GENETIC VARIABILITY AND ASSOCIATION ANALYSIS IN SOYBEAN (*Glycine max*)

THESIS

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Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya,

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By

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CERTIFICATE – I

This is to certify that the thesis entitled “Genetic variability and association analysis in soybean (*Glycine max*)” submitted in partial fulfilment of the requirement of the degree of Master of Science in Agriculture (Plant Breeding & Genetics) of the Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior is a record of the bonafide research work carried out by Shri Mahendra Chachria under my guidance and supervision. The subject of the thesis has been approved by Students Advisory Committee and the Director of Instruction.

No part of the thesis has been submitted for any degree or diploma (Certificate/award etc.) or has been published. All the assistance and help received during the course of investigations have been duly acknowledged by him.

Place : Gwalior

Date :

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CERTIFICATE – II

This is to certify that the thesis entitled "Genetic variability and association analysis in soybean (*Glycine max*)*"* submitted by Shri Mahendra Chachria to the Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior in partial fulfilment of the requirements for the degree of M.Sc. (Ag.) in the Department of Plant Breeding & Genetics, College of Agriculture, Gwalior, has after evaluation, been approved by the external examiner and by the Students Advisory Committee after an oral examination of same.8

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Place: Gwalior

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CHAPTER I
INTRODUCTION

Soybean (*Glycine max* (L). Merill) occupies a unique position among legumes. Most of the food legumes (pulses) are rich in protein but contain limited amount of oil. Soybean contains 40-42% protein and 20-22% of edible oil (Gopalan *et al.*, 1994). It is also rich in lysine (5%), an essential amino acid that is deficient in most of the cereal based diets. Therefore the quality of soy protein is now recognized as being similar to that of meat protein. The edible oil in soybean is approximately 85 percent unsaturated and contains the essential fatty acids. This crop is also a good source of vitamins A, B and D. Soybean is a member of Papilionaceae family and believed to have originated in North Eastern China. This crop is called as "Golden Bean" or "Miracle Crop" of the 20th century, because of its multiple uses. In addition to the nutritional advantages, soybean is also recognized for its benefits to human health such as the cholesterol lowering effect of protein as approved recently by the United States Food and Drugs administration.

Soybean ranks first among the oilseeds in the world. In international market soybean oil trading is next only to palm oil. The crop contributes for nearly 25% of the world's total oil and fats production. In 2010-11 the area under soybean in India was 9.60 Million ha. with a production of 9.60 Metric tones and productivity of 930 kg/ha. The USA, Argentina, Brazil, China and India are the major producer of soybean accounting for 90% of world production. In M.P.(2010-11) area under soybean production was 57.3 Lakh ha. with a productivity of 1076 kg/ha.

Collection of germplasm 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 yield contributing characters controlled by polygenes and also influenced by environment. So, the variability in the collections for these characters is the sum total of heredity effects of concerned genes plus the influence of 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 expressed as percent mean.

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

Most of the times, it may not be possible to identify the desirable genotype from the collections. In such cases, variability will have to be created on which selection can be practiced to identify desirable genotypes from segregating populations. Of the different ways of creating such variability, hybridization is the most widely and commonly used technique in almost all the crop species including soybean. For creating desirable variability, parents should be selected carefully and some biometrical tools can be used. Diversity among genotypes through Mahalanobis D^2 technique is a very useful device.

Soybean being a potential legume crop of India has immense scope for genetic improvement for various qualitative and quantitative characters besides widening the genetic base through induced mutagenesis. Keeping in view all these aspects, the present study in soybean was conducted with the following objectives:

1. To estimate the genetic variability among genotypes.
2. To asses the extent of association among yield contributing characters.
3. To estimate the direct and indirect effects of yield contributing characters on seed yield in soybean.
4. To estimate genetic diversity in genotypes through *D^2 analysis.*

CHAPTER III

MATERIALS AND METHODS

The experimental material used and the method applied during the course of present investigation has been described below.

3.1. Experimental site

The experiment was conducted in the experimental area of College of Agriculture, Gwalior; M.P. the field was fairly uniform with gentle slope, adequate drainage and normal fertility status

3.2. Experimental material

The experimental material consisted 39 genotypes of soybean collected from College of Agriculture, Gwalior. Details of genotypes used in present investigation are given in Table 3.2.

3.3. Experimental details

The experiment was done in Randomized Complete Block Design (RCBD) with three replications and seeds were sown on 13th July 2012. The row length was 3m and the number of rows per plot was 3 with row to row spacing was 30 cm. the space between plant to plant was maintained at 7.5 cm.

A random selection of five plants in each plot was made and the observations were recorded on each selected plant. The mean values of each character under study were computed on the basis of five plants for each genotype in each replication.

Table 3.1: Detail of experimental material used for present investigation

Entry No.	Name of entries	Entry No.	Name of entries
1	RVS 2006-1	21	KDS 693
2	MACS 1407	22	NRC 92
3	RSC 10-01	23	VLS 85
4	NRC 94	24	ASB 22
5	DS 2705	25	AMS 358
6	RKS 115	26	KDS 708
7	DSB 22	27	MAUS 612
8	AMS 475	28	KBS 22-2009
9	SL 982	29	JS 20-69
10	Himso 1684	30	NRC 91
11	VLS 84	31	PS 1520
12	JS 20-71	32	MACS 1394
13	KDS 705	33	SL 925
14	MAUS 614	34	CSB 904
15	RSC 01-05	35	AMS 77
16	NRC 93	36	RKS 113
17	PS 1518	37	JS 95-60 (check)
18	MACS 1416	38	JS 335 (check)
19	PS 1521	39	JS 93-05 (check)
20	SL 979		

3.4. Observation recorded

The following observations were recorded on 5 plants for each entry:

1. Days to 50% flowering:

Number of days taken from the date of sowing to the day on which 50% of the plants in a genotype initiate first flower was recorded as days to flowering.

2. Days to maturity

Number of days taken from date of sowing to physiological maturity of the plant was recorded as days to maturity.

3. Plant height (cm)

Height of the main stem from the ground level to the top of the main stem was measured in centimeters at the time of harvesting.

4. Number of primary branches per plant

The number of primary branches per plant was recorded as total number of primary branches on the main stem.

5. Number of pods per plant

This was recorded by counting the number of pods present on main stem and branches in each of the five selected plants.

6. Number of seeds per pod

Number of seeds per pod was counted from fifty randomly selected pods in each of the five selected plants.

7. 100 grain weight (g)

100 seed weight was computed by weighing 100 seeds which are randomly chosen filled seeds from a complete sample made by mixing the seeds of all the five plants in each replication and recorded in grams.

8. Grain yield per plant (g)

The grain yield per plant was recorded from each selected individual after harvest.

3.5 Statistical analysis:

1. Analysis of variance:

Data were analysed by method outlined by Panse and Sukhatme (1954) using the mean values of five randomly selected plants in each treatment for each replication. The model of analysis of variance table is given below:

ANOVA table for the design of experiment:

Source	Degree of freedom	Mean sum of squares	Variance ratio
Replication	(r-1)	M_r	M_r/M_e
Treatment	(t-1)	M_t	M_t/M_e
Error	(r-1) (t-1)	M_e	-
Total	rt-1	-	-

where, r = Number of replications

t = Number of treatments

2. Estimation of phenotypic and genotypic coefficients of variation:

The phenotypic and genotypic coefficients of variation in per cent were computed by the following formulae given by Burton (1952).

$$\text{Phenotypic Coefficient of Variation (PCV)} = \frac{\text{Phenotypic standard deviation}}{\text{Mean}} \times 100$$

$$\text{Genotypic Coefficient of Variation (GCV)} = \frac{\text{Genotypic standard deviation}}{\text{Mean}} \times 100$$

The PCV and GCV values are ranked as low, medium and high (Shivasubramanian and Menon, 1973) and are mentioned below:

0-10% - Low
10-20% - Moderate
>20% - High

3. Estimation of heritability and genetic advance:

Heritability in per cent in broad sense was estimated by the following formula given by Singh and Choudhary (1977):

$$\text{Heritability } (h^2) = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}} \times 100$$

