

Association analysis, genetic variability and genetic diversity studies in soybean [*Glycine max* (L.) Merrill]

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To study the genetic variability, association analysis and genetic diversity for productivity in soybean, a field experiment was conducted during *Kharif* 2005 at University of Agricultural Sciences, Dharwad, India. The experiment comprised of 84 genotypes of which, most of the cultivars were released in India, along with some indigenous and exotic lines. Observations on 11 productivity traits of soybean were recorded. The data were subjected to variability and multivariate analysis. The analysis of variance revealed the prevalence of significant difference among the genotypes for all the 11 characters studied. Plant height was the only character which showed high phenotypic and genotypic co-efficient of variation while days to maturity, number of nodes per plant and oil content recorded a low phenotypic and genotypic coefficient of variation and rest of characters recorded moderate phenotypic and genotypic coefficient of variation. Number of pods per plant, pod weight per plant, 100 seed weight and oil content showed positive and significant correlation with seed yield per plant. Path coefficient analysis revealed maximum positive direct effect of pod weight on seed yield per plant followed by 100 seed weight and its indirect effect through other characters were also considerably high. Therefore, emphasis may be laid on this character for improving seed yield. There was not much amount of diversity was obtained in the material representing diverse eco-geographical regions of the country revealed no relationship between geographic diversity and genetic diversity.

Key words : Genetic variability, Genetic diversity, Soybean, Co-efficient of variation

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INTRODUCTION

Soybean [*Glycine max* (L.) Merrill] is known as 'Golden bean' and miracle crop of 20th century. Soybean is a native of North China, Asia belongs to family Fabaceae. It is a versatile and fascinating crop with innumerable possibilities of not only improving agriculture but also supporting industries. Soybean besides having high yielding potential (40-45 q/ha) also provides cholesterol free oil (20%) and high quality protein (40%). It is a rich source of lysine (6.4%) in addition to other essential amino acids, vitamins and minerals. Its oil is also used as a raw material in manufacturing antibiotics, paints, varnishes, adhesives and lubricants etc.

Soybean occupies a premier position among crops, being the most important source of both protein concentrates and vegetable oil. As a legume it is capable of utilizing atmospheric nitrogen through biological nitrogen fixation and is, therefore, much less dependent on synthetic nitrogenous fertilizers than most non-legume crops. In addition, since the introduction of

soybean into crop rotations often breaks the building up of pests and diseases in cereals.

Soybean tops in the world production of both oil seeds and edible oil. World harvest of soybean is more than 50 per cent of the total world oilseed production. United States of America (USA), the world leader in soybean production produces 40 per cent of world output with highest productivity of 2.5 t/ha. Apart from USA, China and Brazil are the leading soybean producers, while India ranks fifth in the world soybean production (Anonymous, 2005).

The feasibility for large scale cultivation of soybean in India could be demonstrated with yellow seeded, high yielding varieties introduced from USA in mid sixties (Paroda, 1991). Major soybean producing states in India are Madhya Pradesh, Maharashtra, Rajasthan, Karnataka and Andhra Pradesh. In Karnataka, it is being grown in an area of 1.78 lakh hectares during the year 2004-05 with the production of about 1.14 lakh tonnes with productivity level of 642 kg/ha.

Collection of genotypes and assessment of genetic variability is a basic step in any crop improvement programme. Yield being a complex character is influenced by a number of high yield contributing characters controlled by polygenes and also influenced by the environment. Hence, it becomes necessary to partition the observed variability into heritable and non-heritable components measured as genotypic and phenotypic coefficients of variation (GCV and PCV), heritability and genetic advance.

However, inheritance of quantitative character is often influenced by variation in other characters which may be due to pleiotropy or genetic linkage (Harland, 1939). Hence, knowledge of association between yield and its components obtainable through estimation of genotypic and phenotypic correlations helps in a great deal to formulate selection strategies to develop suitable genotypes.

