of seeds per pod
8. Number of seeds per plant
9. 100 seed weight (g)
10. Oil content (%)
11. Protein content (%)
12. Seed yield per plant (g)



**Fig. 1 :** Heritability and mean data for quantitative characters of 148 RIL population of soybean.

High heritability observed for number of pods per plant (92.00%) and pod bearing length (92.00%) followed by 100 seed weight (89.00%) and number of seeds per pod (82.00%) and oil content (77.00%), whereas moderate heritability was observed for days to maturity (69.00%), number of primary branches per plant (69.00%), number of seed per plant (69.00%) and plant height (52.00%). Similar result was observed by Kumar *et al.* (2012). Result was similar with Reddy *et al.* (2022) for plant height and days to maturity.

Correlation coefficients indicated the measure of

**Table 2 :** Heritability and mean data for quantitative characters of 148 RIL population of soybean.

S. no.	Characters	Mean	Range		Broad sense heritability ( $h^2$ ) (%)
			Min.	Max.	
1	Days to 50% flowering	47.86	38.00	60	43
2	Days to maturity	104.51	95	121	69
3	Plant height (cm)	63.03	23.66	98.66	52
4	No. of primary branches per plant	3.18	2.00	7.00	69
5	Number of pods per plant	26.76	6.66	89.66	92
6	Pod bearing length (cm)	10.87	3.00	43.33	92
7	Number of seeds per pod	22.87	20	28	82
8	Number of seeds per plant	43.80	12.33	144.66	69
9	100 seed weight (g)	10.17	5.87	18.66	89
10	Oil content (%)	18.86	16.05	21.88	77
11	Protein content (%)	38.86	30.76	43.11	30
12	Seed yield per plant (g)	7.49	4.13	14.75	49

of leaf morphology, 47.29% of genotypes were found to have pointed ovate leaves, 33.78% to have rounded ovate leaves, and 6.75% to have lanceolate leaves. The two categories of flower colours were white and purple, with 74.32% of all genotypes being purple and 25.67% being white. The colour of the seed coat is uniformly yellow throughout all genotypes, with no variance. Small seeds were discovered in 64.18% of genotypes, medium seeds in 16.89%, and giant seeds in 6.75% of genotypes.

The analysis of variance showed a significant difference among the genotypes for all the 12 traits. The block effect and the treatment effects were significant in most of the traits indicating the presence of considerable amount of genetic variability. Similarly, the effects due to checks, varieties and checks were significant for most of the traits indicating that the genotypes were significantly different from checks. It provides ample opportunity for the breeder in the selection of lines having traits in the desirable direction. This is in agreement with the result obtained by Koraddi and Basavaraja (2019).

genotypic and phenotypic correlation, but the genotypic correlation magnitude was greater than the phenotypic correlations. Hundred seed weight and oil content showed positive and significant correlation with seed yield per plant both at genotypic and phenotypic correlation. Characters such as number of pods per plant, number of seeds per pod, number of seeds per plant and protein content showed positive and significant correlation with seed yield at genotypic correlation, but days to 50% flowering, number of primary branches per plant showed negative and significant correlation with seed yield per plant at both genotypic and phenotypic correlation. Shekar *et al.* (2018) reported similar results of significant and positive correlation between number of pods/plant and seed yield/plant. However, the seed yield/plant is significantly and negatively associated with days to 50% flowering (Nutan and Gabrial, 2016; Sudhanshu *et al.*, (2015). Reddy *et al.* (2022) reported similar results of significant and positive correlation between number of pods/plant and 100 seed weight.