Heritability values are catagorised as low, moderate and high (Robinson *et al.,* 1949) and are given below,

0-30% - Low
30-60% - Moderate
60% and above - High

The estimates of expected genetic advance from selection, G(s), was obtained by the formula suggested by Robinson *et al.* (1949).

$$G(s) = k \times h^2 \times \sigma p$$

where,

k = Selection differential in standard deviation units which is 2.06 for 5% selection intensity,

h^2 = Heritability in broad sense, and

σ_p = Phenotypic standard deviation

Genetic advance was expressed as percentage of mean by using the formula suggested by Johnson *et al*.(1955).

$$\text{Genetic advance as percentage of mean} = \frac{\text{Genetic advance}}{\text{Grand mean}} \times 100$$

Genetic advance as percent of mean was classified as low, moderate and high (Johnson *et al*., 1955) and values are given below:

0-10% - Low

10-20% - Moderate

20% and above - High

4. Estimation of correlations coefficients:

Phenotypic, genotypic and environmental correlation coefficients between characters were computed utilizing respective components of variance and co-variance, by following formula suggested by Miller *et al.* (1958).

$$r_{xy} = \frac{\text{Covariance x, y}}{\sqrt{(\text{Variance x}) \times (\text{Variance y})}}$$

where,

r_{xy} = Correlation coefficient between character x and y,

To test the significance of correlation coefficients, the estimated values were compared with the tabulated values of Fisher and Yates (1938) at t-2 d.f. at two levels of probability, viz., 5% and 1%.

5. Path coefficient analysis:

The proportion of direct and indirect contributions of various characteristics to the total correlation coefficients with grain yield per plant, was estimated through path coefficient analysis as suggested by Wright (1921, 1934) and elaborated by Dewey and Lu (1959).

Path coefficient is a standardized partial regression, which measures the direct influence of one variable upon another and allows partition of correlation coefficient into components of direct and indirect effects.

To estimate various direct and indirect effects, the following set of simultaneous equations were formed and solved.

$r_{1y} = P_{1y} + r_{12}P_{2y} + r_{13}P_{3y} + \ldots + r_{1I}P_{Iy}$

$r_{2y} = r_{2y}P_{1y} + P_{2y} + r_{23}P_{3y} + \ldots + r_{2I}P_{Iy}$

.

.

$r_{Iy} = r_{I1}P_{1y} + r_{I2}P_{2y} + r_{I3}P_{3y} + \ldots + P_{Iy}$

where,

r_{1y} to r_{Iy} = Coefficient of correlation between causal factor 1 to I and dependent character y,

r_{12} to $r_{I-1,I}$ = Coefficient of correlation among causal factors themselves, and

P_{1y} to P_{Iy} = Direct effects of characters 1 to I on character y.

Residual effect, which measures the contribution of the characters not considered in the causal scheme, was obtained as:

Residual effect (P_{RY}) = $\sqrt{1 - R^2}$

where,

$$\mathbf{R^2} = \sum_{iy} P_{iy}^2 + 2\sum_{\substack{i\neq j \\ i>j}} P_{iy}\, P_{jy}\, r_{ij}$$

6. Multivariate analysis:

(a) Estimation of Wilk's (Λ) criterion:

To test the significance of difference between lines, taking all the characters simultaneously, 'V' statistic was calculated which was based on Wilk's (Λ) criterion (Wilk). The sum of squares and sum of products of error and error + variety were utilized for estimation of "Λ".

To calculate the value of "Λ" following relationship was used:

$$\text{"}\Lambda\text{"} = \frac{|E|}{|E+V|}$$

where,

$|E|$ was the determinant of error sum of squares and sum of products matrix and $|E+V|$ was the determinant of the "error + variety' sum of squares and sum of products matrix.

χ^2 was used to test the significance of "Λ" as

$$\chi^2_{pq} = V = -m \log_e \Lambda$$

where,

m = n - $\frac{p+q+1}{2}$ with pq degree of freedom.

where,

n = total number of observations –1,

p = number of characters,

q = k – 1, and

k = number of lines

(b) Estimation of D^2-statistic:

To estimate divergence between two lines Mahalanobis (1936) D^2- statistic was used. He defined generalized distance between two lines as:

$$\Delta^2 = \sum\sum \lambda^{ij} \delta_i \delta_j$$

where,

λ^{ij} = Reciprocal matrix of the common dispersion matrix λ_{ij},

δ_i = Difference between mean values of two lines for the i^{th} character, and

δ_j = Difference between mean values of two lines for the j^{th} character.

D^2-statistic is the sample estimate of the generalized distance which is estimated as:

$$D^2 = \sum_{i,j=1}^{P} s^{ij} d_i d_j$$

where, s^{ij} and d_i are the sample estimates of λ^{ij} and δ_i, respectively. For calculating D^2 values inversion of matrix was required which is quite cumbersome. To overcome this difficulty original correlated, unstandardized character means (X_i) were transformed to uncorrelated, standardized variables (Y_i) by Pivotel condensation method (Rao, 1952). D^2 between any pairs of populations, for example population 1 and 2, was then estimated as:

$$D_p^2 = \sum_{i=1}^{p} (Y_{i1} - Y_{i2})^2$$

where, p = number of characters used for estimation of divergence.

(c) Determination of population constellations:

Population constellations were determined by Tocher's method described by Rao (1952). A cluster or constellation may be explained as a group of populations or genotypes such that any two populations belonging to the same cluster showed, on the average, a smaller D^2 value than those belonging to different clusters.

Tocher suggested that two closely related populations of low D^2 value be pooled together and then a third population of similar D^2 value be added to this group such that it did not increase the average D^2 value appreciably. This process is continued. Any population, which sharply increases the average D^2 value should not be included in that group.

After formation of first cluster, the process is repeated to form second, third clusters, using remaining populations until all populations are included in one or the other cluster. After cluster formation average intra and inter-cluster distances were calculated. The square root of corresponding average D^2 values represents the distance within and between groups.

(d) Canonical analysis:

To visualize multidimensional picture of variability among genotypes canonical analysis was done. Canonical roots were estimated by transformation of correlated, unstandardized means into uncorrelated, standardized variables (Rao, 1952). From these uncorrelated standardized variables, matrix of variance and covariance (matrix A) was obtained by computing sums of squares and sums of products. From matrix A, matrix $(A)^p$ was derived, where p is the number of characters. The column totals of matrix $(A)^p$ were obtained and each total was divided by the highest value among them to obtain the first approximation trial vector. The canonical variates were determined by iteration. The vectors were then standardized by dividing them with correlated sum of squares of these vectors. The first root, λ_1, was calculated as the p^{th} root of the highest column total of the last approximation.

The second root, λ_2, was obtained by transforming the original $(A)^p$ matrix to reduced matrix $(B)^p$. Each $i \times j^{th}$ element of $(B)^p$ was calculated as: $(i, j)^{th}$ element of $(A)^p = \lambda_1 \times i^{th}$ element $\times j^{th}$ element of the vector.

Estimation of second and third canonical root was done following the same procedure as in the case of 'A' was followed. The utility of estimation of other roots depends on the proportions of the sum of squares accounted for by the first three roots.

CHAPTER-IV
RESULTS

The present experiment was carried out during *kharif* 2012 at experimental area of College of Agriculture, Gwalior; M.P to assess the nature and extent of genetic variability and diversity among 39 genotypes. Yield and yield components recorded were used to estimate the variability parameters, character association and diversity in the material. The experimental results are presented under the following headings:

1. Analysis of variance
2. Mean performance
3. Phenotypic and genotypic coefficient of variation
4. Heritability
5. Genetic advance
6. Genetic divergence
7. Canonical analysis
8. Correlation studies
9. Path analysis

1. Analysis of variance:

The mean sum of squares due to various sources of variation for 8 characters viz., days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of pods per plant, number of seeds per pod, 100 grain weight and grain yield per plant are presented in Table 4.1. The variation due to genotypes was significant for all the studied characters except number of seeds per pod under study at 1 per cent probability levels.

