International Journal of Environment and Climate Change

Volume 13, Issue 9, Page 3173-3180, 2023; Article no.IJECC.103782
ISSN: 2581-8627
(Past name: British Journal of Environment & Climate Change, Past ISSN: 2231–4784)

Characterization and Evaluation of Some Genotypes of Soybean [(*Glycine max* (L.) Merrill] under Acidic Soil Condition in Meghalaya, India

Yengkhom Linthoingambi Devi [a*], K. Noren Singh [a] and S. Samuthirapandi [a]

[a] College of Post Graduate Studies in Agricultural Sciences, CAU, Umiam, Meghalaya, 793103, India.

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Article Information

DOI: 10.9734/IJECC/2023/v13i92561

Open Peer Review History:
This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: https://www.sdiarticle5.com/review-history/103782

Original Research Article

Received: 27/05/2023
Accepted: 29/07/2023
Published: 08/08/2023

ABSTRACT

In the world scenario, although soybean is considered an important oilseed crop with India holding 5th position by contributing about 3.95% share in it's total production, its production in north-eastern region of India especially in Meghalaya is quite less due to its acidic soil condition. With the highlight of the above fact, the present research was conducted using 40 different soybean genotypes from different regions in the country. At different growth stages of the plant, 22 DUS characters and 12 quantitative characters were recorded. Analysis of variance gave highest significant value for number of seeds per plant succeeded by number of pods per plant and the lowest was found for number of seeds per pod and primary branch per plant. Studying the correlation analysis of the agronomic traits, seed yield per plant was showing positively correlation with characters number of seeds per pod, number of pods per plant, 50% flowering, plant height, days to maturity, primary branch per plant and protein content while characters like number of

**Corresponding author: E-mail: linthoiyengkhom123@gmail.com;*

seeds per pods, number of pods per cluster and100 seed weight was found non-significant. The highest yield was found in the genotype TS-53 followed by SKF-SPS-11 and MACS-1493. Lowest yielder genotypes are MACS-1575 followed by NRC-130. Genotype CSB-10112 had the highest protein content(45.1%) and genotype NRC-131 was found to have highest oil content(20.1%). Clustering of genotypes for studying genetic diversity was performed by Tocher's method of D^2 analysis. A total of 9 clusters was formed with cluster I having 23 genotypes, cluster II with 4 genotypes, cluster III with 3 genotypes, cluster IV with 5 genotypes while cluster V, VI, VII, VIII and IX did not fall in any cluster. With these findings, it will be useful for breeders to further undergo molecular level studies to find out the gene responsible for tolerance. Thus, breeders can use the characters which were more positively correlated with yield for crop improvement work and the diverse parents could be used for hybridization program.

Keywords: Soybean; genetic diversity; D^2 analysis; Tocher's method.

1. INTRODUCTION

Soybean domestication started in 7000 BC in central China and was introduced in India in 1000 AD through Himalayan Mountain. But the commercial cultivation of soybean was started since 1970s in Madhya Pradesh. Miracle Crop of 20th Century and Golden bean are the popular names of soybean. Soybean has rich source of minerals like copper, molybdenum, manganese, potassium, phosphorus, vitamin B, omega -3-fatty acid and riboflavin. Soybean can be categorized as oilseeds, vegetables, legumes or even fuel sources based on how they are being used. Soybean is also among those plants which have full array of different amino acids and considered as complete protein or can be compared with milk products, eggs and meats. Popular commercial products of soybean include textured vegetable protein, protein powders, edamame, sprouts, dry beans, vegetable oil, livestock feed, tofu, gluten-free flour, soy cheese, etc.

As per PPV & FR Act, new variety should be distinct from other varieties; stable genetically as well as there must be uniformity in the characteristics. So, identification of variety along with genetic purity is required in breeding programme. Germplasm characterization gives us the knowledge of the character and its heritable traits expressing in certain or all the environments. Evaluation is necessary for assessing the agronomic ability combined with quality parameters and also for checking their response against several biotic and abiotic stress. Collecting germplasm and accessing their genetic variability is mandatory for any improvement work. Morphological markers are influenced by the environment where the crop is grown, besides its genetic composition [1].