Correlation coefficient merely describes the extent of association among the characters. But the relationship between two traits is not so simple. Such correlations can be resolved into direct and indirect effects by the method of path coefficient analysis developed by Wright (1921).

The observations for the last 25 years with respect to production trend was revealed that the soybean yield per hectare has made only modest advances in the past 25 years in the United States and other countries, however, it has not improved in India (Less than 1 t/ha). This is ascribed to narrow genetic base of soybean cultivars resulting in susceptibility to biotic (diseases and insects) and abiotic (unfavourable soils and erratic climatic conditions) stresses resulting in yield stagnation. Many of the Indian soybean varieties have narrow genetic base with more than 50 per cent of popular varieties trace back to only few ancestral lines. Although the rate of yield increase has remained constant, there are concerns that future breeding programmes will be limited by diversity constraints. For this, strategies for broadening genetic base of soybean in breeding and production have suggested (Tiwari, 2001) which comprised of enhancement of genetic resources, pre breeding and ultimate widening of genetic base of the cultivars.

RESEARCH METHODOLOGY

The material used in the study comprised of eighty four genotypes of soybean which includes most of the released varieties in India along with some indigenous and exotic lines, which are presently being maintained at All India Co-ordinated Research Project on Soybean, University of Agricultural Sciences, Dharwad, Karnataka, India. The present field experiment was conducted during *Kharif* 2005 at the Main Agricultural Research Station, University of Agricultural Sciences, Dharwad, Karnataka, India. The experiment consisted of 84 genotypes laid out in a Complete Randomized Block Design with three replications. The

entries were sown in one row each of 3.0 m length with a spacing of 45 cm between rows and 10 cm between the plants. The recommended package of practices was followed for raising a healthy crop. Observations were recorded on five randomly selected plants for different characters in each genotypes and replication. The data was subjected to Randomized Block Design as described by Panse and Sukhatme (1962). The mean values of the genotype in each replication were used for analysis of variance. The significant difference among genotypes was tested by 'F' test at one per cent and five per cent levels of probability. Genotypic and phenotypic coefficient of variability were computed according to Burton and Devane (1953).

Broadsense heritability was estimated based on the ratio of genotypic variance to the phenotypic variance and was expressed in percentage (Hanson *et al.*, 1956).

$$\text{Heritability (h}^2\text{)} = \frac{V_g}{V_p} \times 100$$

Genetic advance (GA) was computed according to the formula given by Johnson *et al.* (1955).

$$\text{Genetic advance (GA)} = ih^2 \sqrt{V_p}$$

The correlation coefficients were calculated to determine the degree of association of characters with yield. Phenotypic correlation coefficients were estimated according to the formula given by Al-Jibouri *et al.* (1958).

Mahalanobis (1928) D^2 statistic was used for assessing the genetic divergence between different populations. The D^2 analysis was carried out using the observations made during the *Kharif* 2004. Mahalanobis generalized distance (D^2) between any two population is given by the formulae.

$$D^2 = \delta_i \delta_j^r$$

RESEARCH FINDINGS AND ANALYSIS

The mean sum of squares due to various sources of variation for eleven characters are presented in Table 1. The analysis of variance revealed that, the prevalence of significant difference among the genotypes for all the 11 characters studied.

The value of mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability, genetic advance and genetic advance expressed as per cent mean for all the eleven characters studied are presented in Table 2. A close correspondence between the estimates of GCV and PCV was noted specially in case of days to flowering, pod weight per plant and oil content. Pod weight per plant and plant weight recorded high GCV and PCV estimates and seed yield per plant recorded high level of PCV and low GCV. Low estimates of PCV and GCV recorded for the character number of nodes per plant, days to maturity,

days to flowering and oil content. Low estimates of GCV and PCV culminated into low heritability and genetic advance. In broad sense heritability and genetic advance as per cent of mean were higher for plant height, number of branches, days to flowering, number of pods per plant, pod weight per plant, 100 seed weight and seed yield per plant. However, days to maturity and oil percentage showed moderate heritability with moderate genetic advance as per cent of mean, while number nodes per plant and number of seeds per pod showed moderate heritability with lower genetic advance as per cent of mean.