2. Mean performance:

The mean values of eight characters for thirty nine genotypes are presented in Table 4.2 and Appendix-I.

(i) Days to 50% flowering:

The range for days to 50% flowering was from 40.33 to 55.00 days with around a mean value of 45.29 days. The minimum days required for 50% flowering were recorded by PS 1520 followed by KDS 705, ASB 22, Himso 1684, VLS 84,

RKS 115, MAUS 612 and RKS 113 while maximum by NRC 92. Twenty one genotypes were below the grand mean.

Table 4.1: Analysis of variance for eight quantitative characters in soybean

S. No.	Characters	Mean sum of squares		
		Replication	Genotypes	error
1.	Days to 50% flowering	0.8281	40.8278**	3.7501
2.	Days to maturity	2.6250	147.1885**	1.6064
3.	Plant height (cm)	20.4062	660.5991**	7.3462
4.	Number of primary branches/plant	0.3675	4.1718**	0.8499
5.	Number of pods/plant	10.4062	880.3112**	43.6384
6.	Number of seeds/pod	2.3163	0.5996	0.7899
7.	100 grain weight (g)	1.4443	5.1218**	0.6431
8.	Grain yield/plant (g)	0.8730	35.6936**	1.9637

** Significant at p=0.01

(ii) Days to maturity:

The range for days to maturity varied from 83 days (RSC 01-05) to 108 days (KBS 22-2009) with a mean value of 97.20 days. Eighteen genotypes were below the grand mean.

(iii) Plant height:

The variability observed for plant height was high, as reflected by its wide range from 24.43 cm (RVS 2006-1) to 79.47 (KDS 705) with mean value of 46.14 cm. Sixteen genotypes have exceeded the grand mean of 46.14 cm.

(iv) Number of primary branches per plant:

The mean number of branches per plant ranged from 3.00 (RVS 2006-1) to 7.67 (NRC 94) with an overall mean value of 5.19. Seventeen genotypes have exceeded the grand mean.

(v) Number of pods per plant:

The range for number of pods per plant was from 25.33 to 107.67. The entry KDS 708 recorded the maximum while the entry RVS 2006-1 recorded the minimum. Eighteen genotypes exceeded the general mean of 54.91.

(vi) Number of seeds per pod:

A range of 2.00 to 3.33 was observed for number of seeds per pod. The mean value for this trait was 2.62. The genotype MAUS 612 had a mean of 3.33 for number of seeds per pod.

(vii) 100 grain weight:

It ranged from 10.70 to 16.08 g with a grand mean of 12.90 g. The maximum was recorded by genotype SL 982 and the minimum by PS 1518. Eighteen genotypes have exceeded the grand mean.

(viii) Grain yield/plant:

Grain yield per plant ranged from 5.61 to 21.14 g. Entry KDS 708 recorded the maximum yield followed by NRC 94 while the minimum by AMS 358. Eighteen genotypes have exceeded the general mean of 12.08 g.

3. Phenotypic and genotypic coefficients of variation (PCV and GCV):

The estimates of phenotypic and genotypic coefficient of variation were worked out and are presented in Table 4.2. The highest genotypic coefficient of variation (GCV) of 31.98 per cent was observed for plant height followed by number of pods per plant, grain yield per plant and number of primary branches per plant recording 30.41, 27.75 and 20.28 per cent, respectively. The characters number of seeds per pod, days to maturity, days to 50% flowering and 100 grain weight recorded the low estimate of GCV. The highest estimate of phenotypic coefficient of variation (PCV) i.e. 33.89% was noted with number of seeds per pod followed by number of pods per plant, plant height, grain yield per plant and number of primary branches per plant recording 32.70, 32.52, 30.08 and 26.97 per cent, respectively. The character 100 grain weight recorded the moderate PCV of 11.33 per cent. The low estimate of PCV of 7.28% was registered with days to maturity followed by days to 50% flowering (8.86%).

4. Heritability:

The maximum heritability estimate of 96.80 per cent was recorded for days to maturity followed by plant height (96.70%), number of pods per plant (86.50%), grain yield per plant (85.10%), days to 50% flowering (76.70%) and 100 grain weight (69.90%). The character number of primary branches per plant recorded moderated heritability estimate of 56.60 per cent while the lowest heritability estimate of 0.10 per cent was registered for number of seeds per pod.

5. Genetic advance:

The genetic advance as percentage of mean ranged from 0.00 to 64.81 per cent. The maximum (64.81%) and minimum (0.00%) were recorded for plant height and number of seeds per pod, respectively. The characters, number of pods per plant, grain yield per plant and number of primary branches per plant, also recorded high genetic advance as per cent of mean, the values being 58.25 per cent, 52.72 per cent and 31.42 per cent respectively. The moderate genetic advance as per cent of mean, 16.28 per cent, was recorded by 100 grain weight followed by days to maturity and days to 50% flowering recording 14.53 per cent and 14.00 per cent respectively.

Table 4.2: Estimation of range, mean and different genetic parameters for different characters in 39 genotypes of soybean

S. No	Characters	Mean	Range	PCV (%)	GCV (%)	Broad sense Heritability (%)	Genetic advance	Genetic advance as % of mean
1	Days to 50% flowering	45.29	40.33-55.00	8.86	7.76	76.70	6.34	14.00
2	Days to maturity	97.20	83.00-108.00	7.28	7.17	96.80	14.12	14.53
3	Plant height (cm)	46.14	24.43-79.47	32.52	31.98	96.70	29.90	64.81
4	Number of primary branches/plant	5.19	3.00-7.67	26.97	20.28	56.60	1.63	31.42
5	Number of pods/plant	54.91	25.33-107.67	32.70	30.41	86.50	31.99	58.25
6	Number of seeds per pod	2.62	2.00-3.33	33.89	1.21	0.10	0.00	0.00
7	100 grain weight (g)	12.90	10.70-16.08	11.33	9.47	69.90	2.10	16.28
8	Grain yield/plant (g)	12.08	5.61-21.14	30.08	27.75	85.10	6.37	52.72

6. Genetic divergence:

Genetic divergence along with genetic variability is of greatest interest to the plant breeder as they play a vital role in framing a successful breeding programme The analysis of variance at univariate level revealed highly significant differences among genotypes for all most of the characters (except number of seeds per pod) under investigation thereby indicating the presence of a considerable magnitude of genetic variability among 39 genotypes of soybean for these characters. From the estimate of variance and co-variance, v-statistic, which utilizes Wilk's criterion a simultaneous test of significance of difference for the aggregate effect of all the eight characters was done, which also showed highly significant differences among the thirty nine genotypes of soybean (χ^2 = 1413.28 for 304 d.f.). Thus the analysis of genetic divergence among the genotypes taken for study was considered to be relevant.

(a) D^2 analysis:

D^2 analysis was carried out using all the 8 characters and generalized distance (D^2) was calculated for each pair of genotypes among 741 possible combinations. The values of D^2 indicates that the highest D^2 values of 1073.04 were observed between the genotypes NRC 94 and RSC 01-05 and the smallest D^2 value of 4.77 between the genotypes Himso 1684 and JS 20-69.

(i) Group constellations

A method suggested by Tocher (Rao, 1952) was used to group the genotypes into different cluster based on D^2 values. Thirty nine genotypes were grouped into 12 clusters. Among 12 clusters, clusters III and VII were biggest with 6 genotypes each, followed by clusters IX, X and XI with 4 genotypes each, clusters II and V contains 3 genotypes each and clusters I, IV, VIII and XII contained 2 genotypes each. The cluster VI was solitary containing single genotype.