Number of seeds per pod, number of seeds per plant, hundred seed weight and oil content had positive

**Table 3 :** List of 12 different phenotypic characters.

S. no.	Characteristics	Class	Symbols	No. of genotypes	Frequency percentage (%)
1	Hypocotyl color	Green	G	38	25.67
		Violet	V	110	74.32
2	Growth type	Determinate	D	30	21.27
		Semi-determinate	SD	111	75
		Indeterminate	ID	7	4.72
3	Growth habit	Erect	E	42	28.37
		Semi-erect	SE	92	62.16
		Spreading	Sp	14	9.45
4	Pubescence	Glabrous	G	113	76.35
		Pubescent	Pb	35	23.64
5	Pubescent color	Tawny	Ta	148	100
6	Leaf shape	Lanceolate	L	10	6.75
		Pointed ovate	PO	70	47.29
		Rounded ovate	RO	50	33.78
7	Flower color	White	W	38	25.67
		Violet	V	110	74.32
8	Pod color	Light	L	20	13.51
		Medium	M	65	43.91
		Dark	D	45	30.40
9	Seed coat color	Yellow	Y	148	100
10	Seed size	Small	S	95	64.18
		Medium	M	25	16.89
		Large	L	10	6.75
11	Seed shape	Spherical	Sp	70	47.29
		Spherical flattened	SpF	45	30.40
		Elongated	E	10	6.75
		Elongated flattened	EF	5	3.37
12	Hilum color	Grey	G	10	6.75
		Brown	B	30	20.27
		Dark brown	DBr	10	6.75
		Black	B	20	13.51
		Dark black	DBl	60	40.50

correlation with days to 50% flowering at genotypic level whereas number of primary branches per plant and number of pods per plant showed positive and significant correlation with pod bearing length, number of seeds per pod and number of seeds per plant at genotypic level. Hundred seed weight showed positive significant correlation with oil content, protein content and seed yield per plant at both genotypic and phenotypic correlation level. Hence, direct selection for Days to 50% flowering, plant height, number of primary branches per plant, number of pods per plant, pod bearing length, number of seeds per plant, hundred seed weight, oil content and protein content may be beneficial for the selection of soybean from the available soybean genotypes. Similar results were recorded by Iqbal *et al.* (2010), Kumari (2011) and Kumar

*et al.* (2018) in soybean.

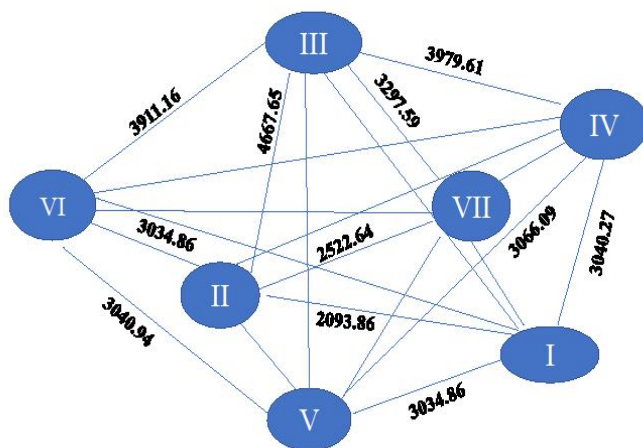
Genetic diversity plays important in the improvement of economic traits in soybean germplasm. Based on  $D^2$  values 148 soybean RILs population were grouped into 7 Clusters. The cluster II was the largest with 82 genotypes, cluster III with 29 genotypes, cluster V with 12 genotypes, cluster VII with 10 genotypes, cluster IV and VI with 7 genotypes and cluster I with 1 genotype. The highest intra cluster distance was found in cluster III (4667.47) followed by cluster IV (3551.06) and cluster VI (3503.7). The highest inter cluster distance was seen in between cluster IV and cluster III (3979.61) followed by cluster VI and cluster III (3911.16), cluster III and cluster I (3648.22) and cluster V and cluster III (3600.79).

Table 4 : Genotypic correlation coefficient for twelve quantitative characters of 148 RIL population of soybean.

