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Genetic divergence in soybean (*Glycine max* (L.) Merrill)

A.K. Datta, M.A. Hossain and L. Rahman
Department of Genetics & Plant Breeding, Bangladesh Agricultural University, Mymensingh-2202, Bangladesh

Abstract

Genetic divergence among twenty-one genotypes of soybean using Mahalanobis D^2 statistics revealed considerable variability among the genotypes for eight characters. The genotypes were grouped into four distinct clusters. The inter-cluster distances were larger than the intra-cluster distances suggesting wider genetic diversity among the genotypes of different groups. The inter-cluster average D^2 values showed maximum distance between cluster II and I followed by between II and III. The genetically diversed genotypes from these groups could be used as parents in hybridization program for getting desirable seggregants. Germplasms much in use of these characters of respective clusters would offer a good scope of improvement of the crops through rational selection.

Keywords: Genetic diversity, Soybean, *Glycine max*, Cluster analysis

Introduction

Soybean [*Glycine max* (L.) Merrill] is considered to be the most important oil and legume crop in the world, in terms of total production and international trade (Yang *et al.*, 1997). The production of this crop has increased in different regions of the world for its multipurpose use and seems to grow well from the tropical to the mid-temperate zones. Soybean is an excellent health food and contains about 40-45% protein and 18-20% oil and provides around 60% of the world supply of vegetable protein and 30% of the oil (Fehr, 1989). It can be a very good source to reduce malnutrition of the people of Bangladesh. But in Bangladesh the average yield of soybean is very low in comparison with other soybean growing countries of the world. Therefore, attempt should be taken to develop high yielding varieties and increase their adaptation in different areas for cultivation.

Information on genetic divergence among the plant materials is vital to a plant breeder for an efficient choice of parents for hybridization. It is an established fact that genetically diverse parents are likely to contribute desirable segregants and or to produce high heterotic crosses. More diverse the parents greater are the chances of obtaining high heterotic F_1s and board spectrum of variability in segregating generations (Murty and Arunachalam, 1996). Improvement in yield and quality is normally achieved by selecting genotypes with desired character combinations existing in the nature or by hybridization. The parents identified on the basis of divergence analysis would be more promising. In both cross and self-pollinated crops genetic diversity is one of the most important tools to quantify genetic variability (Griffing and Lindstrom, 1954; Murty and Arunachalam, 1996; Gaur *et al.*, 1978). The quantification of genetic diversity through biometrical procedure has made it possible to choose genetically diverse parents for a successful hybridization program (Jain *et al.*, 1975). Tomooka (1991) also reported that evaluation of genetic diversity is important to know the source of gene for a particular trait within the available germplasm. In Bangladesh context the information on this aspect of soybean is not sufficient. Therefore, the present investigation was undertaken to estimate the nature and magnitude of genetic diversity in a collection of soybean genotypes.

Materials and Methods

Twenty-one genotypes of soybean were grown in randomized complete block design with three replications at the experimental farm of the Department of Genetics & Plant Breeding, Bangladesh Agricultural University, Mymensingh, during the period of January to May, 2004. Soil of the experimental plot was silty loam in texture and it was medium high land belonging to old Brahmaputra floodplain with soil pH 6.5. Seeds of the soybean genotypes were collected from the BAU-USDA soybean research project. The unit plot size was 2.5 m x 2.0 m. The seeds were sown in lines keeping row-to-row distance 30 cm and 5 cm between seeds within rows. Fertilizers were applied at recommended doses. Other intercultural operations were done as and when necessary. The observations were recorded for ten randomly selected plants of the middle rows in each plot. The data were recorded on leaf area (cm^2), plant height (cm), days to 50% flowering, days to maturity, pods per plant, seeds per pod, 100 seed weight (g) and yield per plant (g). The data were analyzed using Mahalanobis (D^2) statistics and the twenty-one genotypes were recorded into different clusters according to the method described by Rao (1952).

