Original Article

Evaluation of yield contributing characters and cluster analysis of soybean genotypes

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ABSTRACT

Soybean is a major oilseed crop in Bangladesh. Bangladesh is unable to fulfill the demand for soybeans. This experiment was carried out at Sher-E-Bangla Agricultural University to determine the genetic divergence among genotypes established by a Bangladeshi research center and to determine distinct genotypes with their performance for future use. Morphological divergence study among the twenty genotypes of soybean based on nine yield and yield contributing characters through the D^2 statistic indicated the presence of substantial diversity by forming clusters with a wide range of inter-cluster distances. The soybean genotypes under investigation were divided into five clusters. Cluster I had the most genotypes, with 10, followed by clusters III and V, each with five and three genotypes. The relative divergence indicates how much each cluster varies from the others. Cluster I and Cluster III have the most significant order of divergence, followed by Cluster III and Cluster IV. The results revealed that the parents in these clusters are genetically heterogeneous. It's possible that a hybridization program obtained a significant heterotic response. Clusters I and II found the minimum inter-cluster distances, indicating limited genetic diversity. Cluster III had the maximum seed yield per plant cluster value. Individual performance was highest for the genotypes BINAsoybean-3, BINAsoybean-2, and Shohag for the trait seed yield per plant.

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1. Introduction

Soybean (*Glycine max L.*, *Merril*) is an economically significant grain legume that is broadly utilized to supply protein, oil, carbohydrates, minerals, and other nutrients for people and animals [1], and it is therefore widely cultivated for both food and pasture. Unlike most vegetable proteins, Soybean protein contains all of the essential amino acids, along with cardio-friendly oil that meets 30% of the world's vegetable oil requirements. It also has several medicinal components, such as lactose-free fatty acids, antioxidants and folic acid, vitamin B complex, and isoflavones [2].

Genetic variation in traits is essential for breeding and selecting suitable genotypes. Knowledge of diversity patterns will assist breeders in better understanding the evolutionary relationships between accessions and sample germplasm in a more systematic manner and devise ways to incorporate relevant diversity into breeding programs [3]. The introduction of new genetic variation into breeding populations by hybridization with foreign germplasm is one method of increasing genetic variance, which serves as the foundation for selective gain [4]. However, low yield results from common yield variety, lodging, and pod

shattering, substantial production constraints. Hybridization is a helpful strategy for overcoming productivity limits [5]. Moreover, select better genotypes for a hybridization program, it is essential to evaluate the genetic diversity of cultivated agricultural plants. Each breeding program must include genetically diverse parents to form new genetic stocks [6].

Genetic diversity is the most significant tool for a plant breeder when choosing the appropriate type of parent for a hybridization program [7]. D^2 statistics can be used to study the divergence [8]. It is split up into different clusters and is based on multivariate analysis. This approach is thought to be the most efficient for measuring the degree of genetic diversity among genotypes evaluated. The objective of this study was to determine the extent of genetic divergence among genotypes which is developed by the research institute of Bangladesh and identify different genotypes with their performances for future usage.

2.   Materials and Methods
Field research was carried out to examine the cluster, intra and inter-cluster distances, cluster mean performance and mean performance of 20 soybean genotypes. The seeds for these genotypes were obtained from the germplasm banks of the Bangladesh Agricultural Research Institute (BARI), Gazipur, and the Bangladesh Institute of Nuclear Agriculture (BINA), Mymensingh. Table 1 gives a list of genotypes.This study used a randomized block design (RBD) with three replications. All genotypes were planted with a row-to-row spacing of 30 cm and a plant-to-plant spacing of 10 cm. Fertilizers (40 kg N/ha, 40 kg P_2O_5/ha, 40 kg K_2O/ha, and 30 kg S/ha) were applied at the time of sowing. To ensure a healthy crop, all required agronomical techniques and plant protection measures were used [9].

Except for the days to 50% flowering and days to maturity observations, which were recorded on a plot basis, five competitive plants were randomly selected from each replication of each genotype for recorded observation at maturity. The below is the procedure for recording observations / data on various characters: Days to 50% blooming, Days to maturity, Plant height (cm), primary branches per plant, leaves per plant, pods per plant, seeds

per pod, hundred seed weight (g), and seed yield per plant (g) are all factors to consider.