Estimates of heritability and genetic advance in combination are more important for selection than heritability alone. High heritability combined with high genetic advance observed for plant height, days to flowering, days to maturity and number of pods per plant showed that these characters were controlled by additive gene effects and phenotypic selection would be highly effective. Similar results were reported earlier by Singh *et al.* (1997) and Reddy *et al.* (2001).

To know the nature and magnitude of relationship existing between yield and its components characters as well as the association among the components character themselves, the phenotypic and genotypic correlations among the eleven characters are presented in Table 3 and 4. Phenotypic coefficient of variation was higher in magnitude than the genotypic coefficient of variation in respect of all the

characters. Plant height is the only character which showed high phenotypic and genotypic coefficient of variation, while number of branches, days to flowering, number of pods per plant, pod weight per plant, 100 seed weight and seed yield per plant exhibited moderate phenotypic and genotypic coefficient variation. Days to maturity, number of nodes per plant and oil content recorded a low phenotypic and genotypic coefficient of variation.

These results are in consonance with those of Tomar *et al.* (1999) and Singh *et al.* (1997).

Genetic divergence along with genetic variability are of greatest interest to the plant breeder as they play a vital role in framing a successful breeding programme. Analysis of genetic divergence has been used to quantify, a) The genetic distance between the genotypes b) To identify promising types to initiate crossing programme and c) To relate clustering pattern to a geographical origin. There was not much amount of diversity was obtained in the material representing diverse eco-geographical regions of the country revealed no relationship between geographic diversity and genetic diversity. All the 84 genotypes were grouped into five clusters based on D² analysis. Cluster-II was the biggest with 75 genotypes followed by cluster-III and cluster-I. The grouping of 75 genotypes in cluster-II alone indicates similarity in their genetic constitution. Remaining clusters-IV and cluster-V were solitary clusters. The D² values ranged from 0.00 to 246.86 and intracluster D² values exhibited a range of 0.00 to 32.69 and inter

Table 1: Analysis of variance for eleven characters in soybean

Source	d. f.	Plant height	No. of branches	Days to flowering	Days to maturity	No. of nodes/pl	No. of pods/pl	No. of seeds/pod	Pod weight/pl	100-seed weight	Oil content	Seed yield/pl
Replication	2	81.71	0.34	4.01	40.92	8.89	18.75	0.12	5.31	460.23	25.39	33.5
Genotypes	83	6.84**	6.94**	816.31**	11.56**	62.33**	106.84**	6.84*	136.51**	9.39**	48.52**	10.94**
S.E.	-	8.61	0.24	0.73	9.51	0.41	0.67	0.21	0.21	0.11	0.19	0.33
C.D. (P=0.05)	-	17.13	0.48	1.45	18.92	0.82	1.33	0.42	0.42	0.22	0.38	0.66
C.D. (P=0.01)	-	22.73	0.63	1.93	25.11	1.08	1.77	0.55	0.55	0.29	0.50	0.87

** indicates significance of value at P=0.05

Table 2: Estimates of range, mean and different genetic parameters for different characters in 84 soybean genotypes

Characters	Mean	Range	GCV	PCV	h ²	GA	GAM
Plant height (cm)	45.12	21.12-78.12	30.59	38.49	63.20	22.63	50.16
Number of branches per plant	3.28	2.14-4.27	13.67	16.47	68.80	0.77	23.48
Days to flowering	38.15	27.12-56.34	13.61	13.81	97.12	10.53	27.60
Days to maturity	93.13	74.65-109.12	2.75	12.81	46.12	11.14	11.96
Number of nodes per plant	11.42	8.47-14.97	6.35	9.53	44.50	0.33	8.82
Number of pods per plant	33.73	23.78-48.75	13.64	17.81	76.58	8.14	24.13
Number of seeds per pod	2.44	2.12-2.95	9.79	15.87	38.06	0.23	9.43
Pod weight per plant (g)	12.28	7.32-16.88	18.89	19.62	98.60	4.36	35.50
100 seed weight (g)	11.89	8.45-16.71	13.01	16.85	59.70	2.54	21.36
Oil content (%)	16.96	13.90-19.96	7.46	7.58	96.70	2.56	15.09
Seed yield per plant (g)	9.64	4.56-15.42	13.23	20.4	65.50	2.52	26.14