Creating a heritable genetic variability is the key factor in plant breeding program for getting superior variety [2]. So, knowledge of the degree and the nature of diversity are necessary factors for choosing and creating superior varieties. To identify the diverge genotypes, a multivariate D^2 statistics would be useful and will give important information of parents for hybridization work [3]. To fulfill the future demand of soybean, it is necessary to develop high yielding soybean variety with better tolerance to biotic and abiotic stress. So, relationship of component characters of yield would be useful to identify the best performing genotype that can be selected based on the criteria of seed yield, oil and protein content.

2. MATERIALS AND METHODS

The present investigation was carried out in College of Post-Graduate Studies in Agricultural Sciences, Central Agricultural University, Umiam, Meghalaya. The experimental material consisted of 40 genotypes of soybean sown in Randomized Block Design (RBD) with three replications. The 12 agronomic characters viz., primary branch per plant, 50% flowering, number of pods per cluster, number of pods per plant, number of seeds per plant, plant height (cm) , number of seeds per pod, days to maturity, see yield per plant(g), 100 seed weight(g), protein content (%) and oil content(%). Also, 22 DUS characters were recorded viz. Hypocotyl: anthocyanin colour, Plant: growth type, Days to 50% flowering, Leaf shape, Leaf colour, Plant: growth habit, Flower colour, Plant height (cm), Pod: Pubescence, Pod: Pubescence colour, Pod : Colour, Pod: Shattering, Plants: Days to maturity, Seed: Shape, Seed: Colour, Seed: Luster, Seed: Hilum colour, Seed: Cotyledon content, Seed oil content (%), Seed protein content (%).In the field condition, 10 plants are taken for the observation

in all the three replication. The mean of different characters were calculated on the basis of these individual data recorded for each character in each replication and subjected for statistical analysis. Analysis of variance and variability parameter were estimated and Correlation coefficient at genotypic and phenotypic level was computed from the variance and covariance components.

2.1 Mahalanobis D^2 Analysis

The genetic diversity among the plants was calculated based on D^2 analysis. The concept of D^2 was originally given by P.C. Mahalanobis in 1928. Selection of genotype 2. Evaluation of material 3. Biometrical analysis.

D^2 values between i^{th} and j^{th} genotypes for "P" characters was calculated as

$$D^2_{ij} = \sum_{t=1}^{P} (Y_i^t - Y_j^t)^2$$

Y_i^t= uncorrelated mean value of i^{th} genotype for "t" character
Y_j^t = uncorrelated mean valu of j^{th} genotype for "t" character
D^2ij = D^2 value between i^{th} and j^{th} genotype

The contribution of individual character towards divergence was estimated using Singh [4] method which can be calculated by:

$$S_j = \sum_{j=1}^{p} W^{ij}\ d_i\ d_j$$

Where, W^{ij} is the $(ij)^{th}$ element in the inverse of estimates within population variance-covariance matrix, p is the number of characters involved, d_i and d_j are the difference in the mean of two populations for the i^{th} and j^{th} characters.

Grouping of genotypes into different clusters was done by using Tocher's method as described by Rao [5].

Average intra-cluster distance was estimated as:

$$\sum_{i=1}^{n} D_{i^2}/n$$

Where, $\sum_{i=1}^{n} D_{i^2}$ is the sum of distance between all possible combinations of the populations included in the cluster and n is the total number of clusters.

3. RESULTS AND DISCUSSION

Characterization on qualitative characters had low influence of environmental fluctuation and could be used as a morphological marker for soybean varietal identification. Understanding the germplasm characterization gave us the knowledge of nature of the character and its heritable traits expressing in certain or all the environments. Understanding the origin of different accessions of soybean was useful for breeding work to develop improved variety for specific situation. Information on diverse genotypes was obtained through diversity analysis [6]. Crop productivity in the North-eastern states including Meghalaya was limited because of acidic soil condition. So, it is necessary to find out the better performing genotype of soybean in such area.

Therefore, the study was carried out to identify the diverse genotypes, to know the character contributing most towards the yield and to find out the most tolerant genotype under acidic soil condition with pH 4.8.