Table 4.3: Distribution of 39 genotypes into different clusters

S. No.	Cluster No.	No. of genotypes	Name of genotype
1	I	2	**RVS 2006-1, AMS 358**
2	II	3	**KDS 705, PS 1518, RKS 113**
3	III	6	**NRC 93, MACS 1416, PS 1521, SL 979, SL 925, AMS 77**
4	IV	2	**RSC 10-01, SL 982**
5	V	3	**RSC 01-05, MAUS 612, JS 95-60 (check)**
6	VI	1	**NRC 92**
7	VII	6	**RKS 115, Himso 1684, KDS 693, JS 20-69, NRC 91, CSB 904**
8	VIII	2	**DS 2705, KBS 22-2009**
9	IX	4	**DSB 22, AMS 475, MAUS 614, ASB 22**
10	X	4	**JS 20-71, VLS 85, PS 1520, JS 335 (check)**
11	XI	4	**MACS 1407, VLS 84, MACS 1394, JS 93-05 (check)**
12	XII	2	**NRC 94, KDS 708**

(ii) The intra and inter-cluster average distance:

The average D^2 values of intra and inter cluster distance are given in Table 4.4. Maximum differences among the genotypes within the same cluster (intra cluster) was shown by cluster XI (2.277) followed by cluster II (1.844), while cluster VI had the lowest intra cluster distance of 0.000 followed by cluster IV (0.605) and cluster I (0.951). Inter cluster distances varied from 2.983 to 59.305. Cluster I and XII showed maximum inter cluster distance (59.305) followed by clusters V and XII (51.567), cluster I and IV (36.542), cluster I and VI (36.325), cluster XI and XII (35.058), cluster III and XII (32.936) and cluster I and VIII (32.058). The lowest inter cluster distance was noticed between cluster III and VII (2.983) followed by cluster IX and X (3.912), cluster II and IX (4.631), cluster VII and X (4.670), cluster III and XI (4.933) and cluster VII and IX (5.660). Cluster XII followed by cluster I was farthest to other clusters.

(iii) Cluster mean:

Clusters means of all 10 characters are presented in Table 4.5.

1. Days to 50% flowering:

The cluster mean was highest (55.00) for cluster Vi and lowest (42.44) for cluster II.

2. Days to maturity:

Cluster mean was highest (103) for cluster XII and lowest (86.89) for cluster V.

3. Plant height:

Cluster mean was highest (74.09) for cluster II and lowest (26.52) for cluster I.

Table 4.4: Average intra and inter cluster D^2 values of 39 soybean genotypes

Cluster	**I**	**II**	**III**	**IV**	**V**	**VI**	**VII**	**VIII**	**IX**	**X**	**XI**	**XII**
I	0.951	23.021	9.493	36.542	8.503	36.325	13.697	32.058	21.613	20.467	7.161	59.305
II		1.844	12.229	26.688	18.370	19.803	13.720	10.208	4.631	6.812	14.938	20.940
III			1.801	14.040	8.803	21.372	2.983	9.505	10.745	8.762	4.933	32.936
IV				0.605	28.708	18.671	14.615	12.194	18.114	19.158	15.658	16.104
V					1.623	22.582	6.457	20.250	9.604	10.916	7.667	51.567
VI						0.000	20.088	9.260	13.720	10.949	28.058	19.847
VII							1.474	11.560	7.579	4.670	5.660	31.956
VIII								1.438	9.357	8.597	19.794	18.207
IX									1.371	3.912	9.394	21.465
X										1.217	12.334	20.757
XI											2.277	35.058
XII												1.518

4. Number of primary branches per plant:

Cluster mean was highest (7.50) for cluster XII and lowest (3.50) for cluster I.

5. Number of pods per plant:

Cluster mean was highest (101.00) for cluster XII and lowest (30.67) for cluster I.

6. Number of seeds per pod:

Cluster mean was highest (3.11) for cluster V and lowest (2.00) for cluster I and XII.

7. 100 grain weight:

Cluster mean was highest (15.21) for cluster IV and lowest (11.14) for cluster II.

8. Grain yield per plant:

Cluster mean was highest (20.75) for cluster XII and lowest (6.41) for cluster I.

Cluster characteristics:

Table 4.5 revealed that cluster I was characterized by number of tillers per plant and spike length, which had highest mean values for these traits.

Cluster I was characterized by plant height and days to maturity, which had lowest values for these traits.

Cluster II was characterized by days to 50% flowering, which had lowest value for this trait and by plant height, which had highest mean value for this trait.

Cluster IV was characterized by 100 grain weight, which had highest value for this trait

Cluster V was characterized by days to maturity, which had lowest value for this trait and by number of seeds per pod, which had highest mean value for this trait.

Clusters VI and VIII were characterized by number of seeds per pod, which had higher value for this trait.

Clusters VII and XI were characterized by days to 50% flowering, which had lower value for this trait.

Clusters Ix and X were characterized by days to 50% flowering, which had lower mean values for this trait and by number of seeds per pod, which had higher mean values for this trait.

Cluster XII was characterized by grain yield per plant, number of primary branches per plant, number of pods per plant and plant height, which had highest values for these traits.

Cluster III did not show desirable mean for any of the traits.

Table 4.5: The mean values of eight characters in 12 clusters in 39 soybean genotypes

Cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of pods per plant	Number of seeds per pod	100 grain weight (g)	Grain yield per plant (g)
I	44.50	88.17	26.52	3.50	30.67	2.00	12.03	6.41
II	42.44	96.33	74.09	5.89	63.22	2.56	11.14	10.46
III	46.33	103.61	40.41	4.28	42.17	2.44	12.72	10.58
IV	51.00	106.83	42.83	6.67	56.50	2.17	15.21	17.22
V	45.56	86.89	34.47	4.33	37.67	3.11	13.33	8.24
VI	55.00	90.33	49.27	6.00	83.00	3.00	11.85	15.93
VII	43.39	100.06	33.34	4.56	49.78	2.89	13.37	12.88
VIII	50.33	107.50	56.77	6.17	73.50	3.00	12.35	11.04
IX	43.67	91.25	61.78	6.25	58.83	2.92	13.13	12.06
X	43.58	94.92	44.65	5.58	65.00	3.00	11.67	14.70
XI	43.50	93.25	40.75	4.42	46.42	2.08	14.38	10.14
XII	47.17	103.00	70.47	7.50	101.00	2.00	12.68	20.75

(b) Canonical analysis:

The standardized best linear functions (canonical vectors) were obtained and the first four canonical vectors and percentage of variation absorbed by them are presented in Table 4.6. The sum of all canonical roots was 3468.76, which the $Root_1$ = 1961.95, $Root_2$ = 992.05, $Root_3$ = 211.47 and $Root_4$ = 134.57. The first canonical root absorbed 56.56 per cent of total variability and second one accounted for 28.60 per cent of variability. Further, first two roots together accounted for 85.16% of the diversity indicating that the difference for these traits in these entries was nearly complete in the two phases.

Table 4.6: Values of first four canonical vector, which supply best linear function of genotypes

Characters	**Canonical root**			
	CR1	**CR2**	**CR3**	**CR4**
Days to 50% flowering	0.0521	0.0973	0.2861	0.8327
Days to maturity	0.5981	0.6585	-0.3243	0.1008
Plant height (cm)	0.6101	-0.7161	-0.1840	0.1872
Number of primary branches /plant	-0.0248	-0.0458	0.2626	-0.1035
Number of pods/plant	0.2426	0.1688	0.6423	-0.1329
Number of seeds per pod	0.2415	0.0913	-0.0691	-0.1704
100 grain weight (g)	-0.1984	0.0143	0.0920	0.4041
Grain yield/plant (g)	0.3319	-0.0701	0.5333	-0.2016
Percentage of variation absorbed	**56.56**	**28.60**	**6.10**	**3.88**

The relative contribution of characters towards genetic divergence was found out from the canonical coefficients of first two canonical vectors. Plant height recorded the highest coefficient of 0.6101 followed by days to maturity, grain yield per plant, number of pods per plant, number of seeds per pod and 100 grain weight recording 0.5981, 0.3319, 0.2426, 0.2415 and -0.1984, respectively, as reflected by the first vector. In the second vector, the maximum coefficient of -0.7161 was recorded by plant height

followed by days to maturity and number of pods per plant recording 0.6585 and 0.1688, respectively.

6. Correlation studies:

Estimates of environmental, genotypic and phenotypic correlation coefficients between grain yield and contributing characters and among themselves were obtained and are reported in Table 4.7, 4.8 and 4.9, respectively. The genotypic correlation coefficients were in general, slightly higher than the phenotypic correlation coefficients.

