

**GENETIC VARIABILITY, CORRELATION AND PATH ANALYSIS
STUDIES FOR OIL, YIELD AND ROOT NODULATION TRAITS IN
SOYBEAN (*Glycine max* (L.) Merrill.)**

BY

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DISSERTATION

Submitted to the

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2009

The image features two vibrant yellow tulips with green stems and leaves, positioned on the right side. The petals and leaves are covered in fine water droplets, giving them a fresh, dewy appearance. The background is a dark, almost black, surface with a complex, cracked, and marbled texture, resembling stone or aged paper. The lighting is soft, highlighting the texture of the flowers and the background.

*Affectionately
Dedicated*

To

Jadhav Family

&

Research Guide

CANDIDATE'S DECLARATION

I, hereby declare that this dissertation

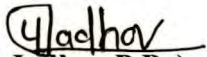
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CERTIFICATE-I

This is to certify that **Shri JADHAV PRASHANT PANDHARINATH** has satisfactorily prosecuted his course and research for a period of not less than four semesters and that the dissertation entitled "**GENETIC VARIABILITY, CORRELATION AND PATH ANALYSIS STUDIES FOR OIL, YIELD AND ROOT NODULATION TRAITS IN SOYBEAN (*Glycine max* (L) Merrill.)**" submitted by him is the result of original research work and is of sufficiently high standard to warrant its presentation to the examination.

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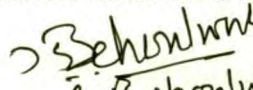



(K. S. Baig)

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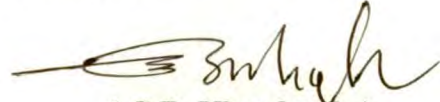
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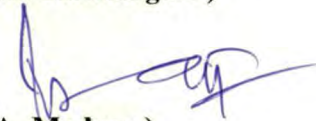
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"Words can not give full justice to express sense of gratitude"

Formal and dead words cannot carry the fragrance of emotions with them, still they are the only available means of expressing emotions in such formal acknowledgement.

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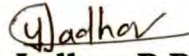
The gentle smile on the face of my niece Sakshi and Divya encouraged me every time.

I wish to express my thanks Mr. M.A. Khaleque and Sajid for printing the manuscript neatly and correctly within time.

Last but never the least, it is difficult to list all those to whom I express my gratitude for their goodwill and moral support during my academic attainments, though nobody is mentioned, none is forgotten too.

PARBHANI

Date : 14/10/09


(Jadhav P.P.)

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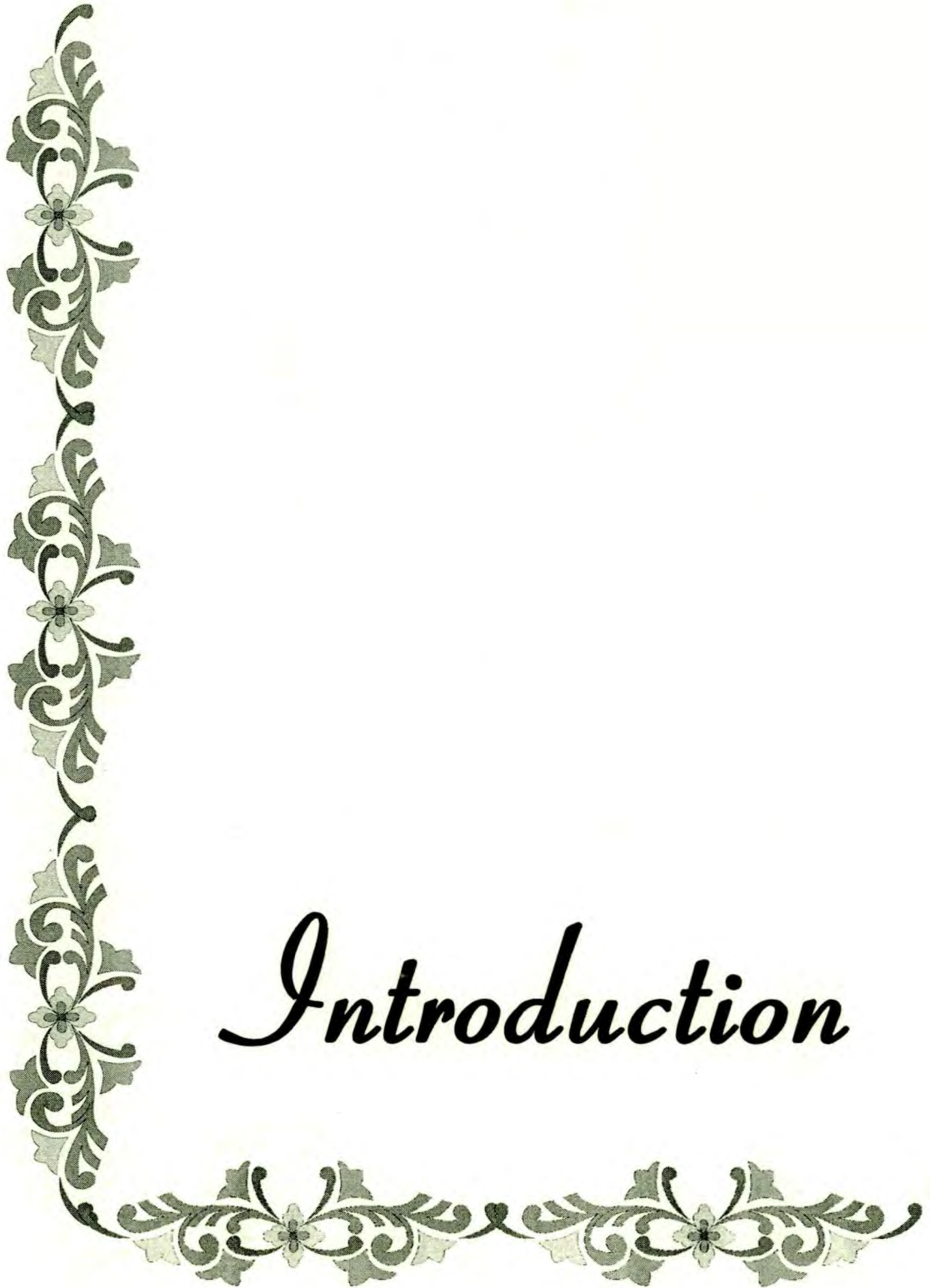
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ABBREVIATIONS

R	=	residual effect
r	=	correlation coefficient
Σ	=	summation
MSS	=	mean sum of square
mm	=	millimeter(s)
b.s.	=	broad sense
EMS	=	error mean sum of square
etc.	=	etceteras
h^2	=	heritability
d.f.	=	degree of freedom
cm	=	centimeter(s)
m	=	meter(s)
mg	=	milligram
viz.,	=	videlicet (namely)
σ^2	=	variance
EGA	=	Expected genetic advance
<i>et al.</i>	=	and other
Fig.	=	Figure
g	=	gram (s)
GCV	=	genotypic coefficient of variation
GM	=	General mean
%	=	per cent
kg	=	kilogram(s)
ha	=	hectare(s)
/	=	per
SE	=	Standard error
CD	=	Critical difference
CV	=	Coefficient of variation
pp	=	pages
P	=	phenotypic correlation
PCV	=	phenotypic coefficient of variation
No.	=	number



Introduction

Chapter-1

INTRODUCTION

Soybean (*Glycine max* (L.) Merrill.) often designated as miracle crop of the twenty first century, contains about 20 per cent of oil, 40 per cent high quality proteins, 23 per cent carbohydrates and reasonable amounts of minerals, vitamins and dietary fibres. Since the yield per unit for many conventional crops has perhaps come to a plateau, search for unconventional source of protein rich food and edible oil supply is a necessity and soybean seems the only crop at present, which has the potential to meet the present and future needs of the world for protein and edible oil.

In India, soybean has emerged as one of the major oilseed crop grown on an area of 9.62 million hectare with estimated production of over 108.02 lakh metric tones during 2008-09 (Anonymous, 2008). Maharashtra state has become second largest soybean growing state contributing nearly 34 per cent area (30.60 lakh ha) of the country next to Madhya Pradesh with average productivity of 1189 kg/ha.

At present about 80% of total soybean produced in the country goes to solvent extraction mills, 10% is retained as seed and remaining 10% is utilized for different food uses such as soy milk, tofu, soy nuts, fortification of wheat flour etc. Out of the 80% going to solvent extraction plants, 18% is used for oil and remaining 82% is utilized as DOC (De-oiled cakes). During last 5-6 years, more than 90% of DOC was being exported leading to earning of about Rs. 3300 million per annum on the

National level. However, at present about 30% of DOC produced is utilized domestically for feed (above 20%). The policy to be conceived is to aim at de linking of soybean farming and industry from foreign market dependence. The programme increase in domestic consumption of DOC provides silver lining in this direction

Overall improvement in yield, oil and protein content in soybean still remains major task for plant breeders. This can be achieved through selection, efficiency of which mainly depends on the extent of the variability existing in the available material. Knowledge of heritability is important to know the extent of genetic contribution to the total variance. This knowledge is also useful in increasing the efficiency of breeding systems, since it is a measure of the success in separating genotypes by selection (Bartley and Weber, 1952). Burton (1952) suggested that the genotypic coefficient of variation together with high heritability estimates would give a better picture of the extent of genetic progress to be expected under selection.

The present study trend in improving soybean crop is mainly through Selection, mutation breeding and hybridization mainly interspecific hybridization i.e. crossing of varieties belonging to different subspecific groups as this methods helps in getting a recombinant with desirable attributes scattered in different habit groups. It has been well established fact that genetically diverse parents are likely to yield desirable segregants and to produce high heterotic crosses. In general utilization of more diverse parents in crossing programme increases greater chances of obtaining high heterotic F_1 and broad spectrum variability in segregating

generations (Arunachalam, 1981). In applied plant breeding, success of the programme may be anticipated if the genetic variability of different selection is known, well in advance. The correlation and path analysis provide information on genetic association of yield contributing characters, which in turn are useful in developing breeding strategies. The information of variability in yield, oil and root nodulation traits will help to manipulate breeding programme for developing a suitable variety.

Association of characters influenced by a large number of genes is elaborated statistically by correlation coefficients. Genotypic correlation coefficients provides a measure of genotypic conjugation between characters. The method of partitioning the correlation into direct and indirect effects by path. Coefficient analysis suggested by Wright (1921) provides useful information on the relative merit of the traits in the selection criteria.

Therefore present investigation was undertaken to evaluate the genetic variability, correlation and path analysis studies for yield, yield components, oil and root nodulation traits in 40 genotypes of soybean with following objectives.

1. To study the pattern of genetic variability.
2. To study the correlation and path analysis for oil, yield and morphological traits.
3. To study the variability for nodulation traits in soybean.



*Review of
Literature*

Chapter 2

REVIEW OF LITERATURE

2.1 Genetic variability, Heritability and Genetic advance

The magnitude of genetic variability in the breeding material determines the speed and precision of the improvement programme in a particular crop. A population with higher variability provides greater opportunity for improvement. Several reports on genetic variability in soybean are available. However, only few of them are reviewed here.

Bartley and Weber (1952) obtained an estimate of heritability from the regression of F_3 progeny on F_2 plants in soybean. Similar estimates were obtained from regression of F_4 on F_3 . Large heritability were observed for maturity date and plant height. Weber and Moorthy (1952) calculated heritability as the per cent genotypic variance of the total F_2 (adjusted for replication differences) variance. Flowering time (75.6) and maturity date (75.3) showed comparatively high heritabilities followed by plant height (62 per cent) and oil content (54 per cent), whereas, seed weight exhibited lowest heritability (54.3 per cent) on the average for three crosses.

Burton (1952) has suggested genetic coefficient of variation as a measure of the extent of genetic variability present in a population for a particular character. Whereas, phenotypic coefficient of variation measures the extent of total or phenotypic variability.

Lal and Haque (1972) recorded wide range of phenotypic variability for the characters days to first flowering, period of flowering,

days to maturity, number of leaves, total leaf area, plant height and number of pods, however, number of nodes, 100 seed weight and seed yield showed a narrow range. Ten characters studied by them showed a wide range in genetic coefficient of variation varying from 10-60 for days to maturity to 46-67 for number of leaves. The total leaf area, number of pods, plant height, seed yield, 100 seed weight and period of flowering showed a high genotypic coefficient of variation. Days to first flowering had a moderate and number of nodes and days to maturity had low genetic coefficient of variation.

Sharma *et al.* (1983) observed substantial genetic variability for days to flower, days to maturity, plant height, number of pods per plant and seed yield per plant. High estimates of broad sense heritability were observed for all characters viz., days to flower, days to maturity, plant height, seed yield per plant and number of pods.

Amarnath *et al.* (1991) reported prevalence of additive gene action for the characters plant height, number of pods per plant, 100 seed weight and number of seeds per plant. Non-additive gene action was detected for days to 50 per cent flowering and days to maturity for the traits viz., number of branches per plant, seeds per pod and seed yield. Combination of both types of gene action was observed.

Harer and Deshmukh (1992) observed wide range of variability for days to 50% flowering and maturity, plant height, nodes and pods/plant, 100 seed weight and seed yield/plant. The characters plant height, branches/plant, pods/plant, 100 seed weight and seed yield per plant showed higher GCV with high heritability estimates and genetic advance.

Ghatge and Kadu (1993) observed highest variability for days to maturity, plant height and seed yield. Genotypic and phenotypic coefficients of variation were highest for seed yield, plant height and plant spread. Heritability was high for days to 50% flowering followed by days to maturity and plant height. Genetic advance was highest for number of seeds per plant and plant height indicating additive genetic control for these traits.

Jagtap and Mehetre (1994) revealed high heritability accompanied by high genetic advance for the characters viz., plant height, number of flowers, pod weight, number of pods, number of branches, single plant yield, number of seed and number of fruiting nodes, indicating presence of additive gene action in their expression. Non-additive heritability was found in the expression of the characters 100 seed weight, days to maturity and days to flowering.

Jangale *et al.* (1994) studied 34 genotypes of soybean and observed high heritability for number of grains per pod, days from anthesis to maturity, days to 50% flowering, number of pods per plant, days to initiation of flowering and 100 grain weight. Estimates of heritability and genetic gain were higher for plant height and number of pods per plant. Days to 50% flowering, days from anthesis to maturity, days to initiation of flowering and 100 grain weight had high heritability estimates but low genetic gain.

Mahajan *et al.* (1994) studied genetic variability and heritability in 51 soybean lines and observed high GCV for the traits viz., number of grains/plant, plant height number of pods/plant and number of

branches per plant, whereas the character plant height, days to 50% flowering, days to maturity, 100 grain weight and number of pods/plant showed high heritability. High heritability coupled with the high genetic advance was observed in respect of plant height and pods/plant.

Taware *et al.* (1995) studied 18 vegetable varieties of soybean and observed highest value for heritability for 100 seed weight followed by days to flower (93.2 %), days to maturity (79.1 %) and seed yield (77.4 %). High amount of heritability coupled with high values of genetic gain was observed for 100 seed weight.

Major Singh (1996) reported high genotypic and phenotypic coefficients of variation for grain yield, pods per plant, 100 seed weight and days to flowering. Heritability estimates were high for days to flowering and days to maturity. Genetic advance was high for plant height, pods per plant, grain yield and days to flowering.