Characters	Correlation coefficient	DF	DM	PH	NBP	PP	PBL	S/P	S/PL	100SW	OIL%	P%
DM	G	-0.103	-									
	P	0.1704										
PH	G	-0.278**	-0.082	-								
	P	-0.0252	-0.1744									
NBP	G	-0.059	-0.064	0.644**	-							
	P	0.0769	-0.0234	0.1245								
PP	G	0.010	-0.377**	0.476**	0.599**	-						
	P	-0.0472	-0.2209	0.3390	0.3798							
PBL	G	0.152	-0.275**	0.491**	0.693**	0.833**	-					
	P	-0.0349	-0.2465	0.3263	0.5014	0.8281						
S/P	G	0.419**	0.095	0.046	0.542**	0.304**	0.270**	-				
	P	0.0521	0.0409	0.0252	0.2550	0.3794	0.3359					
S/PL	G	0.390**	-0.332**	0.521**	0.926**	0.991**	0.910**	0.191*	-			
	P	-0.0865	-0.2723	0.3110	0.4247	0.9164	0.8404	0.4017				
100SW	G	0.247**	0.056	-0.345**	-0.070	-0.565**	-0.513**	-0.372**	-0.768**	-		
	P	0.1079	0.1411	-0.3213	-0.1185	-0.4182	-0.4076	-0.2082	-0.4540			
Oil (%)	G	0.357**	0.142	0.036	-0.314**	-0.370**	-0.395**	-0.162*	-0.523**	0.666**	-	
	P	-0.0024	0.0680	-0.2578	-0.1008	-0.2965	-0.2879	-0.0650	-0.2788	0.6020		
P(%)	G	-0.161*	-0.271**	1.000**	0.894**	-0.424**	-0.128	-0.315**	-0.650**	0.291**	0.882**	-
	P	0.0749	-0.0681	-0.1344	0.0141	-0.1409	-0.1121	-0.0353	-0.1436	0.2098	0.1667	
SY	G	-0.640**	0.128	-0.043	-0.671**	0.326**	0.134	0.236**	0.581**	0.784**	0.638**	0.831**
	P	-0.0413	-0.0211	0.0373	-0.1352	0.0346	-0.0555	-0.1219	-0.0043	0.3070	0.3244	0.1182

**Table 5 :** Distribution of soybean accessions in different clusters based on Mahalanobis D<sup>2</sup> analysis.

Cluster No.	No. of genotypes in each cluster	Name of Genotypes
I	1	RILEJ9752-2
II	82	RILEJ9752-7, RILEJ9752-9, RILEJ9752-10, RILEJ9752-11, RILEJ9752-13, RILEJ9752-16-20, RILEJ9752-24, RILEJ9752-73, RILEJ9752-74, RILEJ9752-70, RILEJ9752-27, RILEJ9752-30, RILEJ9752-35, RILEJ9752-75, RILEJ9752-78, RILEJ9752-83, RILEJ9752-36, RILEJ9752-37, RILEJ9752-39, RILEJ9752-42, RILEJ9752-52, RILEJ9752-53, RILEJ9752-55, RILEJ9752-92, RILEJ9752-97, RILEJ9752-58, RILEJ9752-59, RILEJ9752-62, RILEJ9752-63, RILEJ9752-67, RILEJ9752-77, RILEJ9752-81, RILEJ9752-84, RILEJ9752-85, RILEJ9752-87, RILEJ9752-88, RILEJ9752-90, RILEJ9752-98, RILEJ9752-99, RILEJ9752-100, RILEJ9752-C2, RILEJ9752-102, RILEJ9752-103, RILEJ9752-104, RILEJ9752-105, RILEJ9752-106, RILEJ9752-113, RILEJ9752-107, RILEJ9752-108, RILEJ9752-109, RILEJ9752-110, RILEJ9752-111, RILEJ9752-112, RILEJ9752-115, RILEJ9752-116, RILEJ9752-117, RILEJ9752-118, RILEJ9752-119, RILEJ9752-120, RILEJ9752-121, RILEJ9752-122, RILEJ9752-123, RILEJ9752-125, RILEJ9752-124, RILEJ9752-126, RILEJ9752-127, RILEJ9752-128, RILEJ9752-129, RILEJ9752-130, RILEJ9752-132, RILEJ9752-131, RILEJ9752-134, RILEJ9752-135, RILEJ9752-136, RILEJ9752-137, RILEJ9752-138, RILEJ9752-141, RILEJ9752-142, RILEJ9752-143, RILEJ9752-144, RILEJ9752-145
III	29	RILEJ9752-1, RILEJ9752-3, RILEJ9752-8, RILEJ9752-14, RILEJ9752-15, RILEJ9752-17, RILEJ9752-22, RILEJ9752-23, RILEJ9752-28, RILEJ9752-31, RILEJ9752-33, RILEJ9752-38, RILEJ9752-43, RILEJ9752-45, RILEJ9752-46, RILEJ9752-48, RILEJ9752- 60, RILEJ975261, RILEJ975268, RILEJ9752-69, RILEJ9752-71, RILEJ9752-95, RILEJ9752-79, RILEJ9752-82, RILEJ9752-91, RILEJ9752-93, RILEJ9752-96, RILEJ9752 C3, RILEJ9752-140
IV	7	RILEJ9752-19, RILEJ9752-26, RILEJ9752-41, RILEJ9752-49, RILEJ9752-80, RILEJ9752-114, RILEJ9752-139
V	12	RILEJ9752-12, RILEJ9752-18, RILEJ9752-21, RILEJ9752-29, RILEJ9752-34, RILEJ9752-44, RILEJ9752-64, RILEJ9752-65, RILEJ9752-72, RILEJ9752-86, RILEJ9752-89, RILEJ9752-94
VI	7	RILEJ9752-4, RILEJ9752-6, RILEJ9752-25, RILEJ9752-76, RILEJ9752-47, RILEJ9752-50, RILEJ9752-51
VII	10	RILEJ9752-5, RILEJ9752-32, RILEJ9752-40, RILEJ9752-54, RILEJ9752-56, RILEJ9752-57, RILEJ9752-66, RILEJ9752-C1, RILEJ9752-101, RILEJ9752-133