(i) Correlation with grain yield:

(a) Environmental:

Table 4.7 showed that number of primary branches per plant, number of pods per plant and 100 grain weight had positive correlation.

(b) Genotypic:

Table 4.8 showed that days to 50% flowering, days to maturity, plant height, number of primary branches per plant and number of pods per plant had positive correlation while number of seeds per pod had negative correlation.

(c) Phenotypic:

Table 4.9 revealed that grain yield showed positive correlation with days to 50% flowering, days to maturity, plant height, number of primary branches per plant and number of seeds per pod.

(ii) Correlation among yield attributes:

(a) Environmental:

Days to maturity had positive correlation with 100 grain weight and negative with number of pods per plant and number of seeds per pod.

Plant height had positive correlation with number of pods per plant.

Number of primary branches per plant had positive correlation with number of pods per plant and negative with number of seeds per pod.

Number of pods per plant had positive correlation with plant height and number of primary branches per plant and negative with days to maturity.

Number of seeds per pod showed negative correlation with days to maturity and number of primary branches per plant.

100 grain weight had positive correlation with days to maturity.

(b) Genotypic:

Days to 50% flowering showed positive correlation with days to maturity, number of primary branches per plant, number of pods per plant and 100 grain weight and negative with number of seeds per pod.

Days to maturity had positive correlation with days to 50% flowering, number of primary branches per plant and number of pods per plant and negative with number of seeds per pod.

Plant height showed positive correlation with number of primary branches per plant, number of pods per plant, number of seeds per pod and number of pods per plant and negative with 100 grain weight.

Number of primary branches per plant showed positive correlation with days to 50% flowering, days to maturity, plant height, number of pods per plant and number of seeds per pod.

Number of pods per plant showed positive correlation with days to 50% flowering, days to maturity, plant height, number of primary branches per plant and number of seeds per pod and negative with 100 grain weight.

Number of seeds per pod showed positive correlation with plant height, number of primary branches per plant and number of pods per plant and negative with days to 50% flowering, days to maturity and 100 grain weight.

100 grain weight showed positive correlation with days to 50% flowering and negative with plant height, number of pods per plant and number of seeds per pod.

(c) Phenotypic:

Days to 50% flowering had positive correlation with days to maturity, number of primary branches per plant and number of pods per plant..

Days to maturity showed positive correlation with days to 50% flowering, and number of pods per plant.

Plant height had positive correlation with number of primary branches per plant and number of pods per plant while negative with 100 grain weight.

Number of primary branches per plant had positive correlation with days to 50% flowering, plant height and number of pods per plant.

Number of pods per plant exhibited positive correlation with days to 50% flowering, days to maturity, plant height and number of primary branches per plant while negative with 100 grain weight.

100 grain weight showed negative correlation with plant height and number of pods per plant.

Table 4.7: Estimates of environmental correlation coefficients

Characters	Days to maturity	Plant height (cm)	No. of primary branches	No. of pods/plant	No. of seeds/pod	100 grain weight (g)	Grain yield/plant (g)
Days to 50% flowering	0.012	0.110	0.167	0.089	0.163	-0.025	0.042
Days to maturity		-0.179	0.068	-0.217*	-0.274**	0.211*	-0.073
Plant height (cm)			0.135	0.273**	-0.026	0.001	-0.090
Number of primary branches				0.303**	-0.185*	0.152	0.194*
Number of pods/plant					-0.061	-0.073	0.246**
Number of seeds per pod						0.028	0.006
100 grain weight (g)							0.216*

Table 4.8: Estimates of genotypic correlation coefficients

Characters	Days to maturity	Plant height (cm)	No. of primary branches	No. of pods/plant	No. of seeds/pod	100 grain weight (g)	Grain yield/plant (g)
Days to 50% flowering	0.299	-0.015	0.299	0.256	-2.200	0.193	0.243
Days to maturity		0.056	0.231	0.213	-2.003	0.157	0.380
Plant height (cm)			0.686	0.638	1.006	-0.342	0.341
Number of primary branches				0.916	1.588	-0.119	0.717
Number of pods/plant					0.308	-0.313	0.767
Number of seeds per pod						-2.777	-0.802
100 grain weight (g)							0.039

Table 4.9: Estimates of phenotypic correlation coefficients

Characters	Days to maturity	Plant height (cm)	No. of primary branches	No. of pods/plant	No. of seeds/pod	100 grain weight (g)	Grain yield/plant (g)
Days to 50% flowering	0.258**	-0.004	0.250**	0.225*	0.010	0.135	0.204*
Days to maturity		0.048	0.179	0.181*	-0.119	0.150	0.340**
Plant height (cm)			0.524**	0.602**	0.031	-0.281**	0.303**
Number of primary branches				0.714**	-0.079	-0.020	0.547**
Number of pods/plant					-0.012	-0.258**	0.693**
Number of seeds per pod						-0.067	-0.024
100 grain weight (g)							0.075

7. Path analysis:

Correlation coefficients, which measure the association between any two characters, may not give a true or comprehensive picture of a rather complex situation. Path coefficient analysis is a means of measuring the direct and indirect effects of one variable through the other variables on the end product. The direct and indirect effects of the studied characters viz., days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of pods per plant and 100 grain weight on the grain yield per plant at genotypic level are presented in Table 4.10.

Days to heading had negative but negligible direct contribution and indirect positive contribution through number of pods per plant.

Days to maturity had considerable positive direct contribution. It had positive indirect contribution through number of pods per plant.

Plant height had considerable negative direct contribution and indirect positive contribution through number of pods per plant.

Number of primary branches per plant showed negative and negligible direct contribution. It had positive and substantial indirect contribution through number of pods per plant.

Number of pods per plant showed strong positive direct contribution. It had negligible indirect contribution via rest of the traits.

100 grain weight showed considerable direct positive contribution. It had indirect negative contribution through number of pods per plant.

Table 4.10: Genotypic path

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches	No. of pods/plant	100 grain weight (g)	Genotypic correlation with grain yield
Days to 50% flowering	**-0.107**	0.052	0.003	-0.030	0.269	0.056	0.243
Days to maturity	-0.032	**0.175**	-0.010	-0.023	0.224	0.045	0.380
Plant height (cm)	0.002	0.010	**-0.173**	-0.068	0.669	-0.099	0.341
Number of primary branches	-0.032	0.040	-0.119	**-0.099**	0.960	-0.034	0.717
Number of pods/plant	-0.027	0.037	-0.110	-0.090	**1.048**	0.090	0.767
100 grain weight (g)	-0.021	0.028	0.059	0.012	-0.328	**0.288**	0.039

Residual = 0.2737

Table 4.11: Phenotypic path

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches	No. of pods/plant	100 grain weight (g)	Phenotypic correlation with grain yield
Days to 50% flowering	**-0.059**	0.046	0.001	0.013	0.175	0.030	0.204
Days to maturity	-0.015	**0.179**	-0.007	0.009	0.141	0.033	0.340
Plant height (cm)	0.000	0.009	**-0.139**	0.027	0.468	-0.062	0.303
Number of primary branches	-0.015	0.032	-0.073	**0.051**	0.555	-0.004	0.547
Number of pods/plant	-0.013	0.032	-0.084	0.037	**0.778**	-0.056	0.693
100 grain weight (g)	-0.008	0.027	0.039	-0.001	-0.200	**0.219**	0.075

Residual = 0.4099

CHAPTER-V
DISCUSSION

The investigation entitled "Genetic variability and association analysis in soybean (*Glycine max*)." was carried out during *kharif* 2012-13 at research farm, Department of Plant Breeding and Genetics, College of Agriculture, Gwalior.

The salient finding of this work are interpreted and discussed in this chapter in conjunction with the findings of other workers. The discussion is confined to the relevant topics, viz., mean performance, variability, heritability, genetic advance, genetic divergence, correlation and path analysis.