Singh *et al.* (1996) studied wide range of genetic variability for all the characters. Genotypic coefficients of variation was high for plant height, number of branches per plant, number of pods per plant and biological yield per plant. Number of pods per plant, biological yield/plant, seed index had relatively high heritability value with grain yield per plant.

Dixit *et al.* (2002) studied biometrical parameters in 38 newly developed genotypes of soybean. Harvest index, seed yield per plant and biological yield per plant showed comparatively high estimates of genetic variation and heritability.

Bangar *et al.* (2003) reported highest values of GCV and PCV estimates for branch number per plant and plant height among the characters. The GCV and PCV were of moderate magnitude for the pod number per plant, 100 seed weight and seed yield per plant. Days to 50% flowering and days to maturity had very low GCV and PCV estimates. The difference between GCV and PCV magnitudes were very high for 100 seed weight (12.94) and pod number per plant (10.30). Among the characters, days to maturity (97.80 %), branch number per plant (91.39 %) and plant height (60.82 %) showed the highest magnitude of heritability. Genetic advance was high for number of branch per plant, plant height and seed yield.

Dhillon and Singh (2005) observed that most of the characters possessed sufficient genetic variability. High heritability was accompanied by high genetic advance for seed yield per plant indicating the presence of additive gene action in expression of these characters. Non-additive heritability was observed in expression of characters viz., days to 50% flowering, protein content as these traits had high heritability estimates accompanied by low genetic advance.

Chettri *et al.* (2005) studied genetic variability in 18 soybean genotypes and reported wide range of variation for number of pods per plant. Plant height and grain yield per unit area exhibited high estimates of heritability, genetic advance and genetic advance as per cent of mean along with appropriate broad sense heritability value. Days to maturity, followed by days to 50% flowering recorded the highest phenotypic and genotypic variances and coefficients of phenotypic and genotypic variation. The number of grains per pod and 100 grain weight showed high heritability

values but low genetic advance and genetic advance as per cent of mean indicating the presence of poor genetic variance in the materials

Karad *et al.* (2005) reported that phenotypic coefficients of variation (PCV) were higher than genotypic coefficients of variation (GCV) for all the characters indicating modifying effect of environment on expression of character under study.

Sahay *et al.* (2005) observed high heritability and genetic advance for plant height, number of pods, seed weight/plant number of pod clusters and 100 seed weight in soybean.

Bhairav Bhushan *et al.* (2006) evaluated 198 soybean germplasm and observed high genotypic coefficient of variation (GCV) for branches per plant, pods per plant and biological yield per plant, moderate estimates of GCV for seed yield per plant, plant height and 100 seed weight and low estimate of variability were observed for seed protein, oil content and days to 50% flowering. High heritability was observed for pods per plants, plant height and biological yield per plant, whereas high genetic advance was observed for branches per plant, biological yield per plant and pods per plant and seed yield per plant.

Faisal *et al.* (2006) studied highly significant differences among genotypes for all the characters. High heritability was recorded in 100 grain weight, days to maturity, days to flowering, days to pod initiation, days to 50% flowering, oil content, grain yield per plant, plant height and protein contents respectively indicating for source of additive type of gene action.

Gohil *et al.* (2006) studied genetic variability, broad sense heritability and expected genetic advance for seed yield and its component traits in genotypes of soybean. The highest genotypic coefficient of variation was observed for number of pods/plant followed by seed yield/plant. High heritability was observed for all the characters studied in soybean. Plant height, number of clusters/plant, number of pods/plant and seed yield/plant expressed high genetic advance coupled with high heritability suggesting that these four traits are under the control of additive gene action and can be improved through simple selection procedure.

Malik *et al.* (2006) reported high heritability for 100 grain weight, number of days to maturity, number of days to flowering, number of days to pod initiation, leaf area, number of days to 50% flowering, oil content, number of shattered pods per plant, grain yield per plant, plant height and protein contents indicating the additive type of gene action governing the traits.

Yadav (2006) evaluated 30 diverse genotypes of soybean and revealed that seed yield per plant, number of pods per plant, number of seeds per plant, plant height exhibited maximum genotypic coefficient of variation. High heritability coupled with high genetic advance as percentage of mean was observed for plant height. Significant contribution of additive genetic variance was observed for all the above characters. Coheritability was high for characters like seed yield per plant with all characters.

Alok Kumar Gupta and Punetha (2007) evaluated 23 genetically diverse genotypes of soybean and reported highest amount of

genetic variability for pods per plant followed by seed yield per plant, 100 seed weight. The traits pods per plant expressed highest heritability and expected genetic advance.

Gupta and Punetha (2007) studied genotypic and phenotypic variability, heritability and genetic advance in quantitative traits including seed yield per plant and main seed vigour pods per plant exhibited highest amount of genetic variability followed by 100 seed weight and pods per plant.

Malik *et al.* (2007) observed significance differences among genotypes for different characters viz., first pod height, days to 50% flowering, days to pod initiation, days to 50% maturity, plant height, number of pods per plant, number of branches per plant, 100 seed weight, grain yield and oil content, while protein content was statistically non-significant.

Sirohi *et al.* (2007) observed wide range of variability among 25 genotypes of soybean for days to 50% flowering, days to maturity, plant height, number of primary branches, number of clusters per plant, number of pods per plant, 100 seed weight and harvest index. The estimate of genotypic coefficient of variation (GCV) ranged from 3.33 to 38.13 for number of pods per plant. The estimate of GCV were high for number of pods per plant, number of clusters per plant, seed yield per plant and plant height.

2.2 Variability for nodulation traits

Weiss (1949) reported that there are genetic difference in ability of soybean lines to nodulation.

Bonnier and Sironval (1956); Sironval *et al.* (1957) reported that nodule development is influenced by processes in the leaf and heavier as well as more effective nodules were produced under long days than short.

Bergersen *et al.* (1958) observed that the first nodules appeared on Lincoln soybean after planting and nitrogen fixation began about two weeks later.

Rawat *et al.* (1949) revealed that soybean biological nitrogen fixation (BNF) can be improved through hybridization by utilizing parents viz., JS 71-05, DSB 1, JS 2 and PS 73-22 at Jabalpur for good nodulation traits with pest and disease tolerant lines.

Manishkumar and Rana (2005) observed that there is large variability in the studied germplasm for nitrogen fixation and these traits such as nodules fresh weight, nodules dry weight, highest number of grains per pod exhibited significant positive correlation with the yield. Mid-season peas were found to have better nitrogen fixation potential with *rhizobium* and higher green pod yield in comparison to the early peas. Hence, selection of an efficient nitrogen fixation pea cultivar can lead to the reduction of production cost by improving yield and restricting the use of nitrogenous fertilizers.

Poonam Sharma *et al.* (2007) observed the high number of nodules and their dry weight, shoot dry weight and grain yield in the genotypes viz., SML 742, SML 763 and VC 6369-3065 and suggested use of these genotypes for improvement of these traits in other genotypes. Nodule dry weight significantly correlated with grain yield on the basis of

path analysis leg-hemoglobin content, number of nodules and their weight are important yield contributing traits.

2.3 Correlation and path analysis

Correlation coefficient measures the intensity of association between two characters. Association analysis between quantitative characters is important because it indicates the change brought out in them when selection pressure applied on one character even though the other character is not subjected to any selection. The measure relationship is vital in planning of efficient breeding programme for improvement of one or more economic characters which are known to be dependent on two or more metric traits.

Jonson *et al.* (1955) evaluated two populations of F_3 lines of soybean in F_4 generation. He reported that genetic correlation among characters for which selection is practiced may have important implication in breeding procedure, they pointed out that effective selection for yield in soybean is more difficult and requires more replications over years location and individuals tests that selection for other important characters.

Malhotra *et al.* (1972) reported positive association of yield with the pods per plant and primary branches, but negatively correlated with the 100 seed weight. Partial regression path coefficient analysis revealed that the pods per plant is most important yield contributing traits.

Sharma *et al.* (1983) observed significant positive correlation coefficients for character combinations viz., days to flower with days to maturity, plant height and seed yield per plant days to maturity with plant height, number of pods per plant and seed yield per plant, whereas

significant negative association was observed for plant height with number of pods per plant. Path coefficient and multivariate linear regression analysis revealed a major contribution of number of pods per plant and days to maturity towards seed yield in exotic germplasm lines of soybean.

Tiwari and Joshi (1989) studied positive correlation among seed vigour characters both at genotypic and phenotypic level but not found any association with oil and protein content. Oil content and seed weight had significant positive correlation at genotypic level but not at phenotypic level. Path analysis revealed that seed weight, germinability and root length were the other major components which had significant indirect effect via hypocotyls length.

Singh *et al.* (1994) evaluated 51 genotypes of soybean reported high positive association of seed yield/plant with number of pod/plant and harvest index. Days to 50% flowering showed high positive correlation with plant height, 100 seed weight and plant height showed high positive association with days to maturity. Number of pods per plant showed strong correlation with number of pods bearing nodes per plant and height and negative association with 100 seed weight. Path coefficient analysis revealed that number of branches per plant had moderate direct effect on grain yield.

Jadhav *et al.* (1995) observed that seed yield was positively and highly significant correlation with number of branches, pods per plant leaf area/plant and pod weight per plant.

Taware *et al.* (1995) reported positive and significant correlation of seed yield with days to flowering (0.53), days to maturity

(0.54) and pods/plant (0.56). Days to flower and maturity, plant height and pods/plant were positively and significantly correlated with each other. Path analysis revealed highest positive direct effects of days to maturity (0.44) followed by pods/plant (0.37) and days to flower (0.14) on grain yield.

Major Singh and Gyanendra Singh (1996) observed that grain yield was exhibited significantly and positively correlated with branches per plant, 100 seed weight and pods per plant. Path analysis revealed that pods per plant and 100 seed weight had high direct and positive effect on grain yield.

Major Singh (1996) evaluated on 100 germplasm lines of soybean and reported significant and positive correlation of grain yield with branches per plant, pods per plant, pod length and 100 seed weight. Path analysis revealed that pods per plant and 100 seed weight had high direct and positive effects on grain yield.

Saurabh Shukla *et al.* (1998) reported that seed yield was significantly correlated with number of pods per plant. Significant and positive correlations were also observed between plant height and pods per plant.

Inderjit Singh and Phul (1999) reported that nodule number per plant and pods per plant had significant positive and direct effect on grain yield and are important yield components.

Thorat *et al* (1999) revealed that number of pods and days to 50% flowering had positive and significant correlation with seed yield. However, its indirect effects via number of pods was substantial.

Rajanna *et al* (2000) revealed that significant and positive correlation of number of pods per plant, number of clusters per plant 100 seed weight and yield. Days to maturity, plant height and number of branches per plant exhibited significant and positive correlation with number of clusters per plant and number of per pods/plant. Path analysis revealed that high direct effect of number of pods per plant and 100 seed weight on seed yield per plant.

Raut *et al.* (2001) reported positive and significant association of seed yield with number of clusters per plant, number of pods per plant, 100 seed weight oil content and harvest index both at genotypic and phenotypic level. Path analysis revealed that path analysis maximum positive direct effect of 100 seed weight on seed yield followed by number of clusters per plant, days to maturity and number of pods per plant.

Ganeshmurthy and Seshadri (2002) studied the influence of additive gene action for seed yield and dry matter production. Number of pods and 100 seed weight were found to govern by both additive and non-additive gene action.

Zeinali *et al.* (2002) observed significant positive correlation of protein percentage, days to flowering, 100 seed weight and days to maturity with oil percentage. Results of path analysis showed that increase in oil percentage was primarily due to decrease in protein percentage. Days to flowering and days to maturity had direct and negative effects on oil percentage.

Bangar *et al.* (2003) revealed that seed yield was positively and significantly correlated with 100 seed weight followed by days to maturity, plant height and days to 50 per cent flowering.

Chettri *et al.* (2003) observed significantly correlation of grain yield with days to maturity, plant height and days to 50 per cent flowering at both phenotypic and genotypic levels. The number of days to 50 per cent flowering was positively and significantly correlated with days to maturity but negatively correlated with number of pods per plant and 100 grain weight at the genotypic level. The 100 grain weight did not show any correlation with grain yield. Path coefficient estimates showed that days to maturity, number of pods per plant and plant height had positive effect on grain yield.

Shahid Iqbal *et al.* (2003) observed that seed yield was positively and significantly associated with all parameters studied in soybean. Pods per plant exerted maximum positive direct effect on seed yield per plant followed by 100 seed weight, number of seeds/pod whereas, plant height had negative direct effect on yield/plant.

Mukhedkar *et al.* (2004) reported that seed yield was significantly and positively associated with number of pods per plant, days to 50 per cent flowering, mean internodal length, plant height, days to maturity and number of branches per plant. Pod length had significant and negative correlation with seed yield. Pods per plant had highest direct as well as final contribution towards seed yield and can be considered as most reliable yield indicator in soybean.

Bhairav Bhusan *et al.* (2006) observed that pods per plant, biological yield per plant, branches per plant, 100 seed weight and plant

height had positive and significant correlation with seed yield both at genotypic and phenotypic levels. Path analysis showed highly positive direct effects of biological yield per plant on seed yield per plant.

Gohil *et al.* (2006) reported that genotypic correlation coefficient were higher in magnitude than their corresponding phenotypic correlation coefficients for most of the traits. Seed yield per plant showed significant and positive association with plant height, branches per plant, clusters per plant, pods per plants and 100 seed weight and only negatively correlated with oil content at both levels. Among component attributes, pods per plant showed significant and positive association with plant height, branches per plant. Days to 50 per cent flowering and days to maturity showed significant and positive correlation with each other. The path analysis indicated that number of pods per plant had maximum direct effect on seed yield followed by 100 seed weight and number of clusters per plant which appeared to be major yield contributing traits in soybean.

Malik *et al.* (2006) reported that significant and positive correlation of seed yield with the number of pods per plant. Path analysis revealed that number of days to pod initiation had the highest direct contribution to yield.

Gaikwad *et al.* (2007) observed higher values for genotypic correlation was higher than phenotypic correlation. Number of pods per plant showed a positive and significant correlation with seed yield per plant. Path analysis showed that harvest index, number of pods per plant and pod length exerted highest direct effects on seed yield per plant.