Table 3: Phenotypic correlations among the eleven traits studied in soybean

Traits	Plant height	No. of branches	Days to flowering	Days to maturity	No. of nodes/pl	No. of pods/pl	No. of seeds/pod	Pod weight/pl	100-seed weight	Oil content	Seed yield/pl
Plant height	1	0.49**	0.461**	0.46**	0.425*	0.066	0.023	-0.12	-0.277**	-0.261**	0.059
No. of branches		1	0.06	0.526**	0.414*	0.011	0.356**	-0.035	-0.209*	-0.171	0.02
Days to flowering			1	0.363**	0.139	0.316**	-0.03	-0.03	0.06	-0.353**	-0.07
Days to maturity				1	0.148	0.257	-0.007	-0.007	0.042	-0.126	-0.039
No. of nodes/pl					1	0.382**	0.059	-0.049	-0.092	-0.074	-0.053
No. of pods/pl						1	0.052	0.580**	0.079	0.016	0.671**
No. of seeds/pod							1	-0.145	0.031	-0.003	0.153
Pod weight/pl								1	0.330**	0.039	0.910**
100-seed weight									1	0.058	0.334**
Oil content										1	0.205*
Seed yield/pl											1

* and ** indicate significance of values at P=0.05 and P=0.01, respectively.

Table 4: Genotypic correlations among the eleven traits studied in soybean

Traits	Plant height	No. of branches	Days to flowering	Days to maturity	No. of nodes/pl	No. of pods/pl	No. of seeds/pod	Pod weight/pl	100-seed weight	Oil content	Seed yield/pl
Plant height	1.00	0.758**	0.591**	0.27**	0.544**	0.09	0.032	-0.14	-0.306**	-0.375**	0.09
No. of branches		1.00	0.08	0.947**	0.543**	0.13	0.450**	-0.04	-0.213**	-0.225*	0.01
Days to flowering			1.00	0.687**	0.15	0.421**	-0.14	-0.210*	0.080	-0.366**	-0.07
Days to maturity				1.00	0.208*	0.097	-0.015	-0.074	-0.334	0.120	-0.16
No. of nodes/pl					1.00	0.283**	0.090	-0.05	-0.220*	-0.08	-0.06
No. of pods/pl						1.00	0.07	0.690**	0.110	-0.320**	0.692**
No. of seeds/pod							1.00	0.13	0.170	-0.03	0.10
Pod weight/pl								1.00	0.379**	0.04	0.938**
100-seed weight									1.00	-0.210*	0.353**
Oil content										1.00	0.295**
Seed yield/pl											1.00

* and ** indicate significance of values at P=0.05 and P=0.01, respectively.

cluster D² values 61.82 to 246.86. Bhatt (1970) reported that the crosses between genotypes belonging to the clusters having maximum inter cluster distance will yield better recombinants. The characters contributing maximum to D² values are given greater emphasis for deciding the clusters for the purpose of future selection and choice of parents for hybridization. Among the characters studied, days to maturity contributed maximum towards the genetic divergence followed by plant height. Similar results have also been reported by Kumar

and Nadarajan (1994), Jaylal (1994) and Ramana and Satyanarayana (2006). Satyavathi *et al.* (2003) studied the genetic base of 66 soybean varieties of India and reported that the narrow genetic base of the Indian soybean varieties is because of repetitive of the same parents for the development of the genetic stock or breeding material. The efficient use of unexploited variability available the problem of narrow genetic base and simultaneously improve the average soybean productivity.

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