5.1 Mean performance:

Based on mean performance, the genotypes PS 1520, KDS 705, RKS 115, AMS 475, Himso 1684, VLS 84, MACS 1416, KDS 693, ASB 22, AMS 358, MAUS 612, JS 20-69, MACS 1394, AMS 77, RKS 113, JS 335 (check) and JS 93-05 (check), would appear to be suitable parents for early in 50% flowering while RSC 01-05 would appear to be suitable parents for early in maturity. The genotypes RVS 2006-1 and AMS 358 would appear to be suitable for dwarf varieties. For increasing the number of primary branches, the genotypes NRC 94, DSB 22 and KDS 708 serve as ideal donors. The genotype KDS 708 would be suitable parent for increasing the number of pods per plant. The genotypes MAUS 612, DS 2705, AMS 475, Himso 1684, JS 20-71, KDS 705, MAUS 614, RSC 01-05, VLS 85, ASB 22, KBS 22-2009, JS 20-69, NRC 91, PS 1520, CSB 904, JS 95-60 (check) and JS 335 (check) would serve as ideal donors for increasing number of seeds per pod. Genotypes SL 982, VLS 84, NRC 91 and MACS 1394 would appear to be suitable parent for increasing 100 grain weight. The genotypes KDS 708 and NRC 94 would serve as ideal donor for improving grain yield per plant.

5.2 Variability studies:

A broad spectrum of variability is fundamental for success of a plant breeding programme since it provides an opportunity to the plant breeder to use his skill and art in making useful selections. Wide range of variability for traits is also necessary to isolate significantly superior varieties for commercial cultivation, to be used as parents in hybridization for combination breeding to develop high yielding hybrid varieties, and to create useful genetic diversity for further selection.

Considerable amount of variability for most of the traits was observed in the experimental material. It was revealed by both, univariate and multivariate, analysis. Mean sum of squares due to

genotypes for all the traits (except number of seeds per pod) were highly significant in univariate analysis while value of Wilk's " Λ " criterion was significant in the multivariate analysis.

This suggested that entries were quite divergent and large variability for most of the traits was present. It indicated that the material chosen for study was quite important. Wide variability was also evident from wide range and high values of PCV and GCV.

Plant height and grain yield per plant had wide range and high estimates of PCV and GCV. It suggested that there is lot of scope for selecting parents to develop dwarf and high yielding varieties. The character number of pods per plant exhibited wide range and high PCV and GCV offering ample scope for improvement through selection. Besides this, these characters also had narrow differences between the values of PCV and GCV showing least influence of environment.

On the other hand days to 50% flowering and days to maturity were found to be consistent in its behaviour at both, phenotypic and genotypic, level having lowest coefficient of variation. It suggested that this was least influenced by non-genetic factors and hence was quite stable. The range was also quite wide and there was ample scope for selecting parents to develop an early variety.

Similar results pertaining to high estimates of PCV and GCV for plant height, number of pods per plant and grain yield per plant were also reported by Jagdish *et al.* (2000), Singh *et al.* (2000), Das *et al.* (2001), Bangar *et al.* (2003), Chamundeswari and Aher (2003), Ganesamurthy and Seshadri (2004), Dhillon *et al.* (2005), Karad *et al.* (2005), Sultana *et al.* (2005), Bhushan *et al.* (2006), Gohil *et al.* (2006), Gupta and Punetha (2007), Yadav (2007), Costa *et al.* (2008), Gangarde *et al.* (2009), Borate *et al.* (2010), Saraswathi *et al.* (2010) and Rajeshwar *et al.* (2010).

5.3 Heritability and genetic advance:

The coefficient of variation indicates only the extent of variability existing for various characters, but does not give any information regarding heritable proportion of it. Hence, amount of heritability permits greater effectiveness of selection by separating out the environmental influence from the total variability and to indicate accuracy with which a genotype can be identified phenotypically. In present study, broad sense heritability, which includes both additive and non-additive gene effects was estimated.

The results indicated that estimates of heritability were high for days to maturity, plant height, number of pods per plant, grain yield per plant, days to 50% flowering and 100 grain weight. Yield being a complex character is influenced by many factors. In the present study, high heritability coupled with high genetic advance as per cent mean was observed for plant height, number of pods

per plant and grain yield per plant. Similar results were reported by Jain and Ramgiry (2000), Jagdish *et al.* (2000), Singh *et al.* (2000), Agrawal *et al.* (2001), Bangar *et al.* (2003), Karad *et al.* (2005), Gohil *et al.* (2006), Thakare *et al.* (2006), Nag *et al.* (2007), Yadav (2007), Karnwal and Singh (2009) and Borate *et al.* (2010) for plant height, Jain and Ramgiry (2000), Jagdish *et al.* (2000), Singh *et al.* (2000), Karad *et al.* (2005), Sultana *et al.* (2005), Gohil *et al.* (2006), Thakare *et al.* (2006), Nag *et al.* (2007), Yadav (2007) and Karnwal and Singh (2009) for number of pods per plant and Jain and Ramgiry (2000), Jagdish *et al.* (2000), Singh *et al.* (2000), Dixit *et al.* (2002), Bangar *et al.* (2003), Dhillon *et al.* (2005), Karad *et al.* (2005), Sultana *et al.* (2005), Bhushan *et al.* (2006), Gohil *et al.* (2006), Karthika and Lakshmi (2006), Nag *et al.* (2007), Yadav (2007), Karnwal and Singh (2009) and Borate *et al.* (2010) for grain yield per plant. This indicates the lesser influence of environments in expression of characters and prevalence of additive gene action in their inheritance, since are amenable for simple selection.

High heritability with moderate genetic advance as per cent of mean was recorded for days to maturity, 100 grain weight and days to 50% flowering. The results indicate that these characters were less influenced by environment but governed by additive and non-additive gene action.

Moderate heritability with high genetic advance for number of primary branches per plant indicated less variability and governed by additive gene action.

From the above discussions, it can be concluded that high genotypic coefficient of variability and phenotypic coefficient of variability coupled with high heritability and genetic advance as per cent of mean were observed for the characters plant height, number of pods per plant and grain yield per plant. This indicates that there is a lesser influence of environment in the expression of character which are amenable for selection. The character viz., days to 50% flowering and days to maturity showed high heritability but low level of variability. Hence, these characters are not amenable for selection in the present study.

5.4 Studies on genetic divergence:

The choice of parents is of paramount importance in any breeding programme. It is rather a difficult task for a plant breeder. Selection of parents on the basis of per se performance is good but there is a possibility of related lines being chosen resulting in limited or no advances under selection and, therefore, there is a need for emphasis on a wide genetic base by the utilization of world collection on genetic criterion. Selection of the parents on the basis of geographical diversity is another way of choosing parents and this has led to success in some cases but this need to be supplemented with genetic diversity. The measures based on genetic criteria qualifying diversity have become important in classifying material for the use by the breeders. Further, the genetic

divergence among parents is important because a cross involving genetically diverse parents is likely to produce high heterotic effect and also a broad spectrum of variability could be expected in the segregating generations. The assessment of divergence for a set of genotypes using multivariate analysis like distance analysis, canonical analysis etc. has been attempted and effectively utilized in a number of crop plants with diverse breeding systems (Murty and Arunachalam, 1966). Thus, the genetic divergence has a definite role to play for efficient choice of parents for hybridization programme.

The analysis of variance revealed highly significant differences among genotypes for all the characters except number of seeds per pod. The dispersion amongst variables for the aggregate effect of the 8 characters as tested by Wilk's criterion was also highly significant indicating existence of considerable divergence in the material under study.

Genetic differences among genotypes were quantified by estimating D^2 statistic. The estimates of D^2 values varied substantially from 4.77 to 1073.04. The maximum divergence (D^2 = 1073.04) was recorded between genotype NRC 94 and RSC 01-05. These two genotypes also showed significant differences between them in respect of most of the characters except days to 50% flowering and 100 grain weight (Appendix-I). A cross between these two genotypes is expected to give a heterotic hybrid and wide spectrum of variability. Therefore, these genotypes may be used as parents for hybridization. On the other hand minimum divergence (D^2=4.77) was observed between genotypes Himso 1684 and JS 20-69 which did not differ significantly from each other for all characters taken under study therefore, these may be related in their evolution.