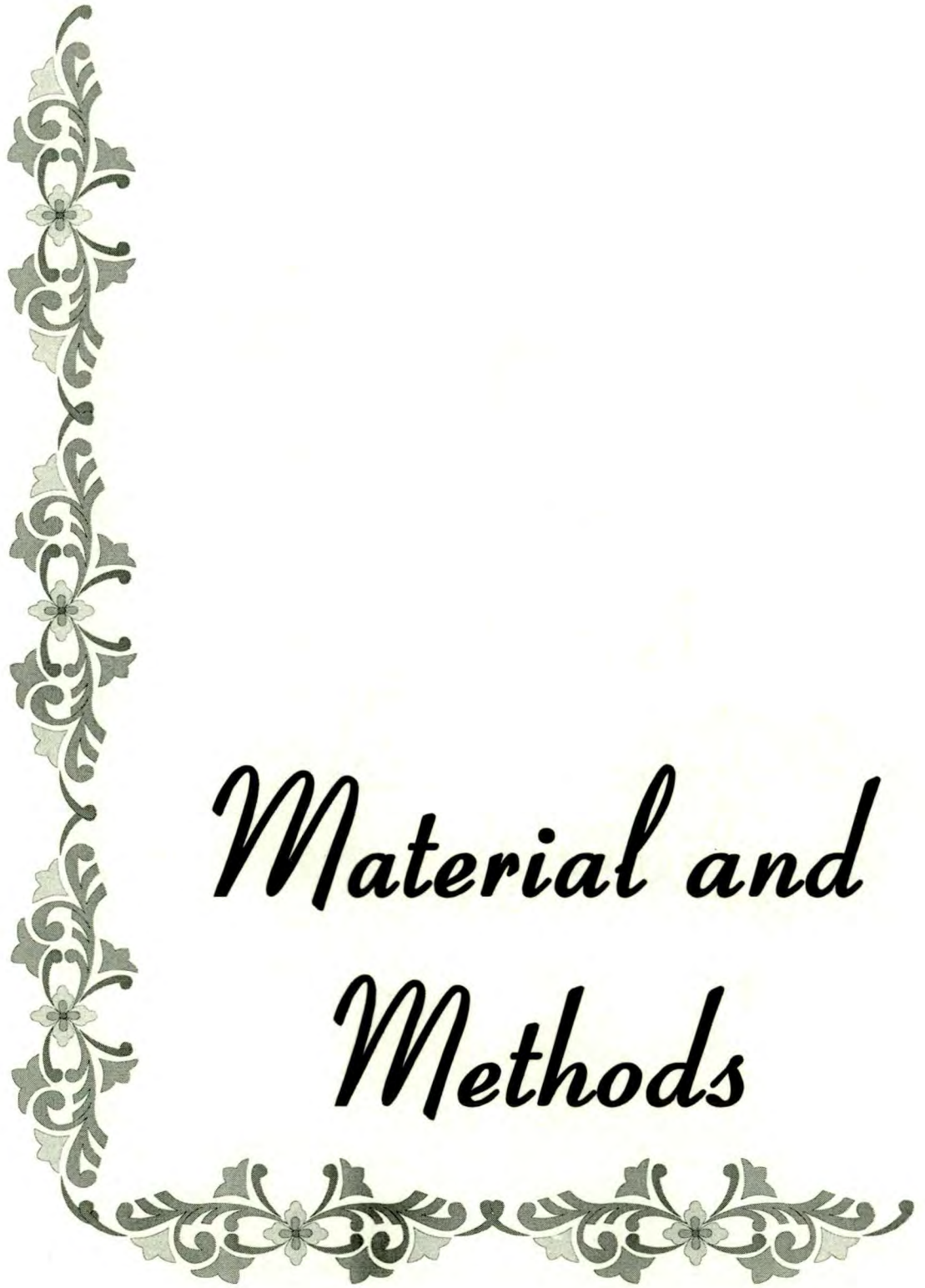
Malik *et al.* (2007) observed higher genotypic correlation than phenotypic and environments for most of the characters exhibiting

high degree of genetic association among the traits under consideration. The correlation coefficient for soybean yield was positive with days to flowering, days to maturity, plant height and number of branches per plant. Path coefficient analysis revealed that days to flowering completion had maximum direct contribution to yield followed by days to pod initiation, number of pods per plant and plant height.

Muhammad Faisal *et al.* (2007) reported positive correlation coefficient for seed yield with leaf area, days to flowering, days to maturity, plant height and number of branches per plant.

Sirohi *et al.* (2007) reported significant and positive correlation of seed yield with days to 50% flowering, number of pods per plant, days to maturity, plant height and biological yield per plant. Path analysis showed that biological yield had highest positive direct effect contributing towards seed yield.

Yadav (2007) evaluated 30 diverse genotypes of soybean and reported that seed yield was highly correlated with plant height, pod bearing length, pod number/plant and seed number/plant.



*Material and
Methods*

Chapter-3

MATERIAL AND METHODS

3.1 Experimental material

The experimental material comprised of 35 promising newly developed cultivars of soybean developed at different centers of the country and five checks viz., Bragg, JS 93-05, JS 335, MAUS 71 and MAUS 81, (Table 1).

3.2 Experimental methods

3.2.1 Layout and sowing

Thirty five different elite lines along with five checks were the experiment was laid out during *khari*f 2008 at experimental farm of All India Coordinated Research Project on Soybean, Marathwada Agricultural University, Parbhani on 26th June 2008.

Two hand weedings were carried out, first at 20 days and second at 45 days after sowing. Two sprayings of endosulfan 35 EC was undertaken for control of leaf miner and leaf eating caterpillar. All recommended agronomic package of practices were followed for satisfactory crop growth.

The experimental details are as follows:

1. No. of entries : 35 + 5 (check) = 40
2. Experimental design: RBD
3. No. of replications : Three
4. No. of rows/entry : Three
5. Spacing :

 - a) Row to row distance: 45 cm
 - b) Plant to plant distance: 5 cm

6. Plot size : 1.35 x 3 m
7. Fertilizer dose : 30:60 NP kg/ha



Table 1. Details of 35 promising lines along with checks with their origin

Sr. No.	Genotypes	Origin
1	Dsb 11	Dharwad
2	JS(SH) 2002-11	Sehore
3	MAUS-417	Parbhani
4	VLS72	Almora
5	Himso 1678	Palampur
6	PS 1454	Pantnagar
7	MACS 1039	Pune
8	BAUS 96	Ranchi
9	DS 2613	Delhi
10	MAUS 282	Parbhani
11	JS 20-14	Jabalpur
12	PS 1444	Pantnagar
13	TS 5	BARC
14	Himso 1677	Palampur
15	MACS 1184	Pune
16	NRC 80	Indore
17	VLS 71	Almora
18	RKS 54	Kota
19	MACS 1140	Pune
20	JS(SH) 2002-14	Sehore
21	TS 2	BARC
22	PS 1450	Pantnagar
23	DS 2614	Delhi
24	NRC 79	Indore
25	AMS 1	Amravati
26	KDS 321	Digraj
27	NSO 383	Pachore
28	RKS 52	Kota
29	Himso 1676	Palampur
30	JS 20-18	Jabalpur
31	MACS 1188	Pune
32	NRC 81	Indore
33	JS 20-05	Jabalpur
34	NSO 29	Pachore
35	AMS 19	Amravati
	Check	
36	JS 335	National check (Jabalpur)
37	JS 93-05	National check (Jabalpur)
38	Bragg	National check (Introduced from USA)
39	MAUS 71	Local check (Parbhani)
40	MAUS 81	Local check (Parbhani)

3.3 Recording of observations

Five plants were selected randomly from each treatment for recording the observations. Average value for each character was computed from these plants separately for each genotype observations were recorded on following traits.

I. Morphological characters

3.3.1 Days to flowering

Number of days from sowing to first flower opening on each plant were recorded and average number of days to flowering was worked out.

3.3.2 Days to 50% flowering

Days required from sowing to flowering an approximately 50 per cent plant in each entry was recorded and average number of days to 50 per cent flowering was worked out.

3.3.3 Days to maturity

Number of days required from sowing to complete maturity of crop were recorded.

3.3.4 Number of branches per plant

At maturity total number of effective branches were recorded.

3.3.5 Plant height (cm)

Average plant height of mature plant was recorded in cm from the ground level to the apex of main shoot.

II. Root nodulation characters

3.3.6 Number of root nodules per plant

The plants were carefully uprooted after 60 DAS from the field with root system intact. The roots were washed in running tap water

and nodules carefully detached with forceps. The number of nodules per plant recorded.

3.3.7 Nodule dry weight per plant (mg)

Nodules from each genotype were dried in an oven at 60°C for two consecutive days and dry weight of nodule per plant was recorded.

3.3.8 Main root length (cm)

Five plants were uprooted carefully and gently washed with tap water to record the main root length in cm. The root length was measured from the crown ring to the apex of the main root at physiological maturity stage.

III. Yield contributing characters

3.3.9 100 grain weight

Weight of randomly sampled 100 grains from each of the entry was recorded in grams.

3.3.10 Number of pods per plant

The total number of pods on randomly selected five plants from each genotype were recorded at maturity and average is worked out.

3.3.11 Oil content

Oil content was estimated through nuclear magnetic resonance (NMR) spectrometer available at Directorate of Oil Seed Research Hyderabad

3.3.12 Grain yield per plant

The five plants from each entry were threshed separately and average weight was recorded in grams as grain yield per plant.

IV. Qualitative characters

3.3.13 Pubescence colour

At maturity stage the pubescence colours present on plant body *viz.*, gray, tan were recorded.

3.3.14 Flower colour

The flower colour *viz.*, white or violet were recorded at the stage of flowering.

3.4 Statistical procedure

Mean values of the five plants selected at random in each plot were used for statistical analysis. The data were subjected to following statistical analysis.

1. Analysis of variance
2. Estimation of mean and range
3. Genetic variability
4. Heritability and genetic advance
5. Analysis of covariance
6. Correlation coefficients
7. Path coefficient analysis.

3.4.1 Analysis of variance

Analysis of variance was performed to test the significance of differences between the genotypes for all the characters. The analysis of variance was done as suggested by Panse and Sukhatme (1967):

Sr. No.	Source of variation	d.f.	Mean sum of squares		Variance ratio 'F' observed	Table 'F' value
			Observed	Expected		
1.	Replication	(r-1)	RMS	$\sigma^2_e + \sigma^2_r$		
2.	Treatment	(t-1)	TRMSS	$\sigma^2_e + r\sigma^2_g$		
3.	Error	(r-1)(t-1)	EMS	σ^2_e		
	Total	(rt-1)				

Where,

r = number of replications

t = number of treatments

The mean squares were tested against error variance by usual 'F' test. The standard error of difference for comparing any two genotypic means was estimated by formula.

$$\text{Standard error (SE)} = \sqrt{\text{EMSS}/r}$$

Where,

EMSS = error mean sum of squares

r = number of replications

$$\text{Critical difference (CD)} = \text{S.E.} \times \sqrt{2} \times 't'$$

Where

t = table value of 't' at error d.f. at 5 and 1 per cent level of significance.

3.4.2 Estimation of mean and range

The mean values of all the treatments for the characters under study were worked out by dividing the total by corresponding number of observations.

$$\text{Mean } (\bar{X}) = \frac{1}{n} \left[\sum_{i=1}^n X_i \right]$$

Where,

\bar{X} = mean of character

X_i = i^{th} observation of population

n = number of observations per replication.

The lowest and highest values of mean of each character represented by range.

3.4.3 Genetic variability

Various parameters of genetic variability were calculated by using appropriate formulae.

The genotypic and phenotypic variance were calculated by using the respective mean squares from variance table (Johnson *et al.*, 1955).

1. Genotypic variance (σ^2g)

$$\sigma^2g = \frac{\text{TRMSS} - \text{EMSS}}{r}$$

2. Error variance = $\sigma^2e = \text{EMSS}$

3. Phenotypic variance (σ^2p)

$$\sigma^2p = \sigma^2g + \sigma^2e$$

Where,

TRMSS = treatment mean sum of squares

EMSS = error mean sum of squares

r = number of replications.

The genotypic and phenotypic coefficient of variation (GCV and PCV) were calculated according to method suggested by Burton (1952).

4. Phenotypic coefficient of variation (PCV)

$$\text{PCV (\%)} = \frac{\sqrt{\sigma^2_p}}{\bar{x}} \times 100$$

5. Genotypic coefficient of variation (GCV)

$$\text{GCV (\%)} = \frac{\sqrt{\sigma^2_g}}{\bar{x}} \times 100$$

Where,

σ^2_g = genotypic variance

σ^2_p = phenotypic variance

\bar{x} = general or grand mean of character

3.4.4 Heritability and genetic advance

Heritability (Broad sense) was calculated according to the method suggested by Allard (1960):

$$1. \quad \text{Heritability (h}^2\text{) (b.s.) (\%)} = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,

σ^2_g = genotypic variance

σ^2_p = phenotypic variance

The genetic advance (at 5 per cent selection intensity) was calculated for each character using the formula suggested by Johnson *et al.* (1955).

$$2. \quad \text{Genetic advance} = h^2 \times K \times \sqrt{\sigma_p}$$

Where,

h^2 (b.s.) = heritability (broad sense)

K = selection difference at 5 per cent selection intensity, the value of

$$K = 2.06$$

σ_p = phenotypic standard deviation

The expected genetic advance (EGA) in percentage of mean is calculated as,

$$3. \quad \text{EGA} = \frac{\text{GA}}{\bar{x}} \times 100$$

Where,

EGA = Expected genetic advance

GA = Genetic advance

\bar{x} = general or grand mean of character

3.4.5 Analysis of covariance

Analysis of covariance was carried out by taking two characters at a time. The genotypic and phenotypic covariances were calculated as per the formulae described by Singh and Chaudhary (1977) as below.

Environmental covariance (Cov. ex.y) = EMSP

Genotypic covariance (Cov. g x.y) = $\frac{\text{TRMSP}-\text{EMSP}}{r}$

Phenotypic covariance (Cov. px.y) = (Cov. gx.y) + (Cov. ex.y)

Where,

EMSP = error mean sum of product

TRMSP = treatment mean sum of product

r = number of replications

3.4.6 Correlation

In order to study the extent of association between different traits, the genotypic and phenotypic simple correlation coefficients were worked out from the respective variances and covariances. The formulae as suggested by Johnson *et al.* (1955) were used for calculating simple correlation coefficient as given below.

1. Genotypic correlation coefficient ($r_{g_{xy}}$)

$$r_{g_{XY}} = \frac{\text{Cov}(g_x \cdot g_y)}{\sqrt{\sigma^2_{g_x} \cdot \sigma^2_{g_y}}}$$

Where,

$\text{Cov}(g_x \cdot g_y)$ = Genotypic covariance between character x and y

$\sigma^2_{g_x}$ and $\sigma^2_{g_y}$ = genotypic variance of characters x and y,

respectively.

Similarly,

2. Phenotypic correlation coefficient ($r_{P_{xy}}$)

$$r_{P_{XY}} = \frac{\text{Cov}(P_x \cdot P_y)}{\sqrt{\sigma^2_{P_x} \cdot \sigma^2_{P_y}}}$$

Where,

$\text{Cov}(P_x \cdot P_y)$ = phenotypic covariance between characters x and y.

$\sigma^2_{p_x}$ and $\sigma^2_{p_y}$ = phenotypic variance of characters x and y, respectively.

Significance of correlation coefficient was determined from the Fisher and Yates table 'correlation coefficient' at 5 and 1 per cent level of significance. The 'r' values were compared against (n-2) degrees of freedom.

3.4.7 Path analysis

The genotypic correlation coefficients between yield and its components were further partitioned into direct and indirect effects with the help of path coefficient analysis originally suggested by Wright (1921) and further outlined by Dewey and Lu (1959).

The first step in path analysis is to prepare the path diagram based on cause and effect relationship. In the present study, path diagram was prepared by taking yield as effect i.e. the function of various

components like x_1 , x_2 , x_3 and these components show following type of association with each other.