Results and Discussion

The analysis of variance showed significant differences among the genotypes of soybean for eight characters at 1% level indicating the presence of genetic variability among the genotypes. On the basis of D^2 values twenty-one genotypes were grouped into four clusters by the Toucher's method as described by Rao (1952). The largest cluster IV was consisted of 10 genotypes, cluster II consisted of 6 genotypes cluster I included 3 genotypes. The cluster II was the smallest with two genotypes (Table 1). Average intra and inter-cluster distances (D^2) between the four clusters were given in Table 2. It was observed that the distance between cluster I and cluster II was the highest (9.63) and was followed by the distance between cluster II & III (6.41) and cluster II and IV (5.61). It noted that the genotypes grouped in these clusters were highly divergent form each other. The inter cluster distance between cluster III & IV was the lowest (3.895), which indicated that the genotypes included in these clusters were closely related. The mutual relationships among four clusters are presented in the diagram (Fig.1). Genotypes belonging to the clusters with maximum inter cluster distance was genetically more diverged. The crosses involving parents belonging to most diversed clusters were usually reported to manifest maximum heterosis and also wide variability in segregation generations (Jagadev *et al.,* 1991). Thus crosses between the genotypes of cluster II with that of cluster I and cluster III would exhibit high heterosis and also likely to produce new recombinant with desirable traits in soybean. Dobhal (1995), Kumar and Nadarajan (1994) and M.M. Rahman (1998) also reported similar information in soybean.

Cluster mean of the eight characters for twenty-one genotypes are given in Table 3. Difference in cluster mean existed for almost all the characters. Cluster I had genotypes with tall plant, late maturing, maximum days to 50% flowering, large leaf area, intermediate 100 seed weight and higher yield/plant. This indicated an isolation of high leaf area, late maturing, tall and high yielding genotypes in this cluster. Genotype of cluster II were late maturating, producing medium number of pods per plant, seeds per pod, semi dwarf plant height, medium days to 50% flowering, lowest 100 seed weight and medium yield per plant. This indicated a grouping of dwarf, early flowering, lower pods per plant and low yielding genotypes. Cluster III included the genotypes that had dwarf plant height, highest 100 seed weight, and maximum days to maturity and minimum days to 50% flowering. Cluster IV included the genotypes, which produced the tallest plant with late maturing, highest number of pods per plant and seeds per pod, lowest 100 seed weight and higher yield per plant. This indicated a grouping of higher plant height, higher pod number and seeds per pod and high yielding genotypes. On the basis of priority in contribution to the total divergence (Table 4) the order of the characters were leaf area, plant height, days to 50% flowering, days to maturity, pods per plant, seeds per pod, 100 seed weight and yield per plant.

Table 1. Clustering pattern of twenty-one soybean genotypes by Tocher's method

Cluster no.	Total no. of genotypes	Genotypes	Origin
I	3	F-85-11347	AVRDC
		MTD-451	USA
		Santarosa	USA
II	6	TG-88	Thailand
		MTD-176	USA
		Shohag	India
		Bragg	USA
		G-2120	AVRDC
		MTD-6	USA
III	2	MTD-459	USA
		Davis	USA
IV	10	Leaflor	AVRDC
		GC-840079-5-1	AVRDC
		CM-3	USA
		Asset 93-19-12	AVRDC
		BS-60	Bangladesh (BCSRP)
		AGS-120	AVRDC
		AGS-302	AVRDC
		SJ-5	Indonesia
		AGS-276	AVRDC
		MTD-178	USA

Table 2. Average intra (bold) and inter-cluster distances (D^2) and D values for 21 soybean genotypes by Tocher's method

Cluster	I	II	III	IV
I	**0.556** **(0.745)**	9.653 (3.107)	4.778 (2.186)	4.296 (2.073)
II		**0.325** **(0.570)**	6.406 (2.531)	5.611 (2.368)
III			**0.618** **(0.786)**	3.895 (1.973)
IV				**0.821** **(0.906)**