3.1 Characterization of Genotypes

A total of 22 DUS characters were used for characterization of 40 soybean genotypes. The characters were observed at different growth stages of the plant. The genotypes were thus characterized and grouped into different categories based on the character of the plant. Talla et al. [7] used 20 DUS characters for characterization of soybean and found characters like pod pubescence, seed size, seed hilum colour to be very effective character for genotype characterization. In the present study, out of the 22 DUS characters in 40 soybean genotypes, the characters like plant growth habit, flower colour, pod pubescence, seed shape, pod shattering, hypocotyl anthocyanin pigmentation and plant growth type were found to be useful for distinguishing genotype effectively. In a study of Ramteke and Murlidharan [8], on the basis of eleven essential DUS characters of 92 soybean varieties, 42 varieties were grouped as distinctive one and on the basis of other 9 characters, 13 were distinct when compared among them.

3.2 Analysis of Variance and Variance Components

Analysis of variance of characters for the genotypes depicted significant value for all the 12 characters under study at 1% level of significance. The highest significant value was recorded for the character seed yield per plant followed by number of pods per plant. Ali et al. [9] also revealed the same in their study on soybean crop.

Number of pods per cluster had highest GCV and PCV followed by number of seeds per plant indicating presence of high genetic variation. Osekita and Ajayi [10] found highest GCV and PCV in seed yield per plant while Chandrawat et al. [11] found high values of GCV and PCV for characters, number of pods per plant succeeded by plant height in soybean crop.

Highest heritability was found for days to maturity succeeded by number of pods per cluster. Osekita and Ajayi [10] also reported similar findings in soybean.

Maximum genetic advance (as per cent of mean) was found in number of pods per cluster followed by seed yield per plant. Aditya et al. [12] also reported high heritability coupled with high genetic advance for number of pods per plant. High genetic advance with high heritability could be used for further improvement work through simple selection method.

3.3 Diversity Analysis

The diversity analysis was carried out on 12 agronomic characters of 40 soybean genotypes. The diversity study showed the nature of relationship among the genotypes under study.

D^2 analysis using Tocher's method of clustering [5] using D^2 value gave 4 clusters with cluster I having 23 genotypes, cluster II 4 genotypes in it, cluster III with 3 genotypes and cluster IV with 5 genotypes. Genotypes CSB 10112, RSC 11-03, NRC 137, VLS 95 and NRC 129 did not fall in any cluster already formed and remain as distinct genotypes from other soybean genotypes as they are different from other genotypes in terms of variation in 12 agronomic characters under study. In the present study, it was also found that grouping of genotypes based on diversity was not related to geographical origin of the genotype. This might be due to the parents involved in developing those genotypes from different geographical region unlike the landraces which was evolved in a certain geographical areas under prolonged exposure in the surrounding environment. Adsul and Monpara [13] also found that the role of genetic makeup of genotype was more important than the geographical origin of a genotype.

Twelve agronomic traits contribute differently towards the diversity analysis. The character number of seeds per pod gave maximum contribution for the diversity study (25.06%) succeeded by the character number of pods per cluster (23.94%). Shadakshari et al. [1] also found the similar findings. The characters like primary branch per plant and oil content gave less shared towards the diversity study with about 0.54% and 1.83% contribution respectively. Adsul et al. [13] explained the importance of giving more emphasis to high contributor characters as these characters could be engaged in further selection and hybridization work.

The highest inter cluster distance was found between the genotype RSC 11-03 and NRC 129 which showed most diverse genotype between them, so the genotypes could be use for hybridization work and through simple selection method the genotypes could be improved for future crop improvement. Cluster IV and the genotype CSB 10112 showed least inter cluster distance showing least diversity between them. The highest intra cluster distance prevailed in cluster IV with distance of 169.20 indicating presence of higher heterogeneity of the genotypes among the cluster. Shadakshari et al. [1] also performed clustering method through D^2 analysis.

The genotypes belonging to Cluster II could be useful for further crop improvement work as they have the genotypes with high seed yield per plant and number of seeds per pod.

3.4 Correlation Analysis of the 12 Agronomic Traits

Correlation study among the characters found highest correlation value between the character seed yield per plant and number of seeds per plant. The findings were correlated with Varnica et al. [14] where they also explained the same findings.

Following correlation analysis, the character seed yield per plant was found to be significant and had positive correlation with primary branch per plant, number of seeds per plant, plant height, number of pods per plant, 50% flowering, protein content and days to maturity. Ali et al. [9] found positive and significant correlation between seed yield per plant and 50% flowering, days to maturity, 100 seed weight, pods per plant and pod length and thus supported the findings.