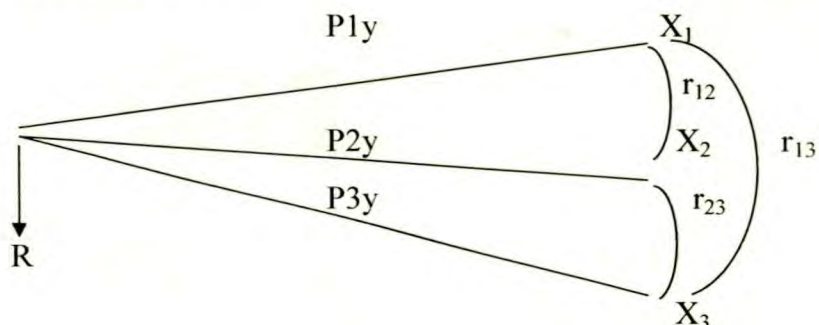


Fig. 1. Path diagram showing the factors influencing yield

In path diagram, the grain soybean yield is the result of x_1 , x_2 , x_3 and some other undefined factors designated by R . The double arrowed lines indicates mutual association as measured by correlation coefficient (r_{ij}) and the single arrowed line represent direct influence as measured by path coefficient (P_{ij}).

Direct and indirect contribution of eight variables to seed cotton yield were calculated by solving a set of simultaneous equations of the form as per Dewey and Lu (1959).

$$r_{ny} = p_{ny} + r_{n2}p_{2y} + r_{n3}p_{3y} + \dots$$

Where,

R_{ny} = represents correlation coefficient between one component and seed cotton yield

r_{n2} = represents correlation coefficient between that character and each of other components

p_{ny} = represents path coefficient between that characters and seed cotton yield.

$$\begin{array}{c}
 \text{Matrix-A} \\
 \left(\begin{array}{c} r_{1,y} \\ r_{2,y} \\ \cdot \\ \cdot \\ \cdot \\ \cdot \\ r_{m,y} \end{array} \right) = \left(\begin{array}{c} P_1 \\ P_2 \\ \cdot \\ \cdot \\ \cdot \\ \cdot \\ P_n \end{array} \right)
 \end{array}
 \qquad
 \begin{array}{c}
 \text{Matrix-B} \\
 \left(\begin{array}{ccc} r_{1,1} & r_{1,2} \dots r_{1,n} \\ r_{2,1} & r_{2,2} \dots r_{2,n} \\ \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot \\ r_{m,1} & r_{m,2} \dots 1 \end{array} \right)
 \end{array}$$

The B matrix was inverted (B^{-1}) and path coefficients (P_{ij}) were obtained as

$$P_{ij} = A \times B^{-1}$$

The coefficients $P_1, P_2 \dots P_n$ are estimates of direct effects of character while the indirect effects of i^{th} character on seed cotton yield character through j^{th} character is $r_{ij}P_{ij}$

The residual factor i.e. variation in yield unaccounted by these associations, was calculated from following formula.

$$\text{Residual factor (Rx)} = \sqrt{1-R^2}$$

Where,

$$R^2 = (P_1y, r_{1y} + P_2y, r_{2y} + \dots + P_ny, r_{ny})$$

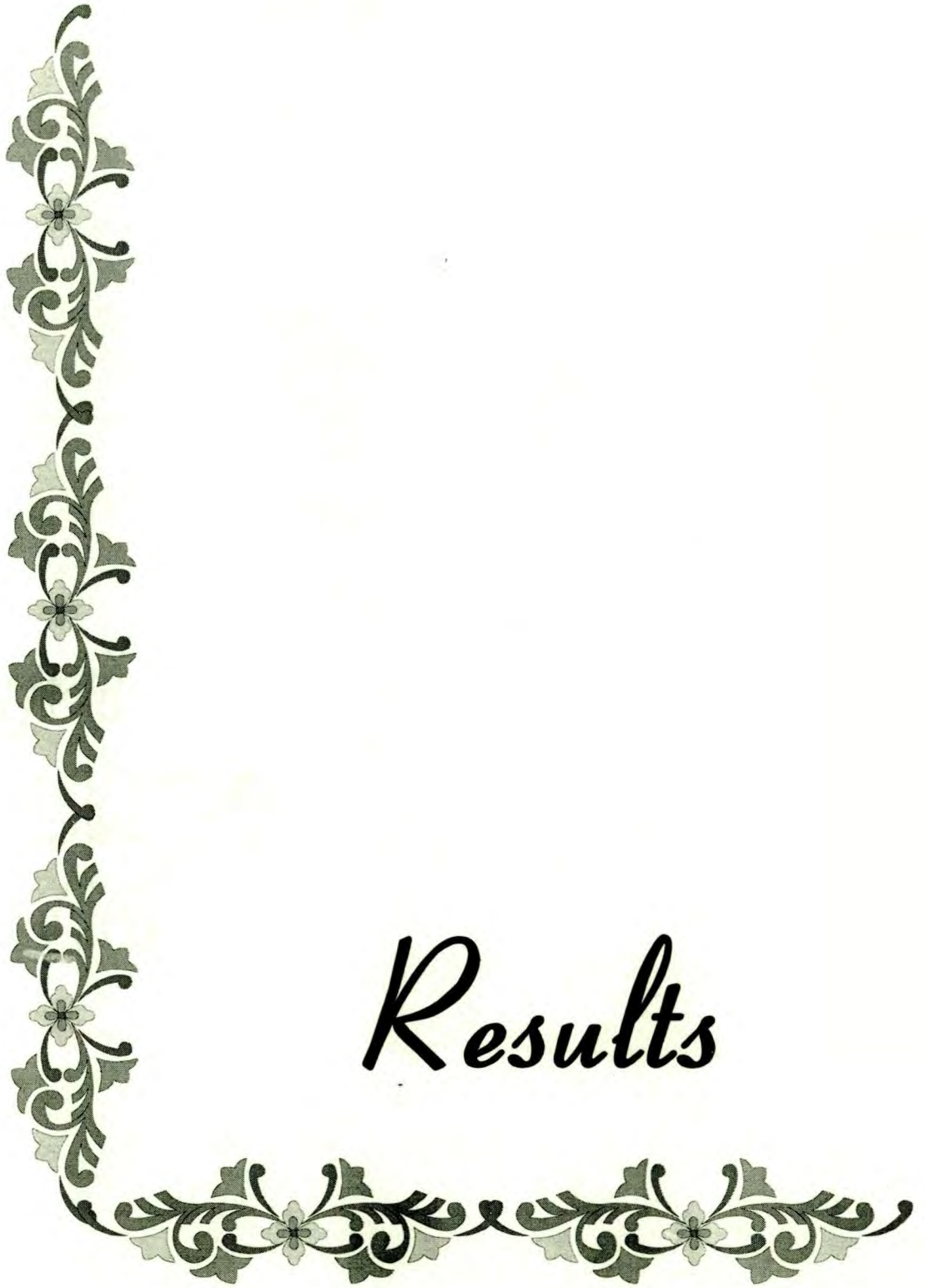
Where,

$$P_1y, P_2y \dots P_ny = \text{path values}$$

$$r_{1y}, r_{2y} \dots r_{ny} = \text{correlation coefficients}$$



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Results

Chapter 4

RESULTS

The present investigation was undertaken with 35 genotypes of soybean developed at different research centers across the country along with three National checks viz., Bragg, JS 93-05, JS-335 and two local checks viz., MAUS-71 and MAUS-81. The objectives of experimental study were to assess the extent of genetic variability for yield and yield contributing characters, root nodulation traits and to study the character association in soybean.

Mean data of genotypes was analyzed as per standard procedure and are presented under the following sub-headings.

- 4.1 Analysis of variance
- 4.2 Mean performance
- 4.3 Genetic variability
- 4.4 Correlation
- 4.5 Path coefficient analysis for yield and yield contributing characters

4.1 Analysis of variance

The analysis of variance showed significant differences among the genotypes for all the twelve characters studied (Table 2).

4.2 Mean performance

The mean performance of 35 genotypes along with 5 checks for twelve characters studied are given in the (Table 3).

Table 2. Analysis of variance for yield and yield contributing characters

Source of variation	d.f.	Mean sum of squares											
		Morphological characters					Root nodulation characters			Yield contributing characters			
		Days to flowering	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Nodule dry wt. (mg)	Number of nodules per plant	Root length (cm)	Oil content (per cent)	100 grain weight (gm)	Number of pods per plant	Yield per plant (gm)
1	2	3	4	5	6	7	8	9	10	11	12	13	14
Replications	2	7.75	14.17	97.75	7.80	0.133	0.717	0.004	0.0073	0.304	11.15	10.00	14.02
Treatments	39	43.32**	37.795**	99.135**	273.57**	9.569**	13.439**	1.582*	4.3613**	57.18**	368.01**	207.07**	15.96**
Error	78	6.27	7.012	9.690	9.637	0.131	0.360	0.014	0.0046	0.627	22.945	3.743	2.735

* and ** indicates significance at 5 and 1 per cent level respectively.

Table 3 : Mean performance of genotypes for yield and yield contributing characters in soybean

Sr. No.	Entry	Morphological characters					Root nodulation characters			Yield and yield contributing characters			
		Days to flowering	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of nodules per plant	Nodule dry wt. (mg)	Root length (cm)	Oil content (per cent)	100 grain weight (gm)	Number of pods per plant	Yield per plant (gm)
1	2	3	4	5	6	7	8	9	10	11	12	13	14
1	Dsb 11	38.33	41.33	93.33	41.33	2.80	10.22	27.67	22.05	21.09	13.33	32.00	16.40
2	JS(SH) 2002-11	33.67	36.67	85.33	41.67	2.00	9.44	23.00	17.83	22.98	12.00	23.33	12.61
3	MAUS-417	40.67	43.67	96.67	48.67	2.13	22.66	47.00	18.21	22.27	13.00	29.00	17.22
4	VLS 72	30.33	33.33	75.33	31.33	3.27	8.66	18.33	18.55	19.67	9.60	21.00	4.77
5	Himso 1678	32.33	35.33	84.00	35.00	3.00	10.33	23.67	20.42	22.23	13.00	29.33	14.58
6	PS 1454	35.67	38.67	92.00	40.00	3.13	18.77	38.33	21.77	21.06	14.00	31.00	14.23
7	MACS 1039	37.67	40.67	94.00	44.00	3.87	10.11	23.33	20.13	22.54	13.70	24.67	14.19
8	BAUS 96	38.67	41.67	94.00	61.67	3.00	13.00	28.00	18.99	21.20	12.50	46.67	13.97
9	DS 2613	33.67	36.67	85.00	48.33	2.07	12.44	28.67	18.94	22.38	13.10	44.67	12.41
10	MAUS 282	36.67	39.67	91.67	43.00	3.93	12.11	28.33	22.61	21.02	13.30	45.67	15.70
11	JS 20-14	34.67	37.67	87.00	40.33	2.07	9.11	23.33	16.61	21.04	10.33	19.33	10.68
12	PS 1444	35.67	38.67	92.00	35.33	3.00	11.67	24.67	19.77	19.79	12.00	37.33	14.34
13	TS 5	32.67	35.67	84.00	61.33	2.80	8.89	18.33	18.50	21.54	10.33	40.00	11.45
14	Himso 1677	33.00	36.00	84.00	38.67	2.87	13.75	29.00	15.77	22.24	13.67	22.67	12.24
15	MACS 1184	38.33	41.33	96.00	33.33	2.00	14.97	31.33	20.38	22.11	14.30	48.00	15.19
16	NRC 80	40.33	43.33	96.00	51.67	3.13	10.38	26.67	21.49	21.67	12.00	56.00	13.27
17	VLS 71	32.33	34.67	82.00	33.00	3.33	8.22	23.00	17.11	24.00	17.00	25.33	13.73
18	RKS 54	41.67	44.67	96.67	52.00	1.80	14.00	32.00	19.50	21.24	9.00	43.67	14.34
19	MACS 1140	36.67	39.67	92.00	54.33	3.00	11.20	29.33	16.05	20.23	13.33	45.67	14.19
20	JS(SH) 2002-14	33.33	36.33	84.00	44.33	2.00	21.78	43.67	21.77	22.47	12.50	52.33	13.19
21	TS 2	38.33	41.33	94.00	62.33	3.87	14.88	30.33	17.39	19.11	13.33	32.33	14.08
22	PS 1450	37.67	44.00	94.00	42.67	3.87	9.66	23.33	21.39	20.21	14.33	28.67	15.62

Table 3 : Contd...

Sr. No.	Entry	Days to flowering	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of nodules per plant	Nodule dry wt. (mg)	Root length (cm)	Oil content (per cent)	100 grain weight (gm)	Number of pods per plant	Yield per plant (gm)
1	2	3	4	5	6	7	8	9	10	11	12	13	14
23	DS 2614	45.67	48.67	102.00	62.00	2.00	12.77	28.33	19.22	20.92	12.67	37.00	17.09
24	NRC 79	36.33	39.33	93.33	43.33	2.87	10.11	26.00	17.88	20.16	13.67	33.00	14.62
25	AMS 1	39.67	42.67	94.00	51.33	2.00	12.33	26.67	18.39	20.49	11.67	52.67	14.77
26	KDS 321	34.67	37.67	85.67	41.33	2.00	8.00	19.00	16.11	18.72	11.30	29.00	11.19
27	NSO 383	34.67	37.67	87.33	46.00	2.00	12.11	24.67	15.39	20.17	14.00	30.33	12.69
28	RKS 52	40.33	43.33	96.00	50.00	2.00	19.78	45.00	17.33	20.75	11.33	57.00	13.60
29	Himso 1676	32.33	35.33	85.33	38.67	3.87	12.44	30.33	17.22	20.29	15.67	31.33	12.88
30	JS 20-18	33.67	36.67	84.00	31.33	2.00	10.00	25.67	16.11	18.83	12.77	44.67	9.06
31	MACS 1188	23.67	47.33	98.67	53.67	2.93	28.33	57.67	20.61	19.81	14.00	61.67	15.63
32	NRC 81	32.33	35.33	82.00	33.33	3.00	15.77	36.00	20.61	21.10	14.00	29.67	13.36
33	JS 20-05	32.33	35.33	84.67	35.33	2.00	8.66	20.00	18.11	19.51	12.67	26.00	11.02
34	NSO 29	39.00	41.33	94.00	44.67	2.07	14.00	32.67	18.72	19.23	16.00	31.67	12.61
35	AMS 19	36.67	39.67	90.67	72.33	2.13	14.88	31.00	21.55	19.31	18.00	30.00	14.50
	Checks												
36	Bragg	36.67	39.67	92.00	43.67	2.00	13.44	43.00	14.83	19.99	11.50	33.00	13.88
37	JS 93-05	34.33	37.33	88.00	40.00	2.93	14.55	30.33	19.66	20.75	13.33	22.33	13.00
38	JS 335	38.33	41.33	92.00	47.00	1.80	19.22	26.00	21.39	20.91	14.00	39.33	16.43
39	MAUS 71	37.67	40.67	93.67	43.33	2.07	12.88	28.00	17.94	20.29	12.33	52.00	14.93
40	MAUS 81	39.67	42.67	98.00	51.67	2.00	14.44	34.00	15.44	20.95	12.33	32.00	14.77
	G. Mean	36.01	39.58	90.36	45.33	2.64	13.25	29.64	18.79	20.86	13.02	36.28	13.61
	SE \pm	1.446	1.528	1.797	1.792	0.209	0.346	0.069	0.039	0.457	2.765	1.117	0.954
	CD at 5%	4.004	4.231	4.973	4.960	0.580	0.959	0.193	0.108	1.365	7.653	3.091	2.643

Table 4. Qualitative characters of soybean genotypes

Sr. No.	Genotypes	Flower colour	Pubescence colour
1	Dsb 11	Violet	Gray
2	JS(SH) 2002-11	White	Tan
3	MAUS-417	Violet	Tan
4	VLS72	Violet	Tan
5	Himso 1678	White	Tan
6	PS 1454	White	Tan
7	MACS 1039	Violet	Absent
8	BAUS 96	White	Tan
9	DS 2613	White	Tan
10	MAUS 282	Violet	Absent
11	JS 20-14	Violet	Tan
12	PS 1444	White	Tan
13	TS 5	Violet	Tan
14	Himso 1677	White	Tan
15	MACS 1184	Violet	Absent
16	NRC 80	White	Tan
17	VLS 71	Violet	Tan
18	RKS 54	White	Tan
19	MACS 1140	Violet	Absent
20	JS(SH) 2002-14	White	Tan
21	TS 2	White	Gray
22	PS 1450	White	Gray
23	DS 2614	White	Tan
24	NRC 79	White	Absent
25	AMS 1	White	Tan
26	KDS 321	Violet	Tan
27	NSO 383	Violet	Tan
28	RKS 52	White	Tan
29	Himso 1676	White	Tan
30	JS 20-18	White	Tan
31	MACS 1188	Violet	Absent
32	NRC 81	Violet	Absent
33	JS 20-05	Violet	Tan
34	NSO 29	White	Absent
35	AMS 19	Violet	Tan
	Check		
36	Bragg	White	Tan
37	JS 93-05	Violet	Absent
38	JS 335	Violet	Absent
39	MAUS 71	Violet	Absent
40	MAUS 81	Violet	Absent

Morphological traits

4.2.1 Days to flowering

Days to flowering is ranged from 30.33 days to 45.66 days with an average mean value of 36.01 days (Table 3). Among the genotypes VLS 72 had shown the earliest mean value for days to flowering (30.33 days) which was earlier than checks viz., Bragg (36.66 days), JS 93-05 (37.67 days) and JS-335 (38.33 days).