Table 1. The code and accession name of 20 soybean genotypes used in the study.

SL. No.	Genotypic Name	SL. No.	Genotypic Name
1	TAS-4	11	FV-4PL-NICE-7
2	DJS 9207	12	BOSS
3	AGS- 95	13	AGS-79
4	K-16	14	BINAsoybean-4
5	GMOT-95	15	BINA soybean-1
6	ASSET-93	16	Sohagh
7	ASOMEME	17	BARIsoybean-6
8	GMOT-13	18	BINA soybean-3
9	AGS-205	19	BINA soybean-2
10	BARIsoybean-5	20	LOCAL

The data was subjected to a variance analysis using the Statistix10 software. Genstat software was used to generate the cluster dendrogram as well as intra and inter cluster distance.

3.   Results and Discussion

The analysis of variance of twenty soybean genotypes is shown in Table 1. Except for the seeds per pod index, the analysis of variance revealed that days to 50% flowering, days to maturity, plant height, primary branches per plant, leaves per plant, pods per plant, hundred seed weight, and seed yield per plant index were significant. The considerable genotype effect implies that the 20 soybean genotypes differed in character. The coefficient of varience values ranged from 1.30 to 18.96%.

Clustering analysis based on nine morphological traits grouped 20 soybean genotypes into five different clusters and indicates that 20 soybean genotypes exhibited notable genetic divergence in terms of morphological traits (Table 8, Figure 1). Cluster I, with ten genotypes, was determined to be the biggest of the five clusters, while cluster III, with five genotypes, was the second largest. Cluster II and cluster IV had the least number of genotypes, with only one. TSA-4, DJS 9207, AGS-95, K-16, GMOT-95, ASSET-93, GMOT-13, AGS-205, FV-4PL-NICE-7 and BOSS formed a distinct cluster in cluster I; ASOMEME

Table 2. Analysis of variance for different characteristics of twenty soybean genotypes.

Mean sum of square	Mean sum of square								
	Days to 50% flowering	Days to maturity	Plant height	Primary branches per plant	Leaves per plant	Pods per plant	Seeds per pod	Hundred seed weight	Seed yield per plant
Replication (2)	4.12	1.67	87.22	0.32	1.32	2.07	0.05	4.62	3.38
Genotype (19)	13.01**	15.63**	381.42**	1.56**	29.22**	71.79**	0.27	24.12**	22.45**
Error (38)	3.87	4.05	34.99	0.44	2.32	8.91	0.24	1.30	0.66
CV%	4.69	1.30	13.61	18.85	9.90	15.78	18.96	9.40	11.30

** Significant at 1% level of probability

formed a cluster in cluster II, BARIsoybean-5, BARIsoybean-6, BINAsoybean-3, BINAsoybean-2 and a local genotype formed in cluster III; the genotype AGS-79 formed cluster IV; Cluster V consist of BINAsoybean-4, BINAsoybean-1 and Sohagh.

Table 3. Distribution of different genotypes of soybean in different clusters

Cluster no.	Name of Genotypes	No. of populations
I	TAS-4, DJS 9207, AGS- 95, K-16, GMOT-95, ASSET-93, GMOT-13, AGS-205, FV-4PL-NICE-7, BOSS	10
II	ASOMEME	1
III	BARIsoybean-5, BARIsoybean-6, BINA soybean-3, BINA soybean-2, LOCAL	5
IV	AGS-79	1
V	BINAsoybean-4, BINA soybean-1, Sohagh	3
	Total	20

Formation of different number of clusters using morphological characters in diverse soybean genotypes was also reported [10, 11, 12]. The dendrogram tends to group some of the genotypes with similar morphological traits into the same cluster. Similar results were also reported in soybean by Cui et al. [11], C. Y. Yu et al. [12] and Z. Iqbal et al. [13], in oil palm by Abdullah et al. [14], in rice by Latif et al. [15], and in physic nut by Rafii et al. [16].