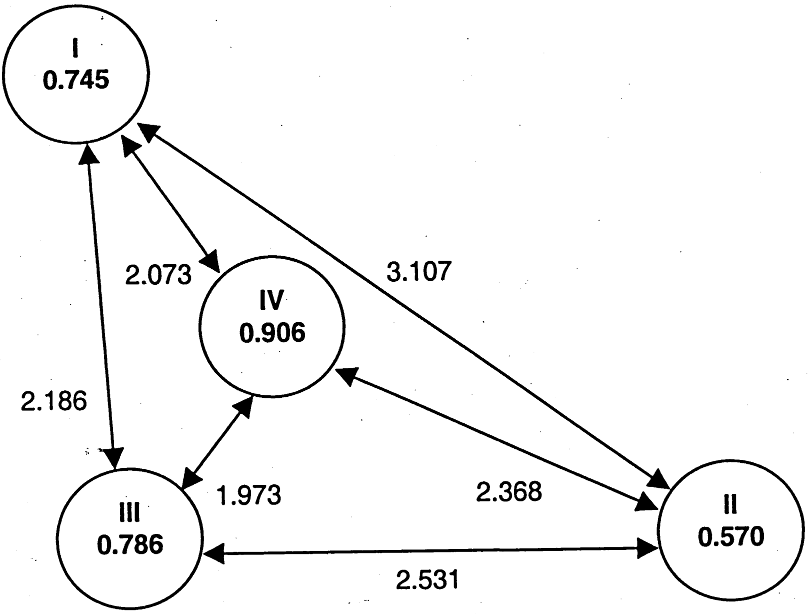

Fig 1. Cluster diagrams showing the average intra and inter cluster distance ($D = \sqrt{D^2}$ values) of the soybean genotypes. The values among the lines indicate inter cluster distance and the values beside the circle indicate intra cluster distances

Table 3. Cluster means of eight quantitative characters in 21 soybean genotypes

Characters	Cluster			
	I	II	III	IV
Leaf area (cm^2)	158.25	67.71	129.38	113.35
Plant height (cm)	74.15	62.19	47.41	74.65
Days to 50% flowering	76.89	64.50	58.00	74.20
Days to maturity	130.44	113.17	121.16	129.77
No. of pods per plant	53.38	38.83	23.10	55.35
No. of seeds per pod	2.09	2.12	2.13	2.13
100 seed weight (g)	11.68	10.94	15.56	10.69
Yield per plant (g)	9.81	8.15	7.07	9.23

Table 4. Relative contribution of the eight characters (%) to the total divergence

Characters	leaf area (cm^2)	plant height (cm)	days to 50% flowering	days to maturity	no. of pods /plant	no. of seeds/ pod	100 seed weight	yield /plant	total
Percent of contribution	65.83	24.28	6.34	1.70	0.81	0.25	0.08	0.01	100

References

Dobhal, V.K. 1995. Genetic divergence in soybean. Legume Research. 18(1): 29-34.

Fehr, W.R.1989. Soybean.In oil crops in the world by Robbelin, G. Downey, R.K. and Ashri, A. McGraw Hill Publishing Comp. London.

Gaur, P.C., Gupta, P.K. and Kishore, H. 1978. Studies on genetic divergence in potato. Euphytica 27: 361-368.

Griffing, B and Lindststorm, E.W. 1954. A study of combining abilities of corn inbreds having varying proportions of corn belt and non-corn belt germplasm. Agron. J. 46: 545-552.

Jagadev, P.N., Samal, K.M. and Lenke, L. 1991. Genetic divergence in rape mustard. Indian J. Genet. 51: 465-466.

Jain, S.K., Quatest, C.O., Bhatt, G.M. and WU, K.K. 1975. Geographical patterns of phenotypic diversity in a collection of durum wheats. Crop Sci. 15: 700-704.

Kumar, M. and Nadarajan, N. 1994. Genetic divergence studies in soybean. Indian J. Genet. 54(3): 242-246.

Murty, B.R. and Arunachalam, V. 1996. The nature of genetic divergence in relation to breeding system in crop plants. Indian J. Genet. 26. 188-198.

Rahman, M.M. 1998. Genetic divergence in soybean. Progress. Agric. 9(1 &2): 185-187

Rao, C.R. 1952. Advanced statistical methods in Biometric Research. 1st Edu. John Wiely and Sons Inc., New York, pp. 357-364.

Tomooka, N. 1991. Genetic diversity and landrace differentiation of mungbean, *Vigna radiata* (L.) wilezek and evaluation of its wild relatives (the Subgenus Ceratotropics) as breeding materials. Tech. Bull. Trop. Res. Centre, Japan No. 28. Ministry of Agr, Forestry and Fisheries. Japan. p. 1.

Yang, Q. and Wang, J.L. 1997.Evaluation and utilization of Genetic potential of semicultivated soybeans.Proc.5th world soybean research conference. pp. 86-90.