**Fig. 2 :** Inter-cluster distances based on Mahalanobis D<sup>2</sup> analysis of 148 RIL population of soybean.

Among seven clusters, cluster IV showed the highest number of seeds per plant (104.81). Cluster V had highest mean for plant height (103.06), number of primary branches per plant (5.30), number of pods per plant (62.76)

and protein content (39.09%). Cluster III reported the highest mean value for the traits number of seeds per pod (2.70) and oil content (19.13%). The genotypes studied are therefore sufficiently accurate for hybridization. Hence, the traits like days to 50% flowering, number of primary branches per plant, pod bearing length, number of pods per plant, number of seeds per pod and 100 seed weight may be selected for the development of high yielding genotypes of Chhattisgarh plains. The above findings of cluster analysis are in general agreement with the findings of Tyagi and Sethi (2011), Bekele *et al.* (2011), Devvart *et al.* (2005), Ganesamurthy and Seshadri (2002) and Shrivastava *et al.* (2000), Alpna *et al.* (2015), Dubey (2015). Results showed that there was huge amount of variability present in studied population. So the genotype can be used in further hybridization programme involving parent from these clusters.

Mean performance of the 148 genotypes revealed that five genotype RILEJ9752-85 (14.75 g), RILEJ9752-

34 (14.01g), RILEJ9752-46 (13.44g), RILEJ9752-131(13.32g), RILEJ9752-1(13.10g) was significantly superior to the best check RILEJ9752-C2 (12.22g) for seed yield.

### Conclusion

Presence of sufficient amount of genetic variability is scope for selection and exploitation of different traits. High heritability indicates characters are less influenced by the environment. Hence, these traits are suitable for crop improvement. The improvement in number of pods per plant, number of seeds per pod, number of seeds per plant, 100 seed weight, oil content and protein will enhance the seed yield. Highly diverse genotypes will be used in hybridization programme. Therefore, improvement of the genotypes like RILEJ9752-C1, RILEJ9752-C2 and RILEJ9752-11, RILEJ9752-7 and RILEJ9752-81 will be useful for further breeding programmes.

### Acknowledgement

The facilities, resources, and materials needed to conduct the inquiry were generously provided by the All India Coordinated Research Project on Soybean, Department of Genetics and Plant Breeding from Indira Gandhi Agricultural University, Raipur, Chhattisgarh.

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