4.2.2 Days to 50 per cent flowering

Range of days to 50 per cent flowering was from 33.33 days to 48.67 with an average mean value of 39.58 days (Table 3). Ten genotypes recorded early flowering compared to checks viz., Bragg (39.67 days) and JS 93-05 (37.67 days).

The genotype VLS 73 recorded lowest value for days to 50 per cent flowering followed by VLS 71, NRC 81 and JS 20-05.

4.2.3 Days to maturity

Days to maturity ranged from 75.33 to 102 days with a mean value of 90.35 days. The genotypes DS 2614 (102 days) and JS 20-18, MACS 1188 (98.67 days) were found late in maturity than checks viz., Bragg (92 days) JS 93-05 (88 days) and MAUS 81 (98 days).

Six genotypes viz., VLS 72 (75.33 days), VLS 71 (82 days), NRC 81 (82 days), Himso 1678, TS 5 and Himso 1677 (84 days) were recorded lowest values for day to maturity over best checks viz., MAUS 71 (93.67 days) and MAUS 81 (98 days).

4.2.4 Plant height (cm)

Wide variation was observed for plant height (cm) at maturity ranging from 31.33 cm to 72.33 cm with a general mean of 45.33 cm.

Maximum plants height were recorded by strain AMS 19 (72.33 cm), whereas, lowest plant height was recorded by VLS 73 (31.33 cm) followed by JS 20-18(31.33 cm), VLS 71 (33.00 cm), MACS 1184 (33.33 cm) and NRC 81 (33.33 cm).

In all, 15 genotypes exhibited higher mean performance for plant height over the best checks viz., MAUS-81 (51.67 cm) and JS 335 (47.00 cm).

4.2.5 Number of branches per plant

Number of branches per plant was ranged from 1.80 to 3.93 with a general mean of 2.64. The highest number of branches were recorded by MAUS 282 (3.93) and BAUS 96 (3.00), compared to checks viz., Bragg (2.0), JS 93-05 (2.93), JS 335 (1.80), MAUS 71 (2.07) and MAUS 81 (2.0).

Seven strains viz., TS 2, PS 1450, Himso 1676 (3.87), VLS 71 (3.33), Himso 1678 (3.0), PS 1454 (3.13), PS 1444 (3.0) were recorded higher number of branches per plant. In all 19 genotypes exhibited higher value for number of branches over the checks.

Root nodulation traits

4.2.6 Nodule dry weight per plant (mg)

Nodule dry weight per plant varied from 18.33 to 57.66 with a general mean value of 29.64. Highest nodule dry weight was recorded by strain MACS 1188 (57.67 mg) followed by RKS 52 (45.00 mg), JS (SH)

2002-14 (43.66 mg) and MAUS 417 (47.00 mg). Six genotypes were recorded highest nodule dry weight than checks viz., Bragg (43.00 mg), JS 93-05 (30.33 mg), JS 335 (26.00 mg), MAUS 71 (28.00 mg) and MAUS 81 (34.00 mg).

The lowest nodule dry weight was recorded by genotypes viz., VLS 73 (18.33 mg), TS 5 (18.33 mg), JS (SH) 2002-11 and VLS 71 (23.00 mg).

4.2.7 Number of nodules per plant

Number of nodules per plant ranged from 8.00 to 28.33 with an average value of 13.24 per plant. The highest number of nodules per plant was recorded by strain MACS 1188 (28.33) followed by MAUS 417 (22.66), JS(SH) 2002-14 (21.78) and RKS 52 (19.78) compared to checks viz., Bragg (13.44), JS 93-05 (14.55), JS 335 (19.22), MAUS 71 (12.88) and MAUS 71 (14.44).

The lowest number of nodules per plant was recorded by strains viz., JS 20-14 (9.11), JS (SH) 2002-11 (9.44), VLS 71 (8.22), KDS 321 (7.99) and PS 1450 (9.66).

4.2.8 Root length (cm)

Root length was ranged from 15.39 cm to 22.61 cm with an average mean value of 18.79 cm.

The strain MAUS 282 (22.61 cm), Dsb 11 (22.05 cm), Himso 1678 and JS(SH) 2002-14 (21.77 cm) had recorded the highest root length than checks viz., Bragg (14.83 cm), JS 335 (21.39 cm) and JS 93-05 (19.66 cm). None of genotype exhibited lower root length than checks except Himso 1677 (15.77 cm).

Yield and yield contributing traits

4.2.9 100 grain weight

100 grain weight varied from 9.00 to 18.00 gm with a general mean of 13.02 gm. The genotype AMS 19 (18.00 gm) recorded high 100 grain weight followed by NSO 29 (16.00 gm), Himso 1676 (15.66 gm), VLS 71 (17 gm) over the checks viz., Bragg (11.50 gm) JS 93-05 (13.33 gm) and JS 335 (14.00 gm).

The lowest test weight was recorded by genotypes RKS 54 (9.00 g) followed by VLS 73 (9.60 gm), JS 20-14 (10.33 gm), RKS 52 (11.33 gm) and KDS 321 (11.30 gm).

4.2.10 Number of pods per plant

Number of pods per plant ranged from 19.33 to 61.67 with an average mean value of 36.28. Nineteen genotypes recorded the high number of pods per plant as compared to checks viz., Bragg (33.00), JS 335 (39.33), MAUS 71 (52.00) and MAUS 81 (32.00). The genotypes MACS 1188 (61.66) recorded highest number of pods per plant followed by RKS 52 (57.00), NARC 80 (56.00), AMS 1 (52.66), JS(SH) 2002-14 (52.33) and MACS 1184 (48.00) are found significant over all the checks.

The strain JS 20-14 (19.33) recorded lowest number of pods per plant followed by VLS 73 (21.00) and JS (SH) 2002-11 (23.33).

4.2.11 Oil content

Oil content was ranged from 18.72 to 24.00 per cent with a mean value of 20.86 per cent. Eighteen genotypes were recorded higher oil per cent than checks viz., Bragg (19.99 per cent), JS 93-05 (20.75 per cent), JS 335 (20.91 per cent), MAUS 71 (20.29 per cent) and MAUS 81 (20.95

per cent). The strain VLS 71 (24.00 per cent) recorded high oil content followed by JS(SH) 2002-11 (22.98 per cent), MACS 1039 (22.54 per cent) and JS(SH) 2002-14 (22.47 per cent).

The strain KDS 321 (18.72 per cent) recorded lowest oil content followed by TS 2 (19.11 per cent), NSO 29 (19.23 per cent), AMS 19 (19.50 per cent) and VLS 73 (19.67 per cent).

4.2.12 Yield (gm/plant)

Grain yield per plant (gm) ranged from 4.77 to 17.22 gm with a general mean value of 13.61 gm. Amongst the strains MAUS 417 (17.22 gm) recorded significantly highest grain yield per plant followed by DS 2614(17.09 g), Dsb 11 (16.40 gm) and were found superior than checks viz., Bragg (13.88 gm), JS 93-05 (13.00 gm), JS 335 (16.43 gm), MAUS 71 (14.93 gm) and MAUS 81 (14.77 gm).

Lowest yield per plant was recorded by strain VLS 73 (4.77 gm) followed by JS 20-18(9.06 gm), JS 20-14 (10.68 gm), KDS 321 (11.19 gm), JS 20-05 (11.09 gm) and TS 5 (11.45 gm).

The strains viz., MAUS 417 (17.21 gm) and DS 2614 (17.09 gm) were found statistically significant over the best check JS 335 (16.42 gm).

Qualitative characters of soybean genotypes

4.2.13 Flower colour

The genotypes showed two types of flower colours viz., violet and white. The genotypes viz., Dsb-11, MAUS 417, VLS 73 etc. and checks JS 93-05, JS 335, MASU 71 and MAUS 81 exhibited violet colour.

Whereas genotypes viz., JS(SH) 2002-11, Himso 1678, PS 1454 etc. and check Bragg showed white flower colour.

4.2. 14 Pubescence colour

The strains exhibited two types of pubescence colours viz., Tan and Gray, while some strains found in absent of pubescence viz., MACS 1039, MAUS 282, MACS 1184 etc. Whereas other strains such as Dsb-11 TS 2 and PS 1450 had show gray pubescence. Most of the strains viz., JS(SH) 2002-11, MAUS 417, VLS 73, Himso 1678 etc. and check Bragg showed tan pubescence colour.(Table 4).

4.3 Genetic parameters

The characters under investigation were analyzed for genotypic variance (σ^2g), phenotypic variance (σ^2p), genotypic coefficient of variation (GCV), phenotypic coefficient variation (PCV), heritability (broad sense) and the expected genetic advance (EGA). The results are presented in (Table 5).

Morphological traits

4.3.1 Days to flowering

The range for days to flowering was from 30.33 to 45.66 days. Genotypic variance (12.34) was lower than the phenotypic variance (18.62). The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for days to flowering were 9.76 per cent and 11.99 per cent, respectively. Moderate estimates for heritability (66.29 per cent) and expected genetic advance (16.37 per cent) were observed for the trait days 50% to flowering.

Table 5 : Parameters of genetic variability for yield and yield contributing characters in soybean

Sr. No.	Characters	Range	General mean	Genotypic variance (σ^2_g)	Phenotypic variance (σ^2_p)	GCV (%)	PCV (%)	Heritability (%)	GA	EGA (%)
1.	Days to flowering	30.33 – 45.66	36.01	12.34	18.62	9.76	11.99	66.29	5.89	16.36
2.	Days to 50% flowering	33.33 – 48.66	39.57	10.26	17.27	8.09	10.50	59.40	5.08	12.85
3.	Days to maturity	75.33 – 102.00	90.35	29.81	39.50	6.04	6.96	75.47	9.76	10.81
4.	Plant height (cm)	31.33 – 72.33	45.33	87.97	97.61	20.69	21.79	90.13	18.34	40.46
5.	Number of branches per plant	1.80 – 3.93	2.64	0.52	0.53	27.38	27.76	97.28	1.46	55.63
6.	100 grain weight (gm)	9.00 – 18.00	13.02	3.12	3.25	13.58	13.86	95.95	3.56	27.40
7.	Number of pods per plant	19.33 – 61.66	36.28	115.02	137.96	29.56	32.37	83.37	20.17	55.60
8.	Oil content (per cent)	18.72 – 24.00	20.86	1.45	1.45	5.78	5.79	99.68	2.47	11.88
9.	Nodule dry wt. (mg)	18.33 – 57.67	13.24	18.85	19.48	32.77	33.31	96.78	8.79	66.41
10	Number of nodules per plant	8.00 – 28.33	29.64	67.51	71.32	27.72	28.49	94.65	16.46	55.55
11	Root length (cm)	15.39 – 22.61	18.79	4.36	4.72	11.11	11.56	92.36	4.13	22.00
12	Yield per plant (gm)	4.77 – 17.21	13.61	4.15	6.88	14.97	19.28	60.29	3.25	23.95

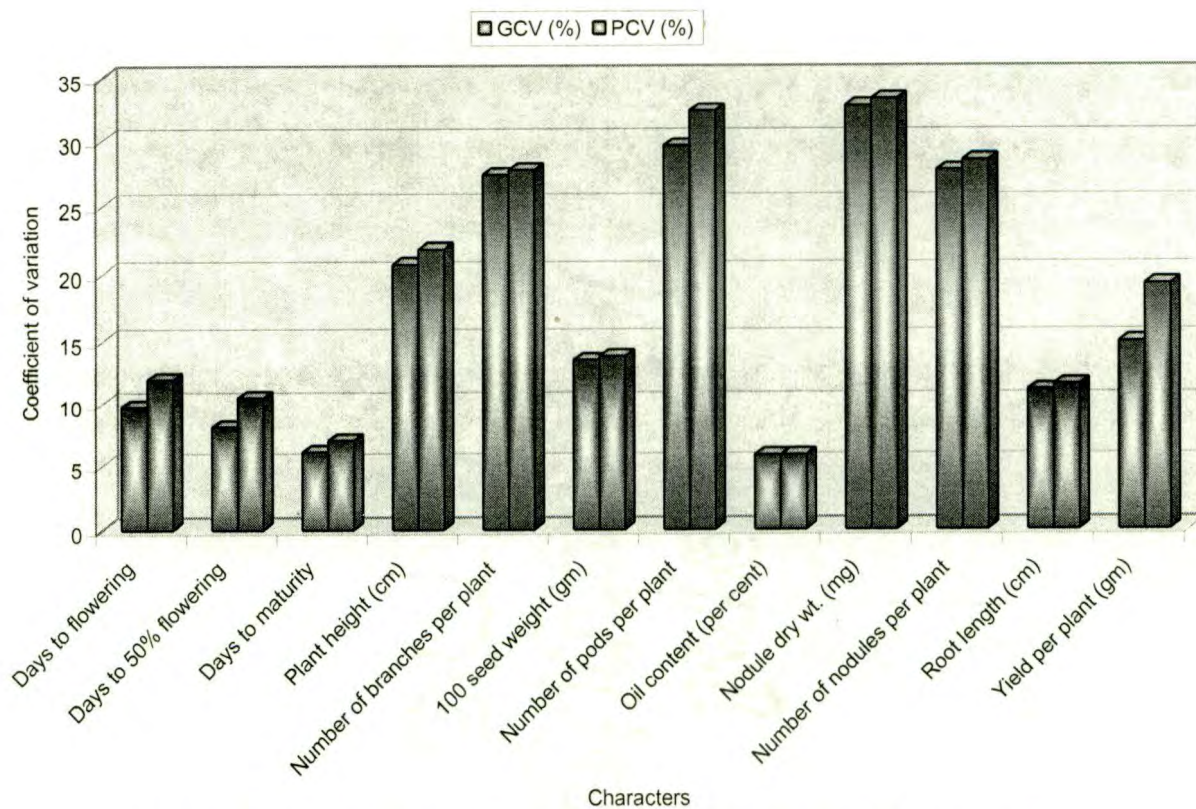


Fig. 1. Genotypic and phenotypic coefficients of variation for yield and its contributing components

Days to 50 per cent flowering

The character days to 50 per cent flowering varied from 33.33 days to 48.66 days. Genotypic variance (10.26) was lower than the phenotypic variance (17.27). GCV and PCV for days to 50 per cent flowering were 8.09 and 10.50 per cent, respectively. The moderate heritability estimates (59.40 per cent) with low expected genetic advance (12.85 per cent) were observed for this trait.