Table 4 shows the mean values of nine distinct attributes for five groups of 20 soybean genotypes. Results showed that among the five clusters, cluster III had the highest average mean for the traits seed yield per plant, pod per plant, and leaves per plant; for the traits plant height, hundred seed weight, and days to maturity, cluster V had the highest average means. The grouping pattern revealed

Table 4. Cluster mean for yield and yield related characters in soybean genotypes.

Characters	I	II	III	IV	V
D50M	41.90	48.00**	42.07	41.00	40.00*
DM	86.83	90.00	88.60	84.33*	90.33**
PH	38.93	24.33*	46.67	45.67	58.89**
PBP	3.83	4.67**	3.27	2.33*	2.89
LPP	16.40	11.67	17.13**	9.67*	12.11
PPP	15.87*	20.67	24.87**	16.33	19.44
SPP	2.60	3.00**	2.67	2.33*	2.44
HSW	10.20	9.33	15.27	8.67*	15.44**
SYP	5.13	5.73	11.01**	4.93*	9.10

* Minimum value ** Maximum value

no link between genetic divergence and geographic diversity, which has long been a source of controversy. Similar observation have also been observed. [17, 18].
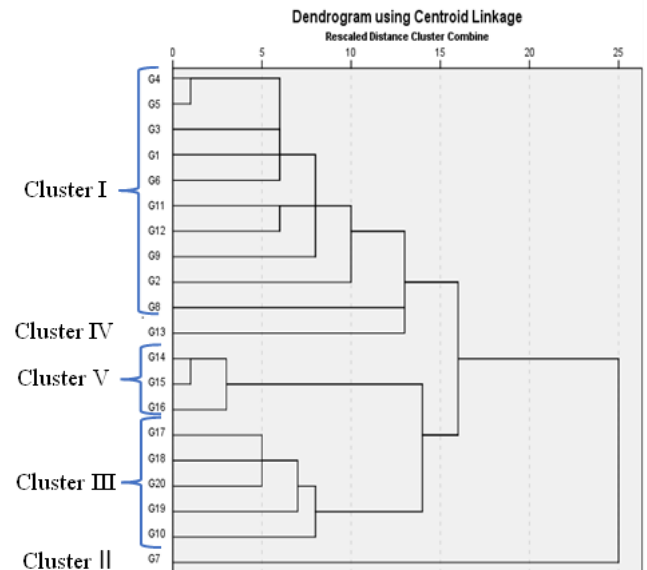

Fig 1 Dendrogram showing six different clusters of 20 genotypes.

Cluster I and cluster III had the highest inter-cluster distance, followed by III and IV, and I and V, respectively, based on D^2 values. Average intra and inter-cluster D^2 values among 20 genotypes revealed that cluster V (4.76) showed maximum intra cluster D^2 value followed by cluster I (3.76), indicating diversity in these clusters. Both Clusters II and IV had only one genotype each, so both of them showed no intra-cluster distance. As determined by inter-cluster distances, the genotype diversity was

Table 5. Intra (Bold) and inter cluster distances (D^2) for soybean genotypes

Cluster	I	II	III	IV	V
I	**3.765**	16.140	38.541	21.690	30.102
II		**0.00**	25.036	27.117	25.868
III			**2.67**	36.024	23.370
IV				**0.00**	17.722
V					**4.76**

significant for hybridization and selection improvement [2, 19]. Crosses between genotypes of clusters separated by considerable inter-cluster distances exhibit significant heterosis [20]. Cluster I and II had the lowest inter-cluster D^2 value (16.14), showing a strong relationship between the genotypes in these two clusters.

To understand the performance of the tested genotype, mean values of several characteristics were analyzed and

are provided in Table 6. Days to maturity were observed significantly different between genotypes.

Soybean yield is significantly and positively correlated to pods per plant and seed per pod [26, 27, 28]. In this

Table 6. Mean performance of different characters of soybean genotypes.

