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Genetic Diversity for Grain Yield and its Components in Soybean (*Glycine max* (L.)*

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ABSTRACT

Thirty four strains of soybean (*Glycine max*) were selected for the study. The D^2 statistic for the strain showed adequate diversity between strains with values ranging from 13.34 to 2095-91. On the basis of D^2 analysis the strains were grouped into 7 clusters with substantial genetic divergence between them. Cluster A and B were very large comprising of 11 strains each C-2 strains, D-4 strains, E-3 strains, F-2 strains and G-single variety cluster.

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INTRODUCTION

In breeing programmes selection of parents for hybridization is largely based on wide adaptation, high yield potential and genetic diversity. Progenies derived from a set of diverse crosses are expected to throw a broad spectrum of genetic variability providing larger scope for isolating high yielding segregants. The present study was undertaken to classify the available variability in diffeent groups giving information which will be helpful in planning the breeding programme.

MATERIALS AND METHODS

For the present study thirty four genotypes of soybean (*Glycine max*) showing varability for different characters were selected from the germplasm collected from the Maharashtra Association for the cultivation of Science, Pune and presently maintained by the Department of Botany, Konkan Krishi Vidyapeeth, Dapoli. These lines were grown in *kharif* season of 1992 in a randomised block design with two replications. In each replication, two rows of 2.6 m length for each variety were planted at spacing of 50 cm between and 20 cm within rows. Observations were recorded on five randomly selected plants for days to initiation of flowering, days for 50% flowering, days from anthesis to maturity, days for maturity, plant height, number of branches per plant, number of pods per plant, number of grains per pod, 100-grain weight and grain yield per plant.

The data were subjected to the statistical analysis as suggested by standard method of Mahalanobis (1936). The clustering

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of genotypes was done by Tochers method as described by Rao (1952) and Majumdar and Rao (1958).

RESULTS AND DISCUSSION

The thirty four strains were grouped into seven clusters. The distribution of thirty four strains in different clusters is given in Table-1. Cluster A and B was very large and comprised of 11 strains, while the cluster D had four strains, cluster E had 3 strains, cluster C and F had 2 strains and G comprised single strain.

The average intra and inter cluster D^2 values are presented in Table 2. The maximum statistical distance appreared between the cluster F and G (1694.291) followed by cluster E and G (1446.31), cluster

TABLE 1

Distribution of 34 strains in various clusters.

Cluster	*No.*	*Strains included*
A	11	MACS 27, MACS 392, MACS 243, MACS 239 MACS 124, MACS 321, MACS 375, MACS 381, MACS 396, MACS 329, MACS 338
B	11	Monetta, MACS 394, MACS 267, MACS 365, MACS 410, MACS 57, MACS 201, MACS 390, MACS 366, MACS 360, MACS 378
C	2	MACS 346, MACS 13
D	4	MACS 58, MACS 397, MACS 391, MACS 226
E	3	MACS 348, MACS 349, MACS 205
F	2	MACS 286, MACS 233
G	1	MACS 409

TABLE 2

Inter and intra cluster divergence (D^2) in soybean.

Cluster	*A*	*B*	*C*	*D*	*E*	*F*	*G*
A	116.030	366.463	180.167	178.439	183.447	374.574	988.74
B		96.968	226.557	274.922	637.529	855.457	269.10
C			20.280	322.419	432.763	630.778	650.89
D				82.361	223.078	411.190	791.21
E					90.780	272.709	1446.03
F						903.479	1694.291
G							0.000

TABLE 3

Cluster means for 10 characters.

Cluster No.	*Day to initiation of flowering*	*Dys to 50% flowering*	*Days from anthesis to maturity*	*Days to maturity*	*Plant height (cm)*	*No. of branches/ plant*	*No. of pods/ plant*	*No. of grains/ pod*	*100-grain weight (gm)*	*Seed yield/ plant (gm)*
A	41.50	44.41	59.36	113.59	66.92	4.74	61.46	2.30	13.01	18.71
B	40.04	42.77	49.54	105.73	47.95	4.66	43.76	2.05	14.75	13.74
C	43.25	45.00	59.00	116.00	41.95	5.10	35.82	2.15	13.72	10.96
D	39.37	43.12	53.25	106.87	80.56	4.71	55.99	2.31	13.95	18.48
E	44.33	46.50	60.17	115.00	85.95	6.38	81.90	2.36	8.72	17.04
F	43.00	46.25	61.00	114.25	88.22	5.32	67.75	2.19	10.22	15.71
G	36.00	37.50	43.00	94.00	29.25	7.45	42.15	1.89	16.35	13.91

A and G (988.674). The lowest degree of divergence was noticed in cluster A and D (178.493) followed by cluster A and C (180.167), suggested the close genetic make up among them.

An examination of Table 3 showed that the means for different characters of cluster G varied considerably from those of clusters F and E. This indicated that strain in cluster G might have entirely different genetic architechture from the strains cluster in clusters F and E. It is suggested that varieties from diverse clusters and having high yield potential thus might be useful in framing a suitable breeding programme since such crosses are expected to throw superior segregates.

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