4.3.2 Days to maturity

The range for days to maturity was from 75.33 days to 102 days. Genotypic variance (29.81) was found lower than phenotypic variance (39.50). Genotypic coefficient of variation and phenotypic coefficient of variation for days to maturity were 6.04 and 6.95 per cent, respectively. High heritability estimates (75.47 per cent) coupled with low expected genetic advance (10.81 per cent) was observed for the trait.

4.3.3 Plant height (cm)

A wide range of variation was observed for this traits ranging from 31.33 to 72.33 cm. The genotypic and phenotypic variance values were 87.97 and 97.61, respectively. The genotypic and phenotypic coefficients of variation for plant height was 20.69 and 21.79 per cent, respectively. High heritability estimates (90.13 per cent) coupled with highest expected genetic advance (40.46 per cent) were observed.

4.3.4 Number of branches per plant

The character number of branches per plant was ranged from 1.80 to 3.93. The genotypic variance (0.522) and phenotypic variance (0.537) values was more or less equal. Phenotypic coefficient of variation

(27.76 per cent) was slightly higher than genotypic coefficient of variation (27.38 per cent). High heritability estimates (97.28 per cent) coupled with high expected genetic advance (55.63 per cent) were observed.

Root nodulation traits

4.3.5 Nodule dry weight per plant (mg)

A wide range of nodule dry weight per plant (mg) from 18.33 to 57.66 mg was observed for this trait. The genotypic variance (67.51) was lower than phenotypic variance (71.32), genotypic coefficient of variation and phenotypic coefficient of variation were 27.71 and 28.49 per cent respectively. High heritability estimates (94.65) coupled with high expected genetic advance (55.55 per cent) were observed for the trait.

4.3.6 Number of nodules per plant

The character number of nodules per plant was ranged from 8.00 to 28.33. The genotypic variance 18.85 was lower than phenotypic variance 19.48. Genotypic coefficient of variation and phenotypic coefficient of variation were 32.77 per cent and 33.21 per cent, respectively. High heritability estimates (99.78 per cent) coupled with high expected genetic advance (66.41 per cent) were observed.

4.3.8 Root length (cm)

The range of root length was from 15.38 to 22.61 cm. The genotypic variance and phenotypic variance were 4.36 and 4.72, respectively. Phenotypic coefficient of variation (11.56 per cent) was higher than genotypic coefficient of variation (11.11 per cent). High heritability estimates (92.36 per cent) coupled with moderate expected genetic advance (21.99 per cent) was observed.

Yield and yield contributing characters

4.3.7 100 grain weight

100 grain weight varied from 9.00 gm to 18.00 gm. The genotypic variance (3.126) and phenotypic variance (3.258) value was more or less equal. Genotypic coefficient of variation (13.57 per cent) was lower than phenotypic coefficient of variation (13.86 per cent). High heritability estimates (95.25 per cent) coupled with moderate expected genetic advance (27.39 per cent) were observed.

4.3.10 Number of pods per plant

A wide range of variation was observed for number of pods per plant ranging from 19.33 to 61.67. Highest genotypic variance (115.02) and phenotypic variance (137.96) were observed. The GCV (29.57 per cent) was lower than PCV (32.37 per cent). High heritability estimates (83.37 per cent) coupled with high expected genetic advance (55.59 per cent) were observed.

4.3.11 Oil content (per cent)

The range of oil content varied from 18.72 to 24.00 per cent. The genotypic (1.452) and phenotypic (1.457) variance value were found more or less equal. Genotypic coefficient of variation and phenotypic coefficient of variation were 5.77 and 5.78 per cent, respectively. The highest heritability estimates (99.68 per cent) coupled with the poor genetic advance (11.88 per cent) were observed for the trait.

4.3.12 Yield per plant (gm)

Yield per plant (g) varied from 4.77 to 17.21 gm. Genotypic variance (4.15) was lower than phenotypic variance (6.88). Genotypic

coefficient of variation and phenotypic coefficient of variation estimated were 14.97 per cent and 19.28 per cent, respectively. This character exhibited moderate heritability estimates (60.29 per cent) coupled with moderate expected genetic advance (23.94 per cent).

4.4 Correlation

Genotypic and phenotypic correlations were calculated among 11 characters with grain yield (gm) per plant to find out inter relationship of different yield component at genotypic and phenotypic levels and are presented in Table 6 and 7, respectively.

Correlation studies revealed that yield per plant was significantly and positively correlated with days to flowering, days to 50% flowering, days to maturity, plant height and all the root nodulation traits viz., nodule dry weight (mg), number of nodules per plant and root length (cm) at both genotypic and phenotypic level, whereas 100 grain weight and number of pods per plant showed positive and significant correlation with yield at genotypic level. Weak positive correlation was observed between number of branches per plant and oil per cent.

The character days to 50 per cent flowering exhibited positive and significant correlation with plant height (cm), nodule dry weight (mg), number of pods per plant and number of nodules per plant at both genotypic and phenotypic level. Days to maturity also exhibited positive and significant correlation with plant height, number of pods per plant, nodule dry weight and number of nodules per plant at phenotypic level.

Plant height (cm) exhibited positive and significant correlation with number of pods per plant at genotypic as well as

Table 6 : Genotypic correlation of soybean yield with yield contributing characters

Sr. No.	Characters	Days to flowering	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	100 grain weight (gm)	Number of pods per plant	Oil content (per cent)	Nodule dry wt. (mg)	Number of nodules per plant	Root length (cm)	Yield per plant (gm)
1	2	3	4	5	6	7	8	9	10	11	12	13	14
1.	Days to flowering	1.000	0.675**	0.767**	0.431**	-0.274	-0.124	0.161	0.027	-0.068	-0.045	0.056	0.552**
2.	Days to 50% flowering		1.000	1.114	0.628**	-0.191	-0.041	0.545**	-0.132	0.484**	0.515**	0.235	0.857**
3.	Days to maturity			1.000	0.561**	-0.166	0.044	0.480**	-0.105	0.424**	0.456**	0.193	0.870**
4.	Plant height (cm)				1.000	-0.145	0.027	0.332*	-0.136	0.260	0.210	0.067	0.406**
5.	Number of branches per plant					1.000	0.321*	-0.210	0.156	-0.206	-0.168	0.240	0.016
6.	100 grain weight (gm)						1.000	-0.159	0.039	0.162	0.132	0.214	0.375*
7.	Number of pods per plant							1.000	-0.048	0.451**	0.444**	0.236	0.316*
8.	Oil content (per cent)								1.000	0.030	0.021	0.196	0.260
9.	Nodule dry wt. (msg)									1.000	0.913**	0.272	0.475**
10	Number of nodules per plant										1.000	0.111	0.447**
11	Root length (cm)											1.000	0.420**
12	Yield per plant (gm)												1.000

* and ** indicates significance at 5 and 1 per cent level respectively.

Table 7 : Phenotypic correlation of soybean yield with yield contributing characters

Sr. No.	Characters	Days to flowering	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	100 grain weight (gm)	Number of pods per plant	Oil content (per cent)	Nodule dry wt. (mg)	Number of nodules per plant	Root length (cm)	Yield per plant (gm)
1	2	3	4	5	6	7	8	9	10	11	12	13	14
1.	Days to flowering	1.000	0.508**	0.513**	0.342*	-0.234	-0.1000	0.100	0.021	-0.045	-0.030	0.039	0.377*
2.	Days to 50% flowering		1.000	0.717**	0.450**	-0.173	-0.042	0.388*	-0.110	0.375*	0.351*	0.186	0.436**
3.	Days to maturity			1.000	0.462**	-0.140	0.024	0.384*	-0.091	0.351*	0.389*	0.1543	0.586**
4.	Plant height (cm)				1.000	-0.134	0.043	0.329*	-0.129	0.247	0.199	0.063	0.312*
5.	Number of branches per plant					1.000	0.313*	-0.193	0.155	-0.199	-0.156	0.227	0.029
6.	100 grain weight (gm)						1.000	-0.134	0.037	0.158	0.127	0.200	0.296
7.	Number of pods per plant							1.000	-0.046	0.4065**	0.410**	0.217	0.255
8.	Oil content (per cent)								1.000	0.029	0.021	0.188	0.207
9.	Nodule dry wt. (mg)									1.000	0.878**	0.258	0.348*
10	Number of nodules per plant										1.000	0.112	0.345*
11	Root length (cm)											1.000	0.303*
12	Yield per plant (gm)												1.000

* and ** indicates significance at 5 and 1 per cent level respectively.

phenotypic level, whereas weak positive correlation was observed for plant height with 100 grain weight (gm), nodule dry weight (mg), number of nodules per plant and root length (cm) at both the levels.

Number of branches exhibited positive and significant correlation with 100 grain weight (gm) at genotypic as well as phenotypic level. Whereas, weak positive correlation was observed with oil content, root length (cm) and grain yield per plant at both the levels.

The character 100 grain weight showed weak positive correlation with oil content, nodule dry weight (mg), number of nodules per plant and root length (cm) at both the levels.

Number of pods per plant exhibited positive and significant correlation with nodule dry weight (mg) and number of nodules per plant at genotypic and phenotypic level, whereas, negative and weak correlation with oil content was observed.

The character oil content exhibited positive but weak correlation with nodule dry weight per plant (mg), number of nodule per plant and root length at both the levels. The character nodule dry weight per plant (mg) exhibited positive and significant correlation with number of nodule per plant at genotypic and phenotypic level and positive correlation with root length (cm) at both the level.

Number of nodules per plant was positively correlated with root length at genotypic as well as phenotypic levels.

4.5 Path analysis

Path analysis between yield, morphological and root nodulation traits were carried out by considering genotypic correlation coefficients (Table 8).

Table 8 : Direct and indirect effects of yield components on soybean yield per plant.

Sr. No.	Characters	Days to flowering	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	100 grain weight (gm)	Number of pods per plant	Oil content (per cent)	Nodule dry wt. (mg)	Number of nodules per plant	Root length (cm)	Yield per plant (gm)
1	2	3	4	5	6	7	8	9	10	11	12	13	14
1.	Days to flowering	-0.1824	0.3143	0.4852	-0.0397	0.0179	-0.0396	-0.0186	0.0095	-0.0108	0.0106	0.0052	0.552
2.	Days to 50% flowering	-0.1231	0.4654	0.7055	-0.0578	0.0124	-0.0133	-0.0631	-0.0468	0.0773	-0.1216	0.0217	0.857
3.	Days to maturity	-0.1398	0.5187	0.6330	-0.0516	0.0128	0.0140	-0.0555	-0.0373	0.0677	-0.1078	0.0178	0.870
4.	Plant height (cm)	-0.0786	0.2924	0.3551	-0.0921	0.0094	0.0086	-0.0384	-0.0481	0.0414	-0.0497	0.0061	0.406
5.	Number of branches per plant	0.0500	-0.0887	-0.1050	0.0133	-0.0654	0.1029	0.0242	0.0555	-0.0328	0.0397	0.0221	0.016
6.	100 grain weight (gm)	0.0225	-0.0193	0.0277	-0.0024	-0.0209	0.3208	0.0184	0.0138	0.0259	-0.0311	0.0198	0.375
7.	Number of pods per plant	-0.0293	0.2538	0.3038	-0.0306	0.0137	-0.0509	-0.1158	-0.0171	0.0720	-0.1049	0.0218	0.316
8.	Oil content (per cent)	-0.0049	-0.0614	-0.0666	0.0124	-0.0162	0.0124	0.0056	0.3551	0.0048	-0.0050	0.0180	0.260
9.	Nodule dry wt. (mg)	0.0124	0.2252	0.2682	-0.0239	0.0134	0.0520	-0.0522	0.0106	0.1598	-0.2155	0.0251	0.475
10	Number of nodules per plant	0.0082	0.2395	0.2888	-0.0193	0.0110	0.0422	-0.05146	0.0075	0.1458	-0.2362	0.0162	0.447
11	Root length (cm)	-0.0102	0.1095	0.1222	-0.0061	-0.0157	0.0688	-0.0273	0.0694	0.4351	-0.0261	0.0924	0.420

Residual effect = 0.0643

Morphological traits

4.5.1 Days to flowering

The result of path coefficient analysis revealed that days to flowering has negative direct effect on yield (-0.1824). It has negative indirect effect on yield through plant height, 100 grain weight (gm), number of pods per plant and nodule dry weight (mg). Positive indirect effect on yield were also observed through days to 50% flowering, days to maturity, number of branches per plant, oil content, number of nodules per plant and root length (cm).

4.5.2 Days to 50% flowering

The direct effect of days to 50% flowering is positive (0.4654). It has positive indirect effect on yield via days to maturity, number of branches per plant, nodule dry weight, root length (cm), whereas it exhibited negative indirect effect on yield via days to flowering, plant height (cm), 100 grain weight, number of pods per plant, oil content and number of nodule/plant.

4.5.3 Days to maturity

Days to maturity exerted highest positive direct effect (0.6330) on yield, whereas, positive indirect effect was also observed via days to 50% flowering, number of branches per plant, 100 grain weight, nodule dry weight and root length (cm).

4.5.4 Plant height

The trait plant height exhibited negative but minor (-0.0921) direct effect on yield. The negative indirect effect was expressed via days

to flowering, number of pods per plant, oil content and number of nodule per plant.

4.5.5 Number of branches per plant

The character number of branches per plant exerted negative (-0.0654) direct effect on yield, whereas positive indirect effect was observed on yield via days to flowering, plant height, 100 grain weight, nodule dry weight and root length (cm).

Root nodulation characters

4.5.6 Nodule dry weight (mg)

The trait nodule dry weight showed positive direct effect on yield and traits viz., days to flowering, days to 50% flowering, days to maturity, number of branches per plant, 100 grain weight, oil content and root length also expressed positive indirect effect. Negative indirect effect were observed through plant height, number of pods per plant and number of nodules per plant.

4.5.7 Number of nodules per plant

The character number of nodules per plant exerted negative direct effect (-0.2362) on yield, while positive indirect effect was observed through days to flowering, days to 50% flowering, days to maturity, number of branches, 100 grain weight, oil content, nodule dry weight and root length.

4.5.8 Root length (cm)

The trait root length showed positive direct effect (0.0924) on yield and positive indirect effect via days to 50% flowering, days to maturity, 100 grain weight, oil content and nodule dry weight.