Seed yield per plant was non-significant with number of seeds per pod, number of pods per

cluster and 100 seed weight. The result was also supported by Malek et al. [15] where they found seed yield to be non-significant with 100 seed weight, protein content and oil content.

Table 1. Genotypic correlation of the 12 agronomic characters

	PBPP	50%F	NPPC	NPPP	NSPP	PH	NSPPo	DTM	SYPP	OC	PC	100SW
PBPP												
50%F	0.071^{NS}											
NPPC	0.073^{NS}	0.206*										
NPPP	0.122^{NS}	0.314**	0.245**									
NSPP	0.140^{NS}	0.358**	0.119^{NS}	0.662**								
PH	0.144^{NS}	0.220*	0.398**	0.368**	0.272**							
NSPPo	-0.003^{NS}	0.160^{NS}	-0.317**	-0.024^{NS}	0.050^{NS}	-0.279**						
DTM	0.112^{NS}	0.044^{NS}	0.139^{NS}	0.355**	0.350**	0.358**	-0.179^{NS}					
SYPP	0.214*	0.371**	0.002^{NS}	0.394**	0.664**	0.248**	0.035^{NS}	0.236**				
OC	0.034^{NS}	-0.301**	-0.034^{NS}	-0.269**	-0.371**	0.066^{NS}	-0.199*	-0.362**	-0.260**			
PC	-0.011^{NS}	-0.005^{NS}	-0.012^{NS}	0.327**	0.095^{NS}	0.052^{NS}	0.038^{NS}	0.317**	0.203*	-0.185*		
100SW	-0.085^{NS}	-0.291**	-0.251**	-0.372**	-0.282**	-0.344**	0.098^{NS}	-0.266**	-0.088^{NS}	0.221*	-0.073^{NS}	

*** maximum; * minimum*

PBPP=Primary Branch per Plant, 50%F=50% Flowering, NPPC=Number of Pods per Cluster, NPPP=Number of Pods per Plant, PH=Plant Height, NSPP=Number of Seeds per Pod,DTM=Days to Maturity, SYPP=Seed Yield per Plant, OC=Oil Content, PC=Protein Content, 100SW=100Seed Weight