Genotype	Plant measurement								
	D50F	DM	PH	PBP	LPP	PPP	SPP	HSW	SYP
Tas-4	42e	90b	21.3p	4b	17d	16h	3a	57g	9.3g
Djs-9207	40f	86f	29n	4b	17.7c	20d	2.3c	52j	11.3e
AGS- 95	42e	89c	45.3fg	5a	17.7c	13j	2.7b	48l	9.7g
K-16	42e	86f	43.3hi	5a	18bc	17g	2.7b	50k	11.7de
GMOT-95	43d	85g	37k	4b	17d	18f	2.7b	56h	9.7g
ASSET-93	45b	87e	44.3gh	3c	18.7b	21d	3a	62e	9.7g
ASOMEME	48a	90b	24.3o	5a	11.7hi	21d	3a	61e	9.3g
GMOT-13	43d	89c	40j	4b	11.7hi	11l	2d	40o	11.7d
AGS-205	41e	85g	49e	3c	14.7f	16h	3a	54i	8.7h
BARI soybean-5	40g	91a	32m	3c	16e	27b	2.7b	81a	14.3c
FV-4PL-NICE-7	41e	86f	45fg	3c	19.3a	12k	2.3c	42n	10.3f
BOSS	40g	86f	35l	4b	12.3gh	15i	2.3c	44m	10f
AGS-79	41e	84h	45.7fg	2d	9.7k	16h	2.3c	57h	8.7h
BINA soybean-4	41e	91a	55.3c	3c	11.3j	22c	2.3c	59f	15.3b
BINA soybean-1	39h	91a	58b	2d	13g	19e	2.3c	60f	14.7c
SOHAGH	40g	89c	63.3a	3c	12h	18f	2.7b	58g	16.3a
BARI soybean-6	44c	89c	52.7d	3c	16.7de	28b	2.3c	74c	15.7b
BINA soybean-3	41e	86f	57.3b	3c	20a	29a	2.7b	78b	17.3a
BINA soybean-2	43d	89c	42.7i	3c	14.7f	19e	3a	64d	16.6a
Local	42d	87d	48.7f	4b	18.3b	22c	2.7b	64d	14.7c

Here, D50F= Days to 50% flowering, DM= Days to maturity, PH= Plant height, PBP= Primary branch per plant, LPP= leaf per plant, PPP= Pods per plant, SPP= Seed per pod, HSW= Hundred seed weight, SPY= Seed yield per plant.

The genotype AGS-79 (84days) matured earlier than the other genotypes, but BINAsoybean-1 (91 days) and BINAsoybean-4 (91 days) took the longest days to mature. The critical photoperiods of various genotypes are responsible for the varying days to maturity [21]. The highest plant was observed in the genotype Sohag (63.3cm) followed by BINAsoybean-3 (57.2cm) and Tas-4 had the shortest plant (21.3cm). Therefore, a shorter plant height is required for adaptation in current agricultural systems that use combined harvesting [22]. Reducing plant height also enhances lodging resistance, another issue in soybean cultivation. On the other hand, low plant height appears to be a disadvantage for larger seed yield since plants of greater height contain more capsules and hence produce more seed [23].

The number of branches is an essential selection criterion in the soybean improvement program. A more significant number of branches allows for more pods to be produced per plant, resulting in a higher seed yield [24]. AGS-95, K-16, and ASOMEME produced the most primary branches per plant in this research, whereas AGS-79 and BINAsoybean-1 produced the fewest. BINAsoybean-3 generated the most leaves per plant, whereas AGS-79 produced the fewest. More leaves might absorb more light, resulting in a plant that is more luminous. More yield and yield-related characteristics were observed with increasing light [25].

study, the highest pods per plant were recorded in BINAsoybean-3 (29), followed by BARIsoybean-6 (28), while the most seed per pod was found in ASOMEME ASSET-93, Tas-4, AGS-205, and BINAsoybean-2. The BARIsoybean-5 had the highest hundred seed weight, followed by BINAsoybean-3 and BARIsoybean-6. The highest seed yield per plant was observed in BINAsoybean-3 (17.3g) followed by BINAsoybean-2 (16.6g) and Sohag (16.3g).

4. Conclusion

According to the initial objectives, the genotypes of clusters I and III might be utilized as parents in a future breeding program to develop soybean varieties. ASOMEME, GMOT-13, and BOSS from cluster I and BARIsoybean-5, BINAsoybean-3 from cluster III, BINAsoybean-4 BINAsoybean-1, and Sohag from cluster V, would be acceptable for future hybridization.

Conflict of Interest

The authors declare that they have no conflict of interest.

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