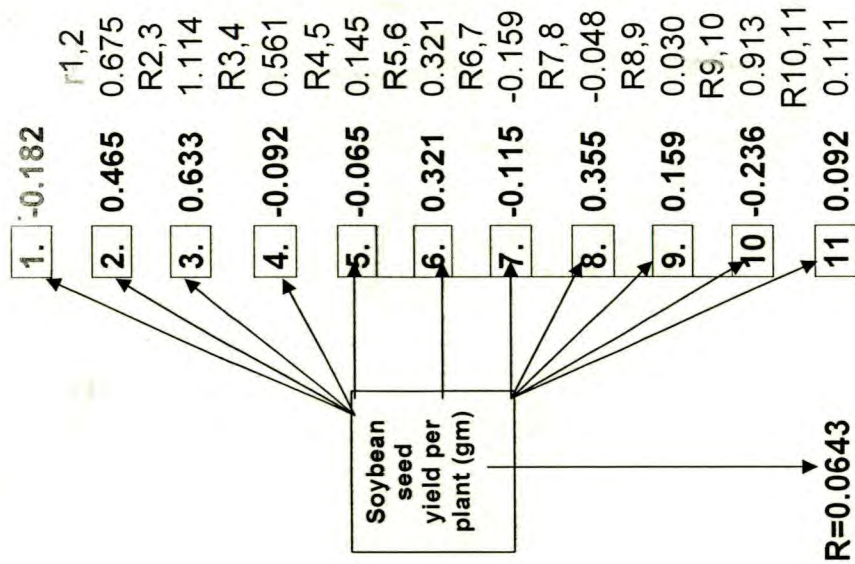


Fig. 2. Path diagram showing the factors influencing soybean grain yield per plant

1.	Days to flowering
2.	Days to 50% flowering
3.	Days to maturity
4.	Plant height (cm)
5.	Number of branches per plant
6.	100 grain weight (gm)
7.	Number of pods per plant
8.	Oil content (per cent)
9.	Nodule dry wt. (mg)
10.	Number of nodule per plant
11.	Root length (cm)

Yield and yield contributing characters

4.5.9 100 grain weight (gm)

The direct effect of 100 grain weight on yield is positive (0.3208). Indirect effect on yield was also observed through days to flowering, days to maturity, number of pods/plant, oil content, nodule dry weight and root length.

4.5.10 Number of pods per plant

The trait number of pods per plant observed negative direct effect on yield (-0.1158), whereas, it showed negative indirect effect on yield through days to flowering (-0.0186), plant height (-0.055), and number of nodules per plant (-0.0514).

4.5.11 Oil content (%)

The character oil content exerted positive direct (0.3551) effect on yield. Negative indirect effect was observed through plant height (-0.0481), number of pods/plant (-0.0171), days to 50% flowering (-0.0468) and days to maturity (-0.0373) whereas it exerted positive indirect effect on yield via days to flowering (0.0095), 100 grain weight (0.0138), nodule dry weight (0.0107) number of nodule/plant (0.0075) number of branches per plant (0.0555).

In general, genotypic path coefficient analysis revealed that days to 50% flowering, days to maturity, 100 grain weight and oil content exerted highest positive direct effect on grain yield per plant, whereas direct positive effect of nodule dry weight and root length was observed minor, while days to flowering, plant height, number of branches per plant, number of pods per plant and number of nodules per plant had exerted negative direct effect on grain yield.



Discussion

Chapter-5

DISCUSSION

Above 97 per cent of soybean in India is cultivated mostly under rainfed or distress prone conditions predominantly in black soils and its area increased from 0.3 lakh ha in 1971 to 88.5 lakh ha in 2007 (295 times increase in 47 years or @ 2.4 per cent per year) (Samara and Ramchandra, 2009). It is a unique example of tremendous diversification of a cash crop and that too in uncertain rainfed agriculture. Soybean is a versatile crop of vegetable oil, pulse, food, animal feed, fodder, industrial uses and foreign exchange earner with a wide range of adaptations both to soil moisture deficit and high rainfall typologies. After palm oil, soybean is the second cheapest source of edible oil. The present cost of 1 kg soya protein is Rs. 48 which is 15 times cheaper as compared to Rs. 714 of paneer (milk product) protein. For the past five years soybean production has occupied first place among the oilseed crops of India. About 75 per cent of deoiled cake (DOC) was exported from which foreign exchange of Rs. 5900 crores was earned during 2006-07 and the rest is being used domestically as feed (20%) and food (5%). Soybean contributed 10% to the total foreign exchange earnings of the agriculture sector and 70 % to the oilseed sub-sector. Whereas, the current production of soybean is 9.5 million tones, domestic demand has been projected at 17 million tones. Soybean market prices ranged from Rs. 1470/q in April 2007 to Rs. 2305/q in June 2008 and remained always higher than minimum support price of

Rs. 1050/q. Both the domestic and export market is growing @ 6-8 per cent per annum and intensification of its cultivation is quite attractive.

Unprecedented growth in the production was realized mainly due to expansion in area and there are vast opportunities to enhance its productivity further. Against an average world productivity of 2.2 t/ha and potential of 2.5 t/ha under rainfed condition of India, the current productivity of 1.07 t/ha presents vast scope for enhancing yield and farm income. Actual yield ranged from 0.65 to 1.38 t/ha under important rainfed typologies of India leaving a gap of 39 to 234 per cent and overall average gap of 102 per cent which can be bridged by improved technologies, enabling policies, marketing, processing, private and public participation. Therefore, there is need to evolve improved, high yielding, non-shattering varieties with intermediate growth, photo-insensitive and having tolerance for important pests and diseases. However, monoculture expansion of JS 335 and JS 93-05 (JNKVV, Jabalpur) on more than 70 per cent area in the country may lead to disaster of pest outbreak and epidemics in coming years.

In applied plant breeding success of any crop improvement programme, mainly depends on the nature and magnitude of genetic variability existed in breeding material. Such improvements are normally achieved by exploiting existing variability either for the selection purpose or for hybridization. Effectiveness of selection directly depends on the amount of heritability and genetic advance.

In the present investigation, genetic variability, heritability, correlation and path analysis has been studied. The results of present investigation were discussed as follows.

5.1 Analysis of variance

The analysis of variance for the characters viz., days to flowering, days to 50 per cent flowering, days to maturity, plant height, number of branches per plant, 100 grain weight, number of pods per plant, oil content, number of nodules per plant, nodule dry weight, root length and grain yield per plant showed significant genotypic differences indicating presence of sufficient variability among the different genotypes selected for present study.

5.2 Mean performance

The mean performance of different characters studied is presented in (Table 2).

The genotypes viz., VLS 73 (30.33 days), Himso 1678 and VLS 71 (32.33 days), Himso 1677 (34 days), NRC 18 (32.33 days), JS 20-05 (32.33 days) and JS (SH) 2002-14 (33.33 days) were relatively early in flowering than checks viz., Bragg (36.66 days), JS 93-05 (37.66 days), JS 335 (38.33 days), MAUS 71 (37.66 days) and MAUS 81 (39.66 days).

Among the genotypes VLS 73 (33.33 days) followed by VLS 71 (34.66 days), Himso 1678 (35.33 days), Himso 1676 (35.33 days), TS 5 (35.66 days), NRC 18 and JS 20-05 (35.33 days) were found significantly superior over all the checks viz., Bragg (39.66 days), JS 93-05 (37.66 days) and JS 335 (41.33 days) for 50% flowering.

The earliness in maturity was observed in seven genotypes viz., VLS 73 (75.33 days), VLS 71 (82 days), NRC 81 (82 days), Himso 1678, TS 5 and Himso 1677 (84 days) compared to all the checks MAUS 71 (93.66 days), MAUS 81 (98 days), Bragg (88 days), JS 93-05 (92 days) and JS 335 (93.66 days).

The character number of branches per plant exhibited least variation. The maximum number of branches was observed in genotype MAUS 282 (3.93) and BAUS 96 (3.00).

Maximum plant height was observed in genotypes AMS 19 (72.33 cm) followed by TS 2 (62.33 cm), DS 2614 (62 cm), BAUS 96 (61.66 cm) and TS 5 (61.33 cm). However, minimum plant height was exhibited by genotype VLS 73 (31.33 cm) and JS 20-18 (31.33 cm).

Highest 100 grain weight was observed in AMS 19 (18 gm) followed by NSO 29 (16 g), Himso 1676 (15.66 g), VLS 71 (17 g). The highest number of pods per plant was observed in genotypes MACS 1188 (61.66) followed by RKS 52 (57), NRC 80 (56) AMS 1 (52.66) and JS (SH) 2002-14 (52.33).

Highest oil content was observed in genotype VLS 71 (24 %) followed by JS (SH) 2002-11 (22.98 %), MACS 1039 (22.54 %), JS (SH) 2002-14 (22.47 %) over the checks Bragg (19.98 %), JS 93-05 (20.75 %) and JS 335 (20.91 %).

Maximum number of nodules per plant was recorded in MACS 1188 (28.33), MAUS 417 (22.66), JS (SH) 2002-14 (21.77) and RKS 52 (19.77). The character nodule dry weight was highest in genotype MACS 1188 (57.66 mg), followed by RKS 52 (45 mg), JS (SH) 2002-14

(43.66 mg) and MAUS 417 (47 mg) than all the four checks viz., Bragg (43 mg), JS 93-05 (30.33 mg), JS 335 (36 mg) and MAUS 81 (34 mg).

Maximum root length was recorded in genotypes viz., MAUS 282 (22.60 cm), Dsb 11 (22.05 cm), Himso 1678 and JS (SH) 2002-14 (21.77 cm) than checks viz., Bragg (14.83 cm), JS 335 (21.38 cm) and JS 93-05 (19.66 cm).

Three genotypes viz., MAUS 417 (17.21 gm), DS 2614 (17.09 gm), Dsb 11 (16.40 gm) were found statistically significant over all the checks Bragg (13.88 gm), JS 93-05 (12.99 gm), JS 335 (16.42 gm), MAUS 71 (14.92 gm) and MAUS 81 (14.77 gm) for grain yield per plants.

5.3 Genetic variability

Genetic variability is prerequisite in crop improvement programme. The heritable variation is masked by non-heritable variation which creates difficulty in exercising selection. Hence, it becomes necessary to split overall variability into heritable and non-heritable components with the help of certain genetic parameters which may enable the breeder to plan out proper breeding programme since many characters of economic importance are highly influenced by environmental condition. Hence, progress of population mainly depends upon the magnitude of genetic variability present in population. In the present study efforts have been made to analyze the component of variability in different genotypes with an object to exploit in future breeding programme.

5.3.1 Range of variability

In general wide range of variability was observed for all the characters. In soybean significant amount of genetic variability has been

reported by Harer and Deshmukh (1992) for characters days to 50% flowering, days to maturity, plant height, pods per plant, 100 grain weight and grain yield per plant. Similarly, Mahajan *et al.* (1994) reported considerable amount of genetic variability for all the characters and Gohil *et al.* (2006) reported highly significant difference for all the 10 characters in 55 genotypes of soybean.

Estimates for phenotypic variance are higher than genotypic variance in all the characters. High genotypic and phenotypic variance were observed for the character for number of pods per plant followed by plant height, nodule dry weight per plant, days to maturity, number of nodules per plant and days to flowering. The results of present findings are in agreement with those of Bangar *et al.* (2003) and Karad *et al.* (2005), Sirohi *et al.* (2007) observed high values of genotypic and phenotypic variance for pods per plant, 100 grain weight and days to maturity, Poonam Sharma *et al.* (2007) for number of nodule and nodule dry weight in soybean.

The lowest genotypic and phenotypic variance were observed for the characters number of branches per plant and oil content. These findings are in conformity with the findings of Bhairav Bhusan *et al.* (2006).

5.3.2 Genotypic and phenotypic coefficient of variation

In the present investigation, GCV estimates are lower than PCV indicating that these characters responded more to environmental

fluctuations. Similar trend of results were reported by Lal and Haque (1972), Ghatge (1993), Singh *et al.* (1996) and Bangar *et al.* (2003). Therefore, there is ample scope for selection for increased expansion of PCV and GCV values as there is great influence of environmental factors.

In the present study, High genotypic and phenotypic coefficient of variation were observed for the character viz., number of pods per plant, number of branches, number of nodules per plant, nodule dry weight per plant, plant height and 100 grain weight. Harer and Deshmukh (1992) observed high genotypic and phenotypic coefficient of variation for plant height, pods per plant, number of branches per plant, 100 grain weight and grain yield. These results are in conformity with those reported by Mahajan *et al.* (1974). Poonam Sharma *et al.* (2007) for nodules per plant and nodule dry weight. High magnitude of variation was observed for number of branches per plant, nodule dry weight, number of branches per plant and number of nodules per plant indicating better scope for genetic improvement of these traits.

5.3.3 Heritability and genetic advance

The heritability estimates along with expected genetic advance are more useful in predicting yield under phenotypic selection than heritability estimates alone (Johnson *et al.*, 1955). In the present study the range of heritability (bs) was from 59.40 per cent for days to 50% flowering to 99.68 per cent for oil content.

The character days to maturity, number of pods, plant height, root length, nodule dry weight (mg), 100 grain weight, number of nodules per plant and oil content recorded higher (> 70 %) broad sense heritability.

High heritability estimates were reported for number of branches per plant, days to maturity, plant height by Banger (2003), number of pods/plant and grain yield per plant by Gohil *et al.* (2006) and Bhairav Bhushan *et al.* (2006), days to flowering by Sharma *et al.* (1983), for 100 grain weight and days to 50% flowering by Jangale *et al.* (1994) and Mahajan *et al.* (1994) for grain yield by Sharma *et al.* (1983) and Taware *et al.* (1995) and for oil content by Bartly and Weber (1982).

In present study for all the important characters the heritability estimates are very high. However, as in broad sense heritability the contribution of dominance and epistasis are also included, such estimates alone does not hold the repeatability of expression of characters in the selection programme. Similarly, the broad sense heritability estimates are prone to change from location to location and interaction with the environment. The heritability estimates for yield contributing characters were also reported by Johnson *et al.* (1955), Mahajan *et al.* (1994), Chettri *et al.* (2005), Dhillon *et al.* (2005) and Yadav (2006).

The high heritability estimates are associated with low expected genetic advance indicating the non additive genetic control. Association of heritability, expected genetic advance and genotypic coefficient of variability has been reported by several workers including Mahajan *et al.* (1994), Chettri *et al.* (2005), Dev Vart *et al.* (2005) and Bhairav Bhushan *et al.* (2006).

High heritability estimates coupled with high expected genetic advance were observed for number of branches per plant and plant height by Bangar *et al.* (2003). Gohil *et al.* (2006) for number of pods per

plant and grain yield per plant. Sharma *et al.* (1983) for days to flowering and days to maturity. Mahajan *et al.* (1994) for plant height and pods per plant. Taware *et al.* (1995) for 100 grain weight and Jangale *et al.* (1994) for 50% flowering. High heritability also observed for number of nodules per plant, nodule dry weight and root length.

Thus from the foregoing discussion it is clear that the characters oil content, number of branches per plant, number of nodules per plant, nodule dry weight per plant, plant height, root length recorded high heritability and high expected genetic advance, indicating the presence of additive gene action and effective in phenotypic selection. Thus while exploiting genetic variability a due weightage should be given to these characters.