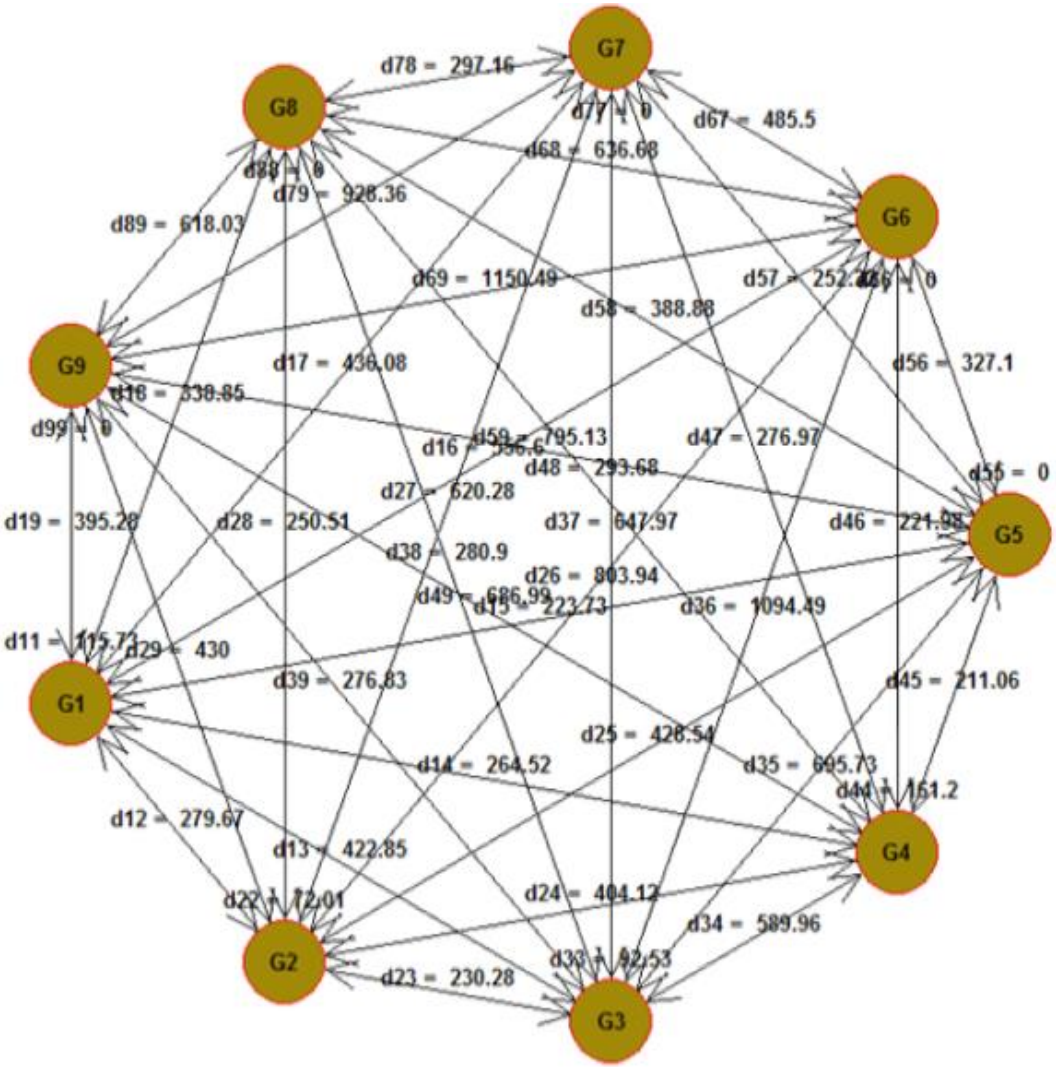

Fig. 1. Cluster diagram based on D^2 distance by Tocher's method

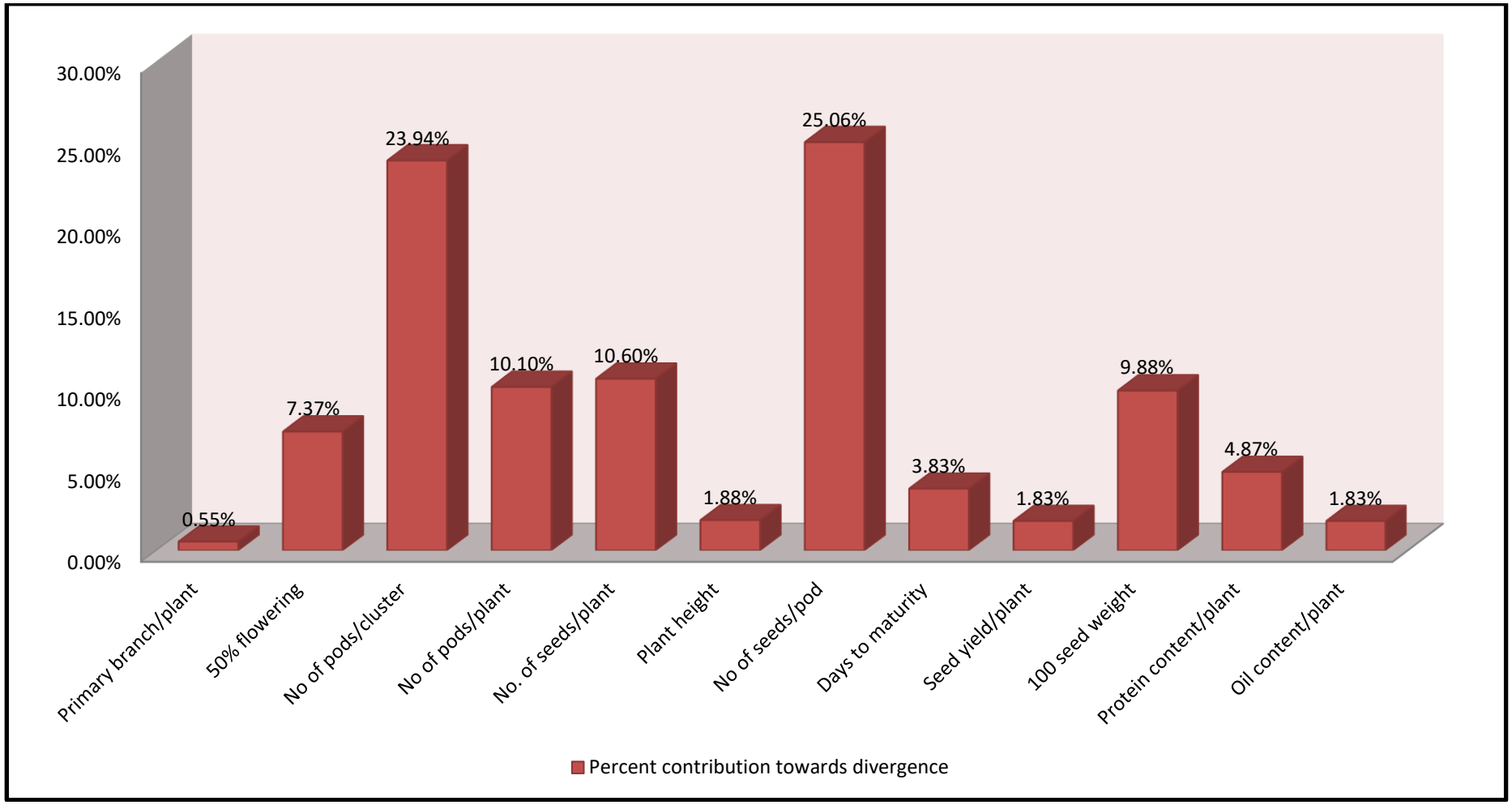

Fig. 2. Percent contribution of characters towards the diversity analysis

Table 2. Name of genotype and their belonging cluster group

Cluster	Number of genotypes	Name of genotypes
I	23	NRC 128, SL 106,JS 21-15,CSB 10084, MACS 1493, JS 20-17, TS 53, MAUS 731, AMS 2014-1, KDS 1095, NRC 133, AMS 100-39, NRC 136, RVS 2011-1, PS 1613, NRCSL-1, PS 1611,RVS 2011-2, SKF SPS-11, PS 1556, JS 20-116, JS 335, RKS 18
II	4	RVS 2011-3, DSb 34, MAUS 725, DS 3108
III	3	NRC 130, MACS 1575, NRC 131
IV	5	AUKS 174, NRC 132, KDS 992, RSC 11-07, JS 97-52
V	1	CSB 10112
VI	1	RSC 11-03
VII	1	NRC 137
VIII	1	VLS 95
IX	1	NRC 129

Table 3. Inter-cluster and intra-cluster distance between and within the clusters based on D^2 value

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	115.731								
II	279.67	72.01****							
III	422.85	230.28	92.53						
IV	264.53	404.12	589.96	161.20***					
V	223.74	428.54	695.74	211.07**	0				
VI	556.60	803.94	1094.49	221.98	327.10	0			
VII	436.08	620.28	647.97	276.97	252.32	485.50	0		
VIII	338.85	250.51	280.90	293.68	388.88	636.68	297.16	0	
IX	395.28	430.00	276.83	686.99	795.13	1150.49*	928.36	618.03	0

** maximum inter- cluster distance*
*** minimum inter-cluster distance*
**** maximum intra-cluster distance*
***** minimum intra-cluster distance*

100 seed weight showed negative correlation with protein content which was supported by the findings of Malek et al. [15]. Protein content was also negatively correlated with oil content. The result was supported by many research works. Dombos and Mullen (1992) found soybean seed protein to be negatively correlated with seed oil. Similar findings were also given by Malek et al. [15] and Liang et al. [16] where they found seed protein content to be negatively correlated with seed oil content.

4. CONCLUSION

The study conducted would be helpful for further research work. The study gave an idea of characterization of the DUS characters which will provide breeders a faster form of screening for their research work and the nature and characters of the genotypes could be easily accessed. The genotypes with most diverse form could be used for hybridization and further crop improvement work. The characters which are found positively correlated with yield could be used for further crop improvement work through selection of the characters

ACKNOWLEDGEMENT

The author are grateful to Dr. Noren Singh, for guiding me throughout the research work. I would also like to take the privilege to thank Dr. N.B Singh Dean, College of Post Graduate Studies, Umiam, Meghalaya and all the staff members of the college for the ceaseless support I received during the course of my study. I extend my profound thanks to the College of Post Graduate Studies for providing me scholarship and financial assistance for completion of my master's programme.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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