The inter cluster distance revealed that cluster I and XII were most divergent followed by cluster V and XIII. Crosses between lines carefully selected from these clusters are expected to throw a wide range of segregants.

Average intra-cluster distance revealed that cluster IV followed by cluster I, which contained two genotypes, had little intra-cluster distance. It indicated these lines could be closely related in their evolutionary process and passed through similar evolutionary factors.

Sometimes a breeder is asked to improve a particular trait of a variety, which is otherwise suitable. For this a donor parent is required. Information about a range of suitable donors thus becomes inevitable. Estimates of cluster mean make this information readily available. Cluster means for the 8 traits of all the 12 clusters were worked out. It was found that Cluster I had lowest mean value for plant height. Cluster II had lowest mean value for days to 50% flowering and highest mean value for plant height. Cluster IV had highest mean value for 100 grain weight. Cluster V had highest mean value for number of seeds per pod and lowest mean value for days to maturity. Cluster XII had highest mean values for number of primary branches per plant, number of pods per plant and grain

yield per plant. To improve any particular trait donor for hybridization could be chosen from an appropriate cluster.

For example, to improve grain yield per plant, number of primary branches per plant and number of pods per plant a line from cluster XII, viz., genotype KDS 708 would be a right choice.

Lines from cluster I, for example genotype RVS 2006-1 could be used to develop early varieties. To develop early and tall variety genotype KDS 705 would be an ideal choice. To improve 100 grain weight SL 982 from cluster IV would be an ideal choice.

The following genotypes of marked mean performance from the selected clusters may serve as parents for hybridisation programmes.

Cluster	Characters	Genotypes
XII	Grain yield per plant , number of primary branches per plant, number of pods per plant	**KDS 708**
I	Plant height (dwarf)	**RVS 2006-1**
II	Early in 50% flowering, Plant height (Tall)	**KDS 705**
V	Early in maturity	**RSC 01-05**
	Number of seeds per pod	**MAUS 612**
IV	100 grain weight	**SL 982**

Canonical analysis:

Generalized distance, D^2 statistic of Mahalanobis (1936) is an important parameter to ascertain the genetic divergence among genotypes. It provides degree of divergence based on multiple variables. However, it does not provide any indication about the quantum of contribution of each trait towards the total genetic divergence. Thus, it becomes difficult to discriminate through D^2 statistic, among the major or secondary traits of genetic diversity based on their relative contribution. To circumvent this problem another technique, the canonical analysis, is used to determine the contribution of each trait towards the total genetic divergence.

The divergence as determined by canonical analysis revealed that the first two roots together accounted for 85.16% of the total variation present in the genotypes. The coefficient of Ist canonical root revealed that the primary axis rotated around plant height, days to maturity, grain yield per plant, number of pods per plant, and number of seeds per pod. These traits thus, were primarily responsible for variation between genotypes. It indicated that these yield components were the major traits for genetic divergence. Therefore, greater significance needs to be attached to these traits during selection.

The estimates of coefficients of canonical root II revealed that the second axis was primarily concerned with plant height, days to maturity and number of pods per plant. It suggested that these traits were secondary in importance in contributing to total genetic divergence. It could be concluded that these traits contributed moderately to the genetic differences and thus be given careful attention while selecting parents to improve these traits.

5.5 Correlation studies:

Information about correlations is of great significance to a plant breeder because all the phenotypic traits are the result of interplay of several genetic factors among themselves and their individual and combined interaction with the environmental factors.

Knowledge of correlation helps a plant breeder to determine the methodology to improve a particular trait which is not readily amenable to direct selection and so indirect selection becomes inevitable. It also provides information about the correlated response to directional selection to predict genetic advance and thus can be used as selection indices for operating more efficient selection programme.

Correlation could be phenotypic, genotypic or environmental. Phenotypic correlation is between values directly measured on individuals and includes genetic and non-genetic effects. Genotypic correlation is between breeding values and accounts for only genetic causes, which could be pleiotrophy, linkage or gene frequency disequilibrium. Environmental correlation is between non-

genetic values and arises due to the fact that several observations are affected by the same amount of environment. Information on all the three is, therefore, very useful to a plant breeder.

The estimate of phenotypic correlation coefficients revealed that grain yield per plant was positively correlated with number of primary branches per plant and number of pods per plant. Improvement in any one of them through indirect selection would result in improvement in grain yield.

Grain yield per plant exhibited positive association with days to 50% flowering, days to maturity and plant height both at phenotypic and genotypic level. The positive correlations of grain yield per plant with days to 50% flowering, days to maturity and plant height were undesirable because early, dwarf and high yielding genotypes are preferred.

The estimates of genotypic correlation coefficients with yield were similar to those of phenotypic correlation coefficients in direction. However, these were higher in magnitude. It suggested that these correlations were due to breeding values and therefore, more dependable.

Correlation of number of seeds per pod with days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of pods per plant, 100 grain weight and grain yield per plant and of days to maturity with number of primary branches per plant which were missing at phenotypic level were apparent at genotypic level.

The appearance of correlation at genotypic level indicated that the character like number of seeds per pod was highly influenced by the environment. Such character need to be carefully included in selection indices to exploit correlated response.

The estimate of environmental correlation coefficients revealed that grain yield per plant was correlated with number of primary branches per plant, number of pods per plant and 100 grain weight. Number of pods per plant was found correlated with days to maturity, plant height and number of primary branches per plant. Number of seeds per pod was observed to be correlated with days to maturity and number of primary branches per plant. 100 grain weight was found to be correlated with days to maturity. It suggested that non genetic factors were operating in determining these traits. Attention needs to be given to these correlations while formulating selection indices.

Jagdish *et al.* (2000), Nimbalkar and Gujar (2000), Singh *et al.* (2000), Bandyopadhyay (2003), Chettri *et al.* (2003), Ganesamurthy and Seshadri (2004), Dev *et al.* (2005), Sahay *et al.* (2005), Sultana *et al.* (2005), Nag *et al.* (2007), Karnwal and Singh (2009), Burli *et al.* (2010), Iqbal *et al.* (2010), Showkat and Tyagi (2010) and Machikowa and Laosuwan (2011) also reported similar results.

5.6 Path analysis:

Path analysis allows us to partition the observed correlation coefficient into different components. Path coefficient analysis is an efficient statistical technique specially designed to quantify the inter-relationships of different components and their direct and indirect effects on grain yield. Through, this technique, yield contributing components can be ranked and specific traits producing a given correlation can be revealed.

The correlations (genotypic) were further partitioned into direct and indirect effects to establish the cause and effect relationship between the yield and its component characters. As a result of this study it was revealed that number of pods per plant exhibited the highest direct effect on grain yield per plant, while the correlation of these two traits was highly positive. Therefore, a true relationship exists between number of pods per plant and grain yield per plant.

The direct positive effect of number of pods per plant on grain yield has been reported Khan *et al.* (2000), Chettri *et al.* (2003) and Machikowa and Laosuwan (2011).

100 grain weight, which did not show correlation with grain yield per plant, exhibited considerable positive direct contribution. This positive direct contribution was converted into negligible correlation mainly due to its negative indirect effects *via* number of pods per plant.

The direct effect of days to 50% flowering, days to maturity, plant height and number of primary branches per plant was low, though these trait showed positive correlation with grain yield per plant. Therefore, it appears that correlation of days to 50% flowering, days to maturity, plant height and number of primary branches per plant with grain yield per plant may be a reflection of positive indirect effects of these traits through number of pods per plant.

Residual effect was found to be moderately high (27.37%). Therefore, the some of the growth, yield and quality characters may also be included in the further study.

Critical analysis of the results obtained from genotypic correlation coefficients and path analysis indicated that the number of pods per plant had positive correlation and high magnitude of positive direct effects on grain yield. It is therefore suggested that preference should be given to number of pods per plant in selection programme to isolate superior lines with genetic potentiality for higher grain yield.

CHAPTER VI
SUMMARY, CONCLUSION AND SUGGESTIONS

The present experiment entitled "Genetic variability and association analysis in soybean (*Glycine max*)" was carried out during *kharif* 2012 at experimental area of College of Agriculture, Gwalior; M.P to assess the nature and extent of genetic variability and diversity among 39 genotypes.

The observations were recorded on days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of pods per plant, number of seeds per pod, 100 grain weight and grain yield per plant.

The data on all characters studied were subjected to statistical analysis and the following conclusions were drawn:

1. Analysis of variance revealed highly significant differences among genotypes for all the characters except number of seeds per pod. It indicated that a sizeable amount of variability present in the material. Estimates of population mean were high and range was wide for most of the traits. Trend of variability at genotypic level was similar to that of at phenotypic for most of the characters. The genotypic coefficient of variation was highest for plant height, number of primary branches per plant, number of pods per plant and grain yield per plant.
2. In broad sense, high heritability was observed for days to 50% flowering, days to maturity, plant height, number of pods per plant, 100 grain weight and grain yield per plant while moderate heritability for number of primary branches per plant.
3. High heritability estimates coupled with high genetic advance as per cent of mean observed for plant height, number of pods per plant and grain yield per plant. Moderate heritability combined with moderate genetic advance as per cent of mean was observed for days to maturity, 100 grain weight, number of primary branches per plant and days to 50% flowering.
4. All the 39 genotypes were grouped into 12 clusters based on D^2 analysis. Cluster III and VII were the biggest with 6 genotypes each followed by cluster IX, X and XI. The cluster VI was solitary cluster. The D^2 values ranged from 4.77 to 1073.04. Intra cluster D^2 values exhibited a range of 0.00 to 2.277 and inter cluster D^2 values ranged from 2.983 to 59.305.
5. The entries KDS 708, RSC 01-05, NRC 94, MAUS 612, RVS 2006-1, KDS 705 and SL 982 may serve as potential parents for hybridization programme in the improvement of potentiality of the yield and its contributing traits in soybean.

6. Canonical analysis revealed that plant height, days to maturity, grain yield per plant, number of pods per plant and number of seeds per pod relatively contributed more to the divergence as seen in the primary axis of differentiation. In the secondary axis of differentiation, plant height was the most important followed by days to maturity and number of pods per plant.

7. Out of 7 yield attributing traits, 5 characters, viz., days to 50% flowering, days to maturity, plant height, number of primary branches per plant and number of pods per plant had positive and significant correlation with grain yield per plant.

8. The days to 50% flowering, number of primary branches per plant and number of pods per plant recorded positive inter correlation among them, indicating the possibility of simultaneous improvement of these traits by selection programme.

9. Path analysis revealed that number of pods per plant recorded positive direct effects on grain yield per plant.

Suggestions:

- The traits viz., plant height, number of pods per plant and number of seeds per pod possessing high genetic advance as per cent of mean coupled with high heritability may be further improved through simple selection.
- While making selection, maximum weightage should be given to more number of pods per plant for getting higher yields in future breeding programmes.
- Cluster XII had high yielding along with more number of primary branches per plant and number of pods per plant entries while cluster V had highest number of seeds per pod earliest entries. Cluster II had tallest and early in 50% flowering entries while cluster IV had bold grained entries. Cluster II had earliest in 5o% flowering entries and tallest entries. Hybridization among the entries from these clusters might produce high yielding genotypes having broad genetic base.
- On the basis of genetic divergence and mean performance the entries KDS 708, RSC 01-05, NRC 94, MAUS 612, RVS 2006-1, KDS 705 and SL 982 have been suggested for further use in breeding programme.

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Mean performance of thirty ninet entries of soybean for eight characters

S. No.	Entries c1	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches/plant	No. of pods/ plant	No. of seeds/ pod	100 grain weight	Grain yield/ plant (g)
1	RVS 2006-1	45.67	90.33	24.43	3.00	25.33	2.00	13.03	7.20
2	MACS 1407	47.67	87.67	29.07	5.33	55.33	2.00	14.31	8.52
3	RSC 10-01	50.67	107.00	39.73	6.67	57.33	2.00	14.34	16.96
4	NRC 94	50.00	107.00	75.87	7.67	94.33	2.00	13.46	20.36
5	DS 2705	53.00	107.00	55.47	5.67	66.00	3.00	13.40	10.42
6	RKS 115	41.67	96.33	29.93	4.67	49.67	2.67	13.71	12.40
7	DSB 22	44.33	95.67	55.73	7.33	56.00	2.67	14.42	10.77
8	AMS 475	43.33	92.00	58.73	5.67	51.67	3.00	12.12	10.26
9	SL 982	51.33	106.67	45.93	6.67	55.67	2.33	16.08	17.48
10	Himso 1684	41.33	98.67	36.00	4.33	48.67	3.00	12.20	10.78
11	VLS 84	41.33	93.67	52.07	3.67	39.33	2.33	15.22	9.37
12	JS 20-71	47.33	99.00	41.07	5.00	66.67	3.00	12.28	13.82
13	KDS 705	40.67	97.33	79.47	5.00	49.33	3.00	11.77	10.48

14	MAUS 614	46.00	88.33	68.53	6.33	71.00	3.00	12.74	13.95
15	RSC 01-05	49.00	83.00	35.00	3.67	31.00	3.00	13.58	6.57
16	NRC 93	45.00	103.33	38.33	3.67	38.67	2.00	12.26	10.48
17	PS 1518	45.00	93.00	77.33	6.33	70.67	2.67	10.70	10.12
18	MACS 1416	43.33	104.00	41.20	3.33	45.00	2.67	12.12	10.39
19	PS 1521	47.00	97.33	46.93	4.00	39.00	2.33	13.06	12.77
20	SL 979	49.33	106.67	41.20	5.00	42.00	3.00	12.89	10.51
21	KDS 693	43.33	107.00	33.53	5.00	55.00	2.67	13.81	13.90
22	NRC 92	55.00	90.33	49.27	6.00	83.00	3.00	11.85	15.93
23	VLS 85	44.67	91.67	58.73	5.67	66.33	3.00	11.20	13.43
24	ASB 22	41.00	89.00	64.13	5.67	56.67	3.00	13.23	13.25
25	AMS 358	43.33	86.00	28.60	4.00	36.00	2.00	11.03	5.61
26	KDS 708	44.33	99.00	65.07	7.33	107.67	2.00	11.89	21.14
27	MAUS 612	41.67	89.00	35.33	4.33	41.33	3.33	14.27	8.06
28	KBS 22-2009	47.67	108.00	58.07	6.67	81.00	3.00	11.30	11.65
29	JS 20-69	42.33	98.67	38.93	4.00	48.00	3.00	12.68	12.65

30	NRC 91	45.00	98.00	29.40	5.00	53.33	3.00	15.17	15.14
31	PS 1520	40.33	95.33	41.13	5.33	61.67	3.00	11.12	15.95
32	MACS 1394	42.00	99.33	33.40	4.00	37.00	2.00	15.18	9.72
33	SL 925	50.67	107.00	33.27	4.67	47.00	2.00	13.02	10.91
34	CSB 904	46.67	101.67	32.27	4.33	44.00	3.00	12.67	12.44
35	AMS 77	42.67	103.33	41.53	5.00	41.33	2.67	13.00	8.42
36	RKS 113	41.67	98.67	65.47	6.33	69.67	2.00	10.94	10.77
37	JS 95-60 (check)	46.00	88.67	33.07	5.00	40.67	3.00	12.13	10.09
38	JS 335 (check)	42.00	93.67	37.67	6.33	65.33	3.00	12.06	15.61
39	JS 93-05 (check)	43.00	92.33	48.47	4.67	54.00	2.00	12.81	12.96
c.d. (P=0.05)		**3.13**	**2.05**	**4.38**	**1.49**	**10.68**	**NS**	**1.30**	**2.27**

VITA

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He acquired his primary, high school and higher secondary education in local schools of Sanawad. After that he passed his B.Sc. (Ag.) from Gwalior obtaining 65.8 per cent marks.

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During all the period of his education, from schooling to post graduation he was very sincere and honest towards his studies.

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