5.4 Correlation

Correlation coefficient is an important statistical constant which gives the degree of association among the various characters. Grain yield is a complex character and depends upon the other agronomic traits, therefore, study of the relationship of characters with each other and with yield become more important in crop improvement programme. It is very essential to find out the relative contribution of each component character in yield so as to give weightage during the selection. In present investigation genotypic and phenotypic correlations were calculated for yield and yield components.

The characters days to flowering, days to 50% flowering, days to maturity, plant height, number of pods per pant, 100 grain weight, number of nodules per plant, nodule dry weight and root length showed

positive and significant correlation with grain yield at both the levels. Amarnath *et al.* (1990) reported significant correlation of grain yield with days to 50% flowering, number of pods per plant, days to maturity, plant height, number of branches per plant, 100 grain weight. Similarly, Taware *et al.* (1995) for days to flowering, days to maturity and number of pods per plant. Inderjit Singh *et al.* (1999) for nodules per plant and number of pods per plant, Poonam Sharma *et al.* (2007) for number of nodules and nodule dry weight per plant.

Days to flowering exhibited positive and significant correlation with days to maturity and plant height at both the levels. Days to maturity showed positive and significant correlation with plant height and number of pods per plant. Similar findings were reported by Sharma *et al.* (1983), Taware *et al.* (1995) and Gohil *et al.* (2006).

The positive and significant correlation existed between days to flowering with days to maturity and plant height, plant height with number of pods per plant in turn their association with grain yield was positive at both the levels. It is important to note that the characters days to flowering, days to maturity, plant height, number of pods per plant, 100 grain weight, number of nodules/plant, nodule dry weight and root length were positively correlated with grain yield. Selection based on the knowledge and direction of association becomes yield with one character will be very useful in identifying key characters which can be perfectly exploited in a short time to achieve yield improvement in soybean.

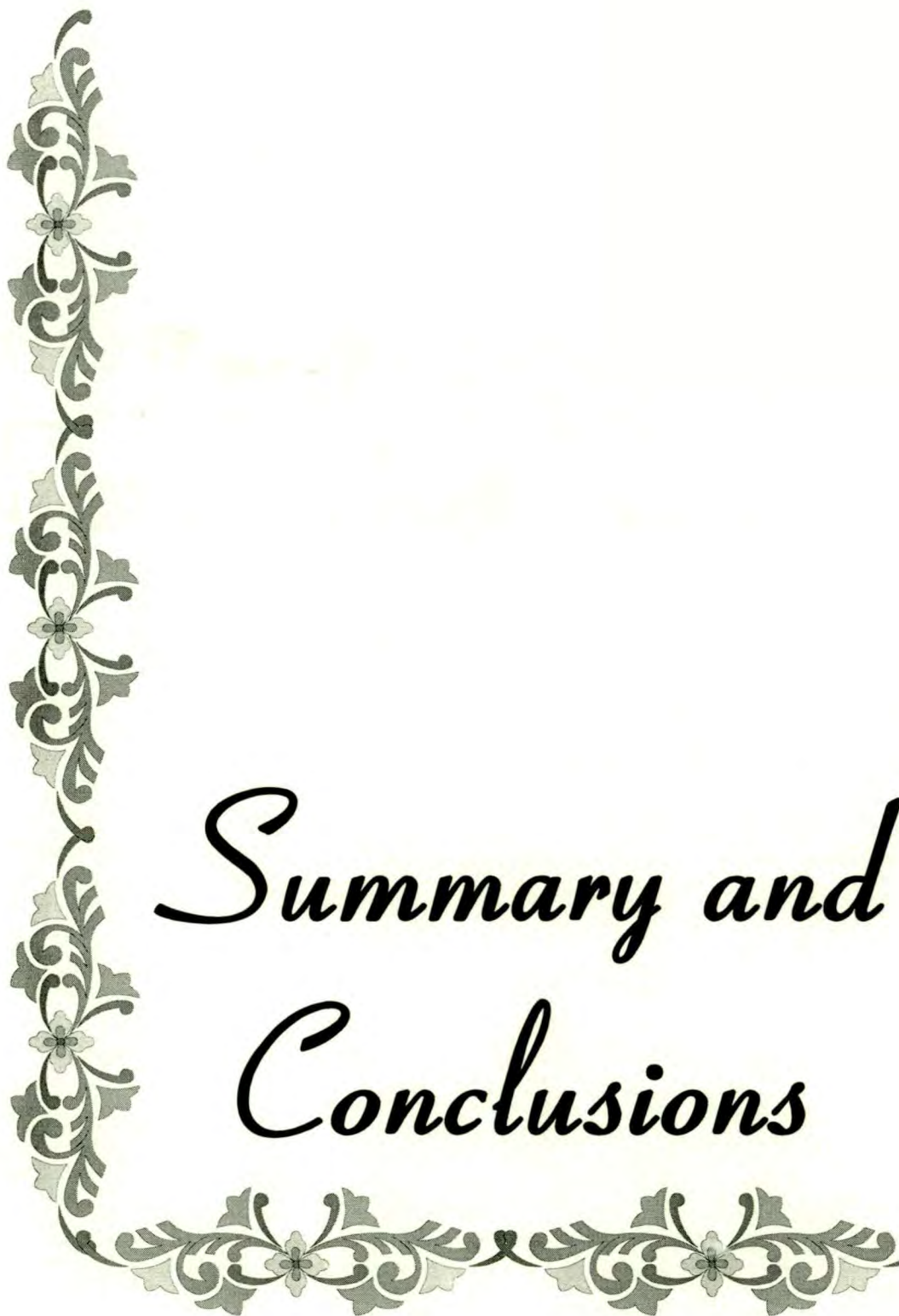
Path analysis

Path coefficient analysis is a standardized partial regression analysis which permits the separation of correlation coefficient into the measure of direct and indirect effects. This helps in giving the weightage to particular character during the selection.

The path analysis indicated that days to maturity and days to 50% flowering exerted the highest direct effect to grain yield at genotypic level. Similar results reported by Sharma *et al.* (1983), Taware *et al.* (1995) and Chettri *et al.* (2003) and Inderjit Singh (1999) for number of nodules per plant had positive and direct effects on grain yield.

Significant and positive correlation of days to maturity with grain yield could be explained by its positive direct effect. Taware (1995) reported indirect effect on yield via days to 50% flowering, number of nodules per plant and 100 grain weight.

The present investigation clearly revealed that the characters days to maturity, days to 50% flowering, 100 grain weight, number of nodules per plant, root length had strong association with yield also showed the highest direct effect and indirect effect through other component traits. This indicated that direct selection for these characters will help to enhance the breeding efficiency for grain yield in soybean.



*Summary and
Conclusions*

Chapter-6

SUMMARY AND CONCLUSION

The present investigation was undertaken with the object to estimate genetic variability for oil, yield and yield contributing characters and association of yield and yield contributing characters in soybean (*Glycine max* (L.) Merrill.). The experiment was conducted in a randomized block design with three replications. Results obtained are as follows:

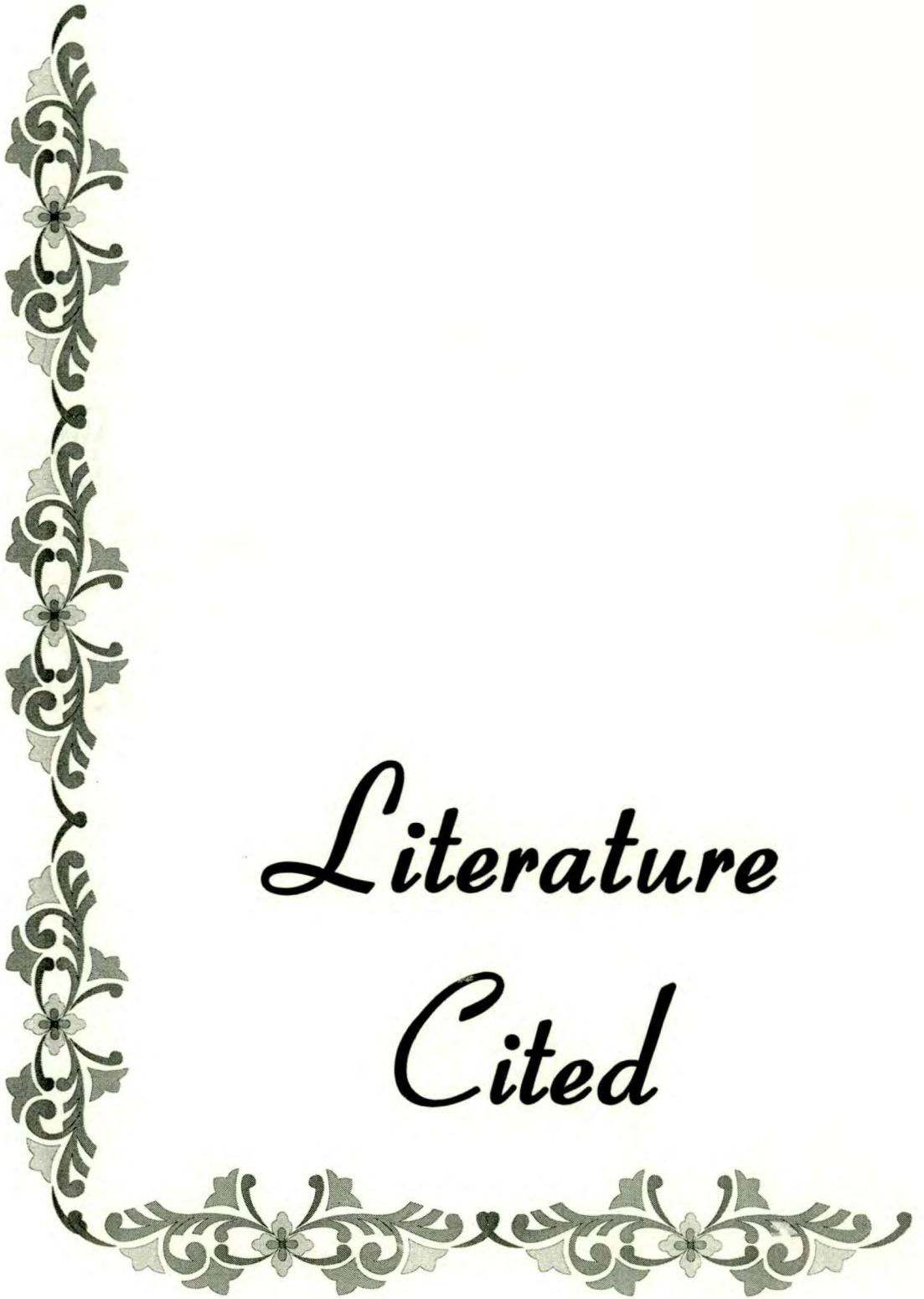
1. Analysis of variance showed significant genetic variability for all the characters.
2. Early maturity were recorded by VLS 72 (75.33 days), VLS 71 (82 days), MACS 1188 (82 days), Himso 1678, TS 5 and Himso 1677 (84 days).
3. The genotypes TS 2, MAUS 282, BAUS 96, PS 1450, Himso 1676 (3.86), VLS 71 (3.33), Himso 1678, PS 1454 and PS 1444 (3) recorded maximum number of branches per plant.
4. Number of pods per plant were higher in MACS 1188 (61.66), RKS 52 (57.00), NRC 80 (56.00), AMS 1 (52.66), JS (SH) 2002-14 (52.33) and MACS 1184 (48.00).
5. High oil content were recorded by VLS 71 (24.00 %), JS (SH) 2002-11 (22.98 %), MACS 1039 (22.54 %) and JS (SH) 2002-14 (22.47 %).
6. Nodule dry weight per plant and number of nodules per plant were higher in MACS 1188 (57.66 and 28.33 mg), MAUS 417

- (47 and 22.66 mg), JS (SH) 2002-14 (43.66 and 21.77 mg), RKS 52 (45 and 19.77 mg).
7. The strain MAUS 417 (17.21 gm), DS 2614 (17.09 gm), Dsb 11 (16.40 gm), MACS 1188 and PS 1450 (15.62 gm) recorded highest grain yield per plant.
 8. The range of variation was more for almost all the characters.
 9. High genotypic coefficient of variation were observed for six characters.
 10. High heritability coupled with high expected genetic advance was observed for oil content, number of branches per plant, number of nodules per plant, 100 grain weight, nodule dry weight, plant height and root length.
 11. Correlation studies indicated the importance of days to maturity, plant height, 50% flowering, 100 grain weight, number of pods per plant, number of nodules/plant, nodule dry weight and root length.
 12. The path coefficient of analysis revealed maximum contribution of days to maturity, days to 50% flowering, oil content, number of nodules per plant, plant height, 100 grain weight and root length.
 13. The promising genotypes should be evaluated for yield and other characters in large plot size.

CONCLUSION

The present study revealed that the genotypes viz., MACS 1188, MAUS 282, MAUS 417, Dsb 11, DS 2614, PS 1450, PS 1444, RKS

54 exhibited better performance for days to maturity, number of branches, number of pods, plant height, oil content and number of nodules. These characters also showed positive correlation with yield per plant through their direct and indirect effect. Most of these characters exhibited high heritability coupled with high expected genetic advance. Hence, direct selection on these characters in soybean will increase the breeding efficiency. The promising genotypes MACS 1188, MAUS 282, MAUS 417, Dsb 11, DS 2614, PS 1450, PS 1444 and RKS 54 should be evaluated for yield and other characters in future.



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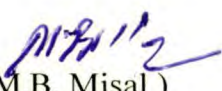
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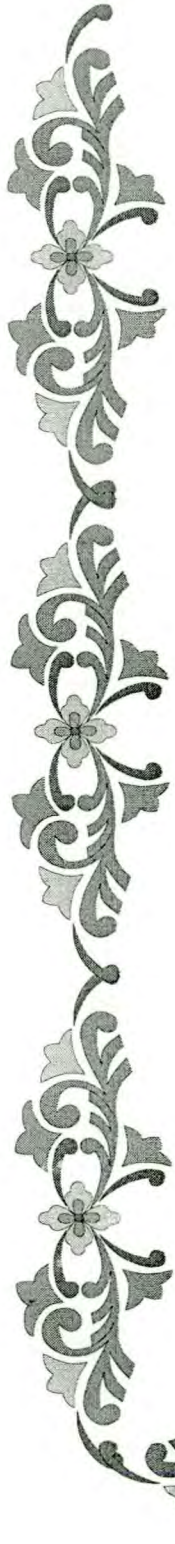
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THESIS ABSTRACT

- a) Title of the thesis : **GENETIC VARIABILITY, CORRELATION AND PATH ANALYSIS STUDIES FOR OIL, YIELD AND ROOT NODULATION TRAITS IN SOYBEAN (*Glycine max* (L) Merrill.)**
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Thesis Abstract



ABSTRACT

The present studies on “Genetic variability correlation and path analysis studies for oil, yield and root nodulation traits in soybean (*Glycine max* (L.) Merrill.)” involved the assessment of genetic variability, correlation and path analysis in 35 soybean strains with 5 checks for 12 component characters including seed yield during *kharif* 2008 at AICRP on soybean, MAU, Parbhani. It was revealed that most of the characters possessed sufficient genetic variability. High heritability coupled with high expected genetic advance was observed for number of branches per plant, 100 seed weight, number of nodules per plant, nodule dry weight and oil content indicating the presence of additive gene action in expression of these traits. Non-additive heritability was observed for days to flowering, days to 50% flowering, days to maturity, plant height and seed yield as these traits expressed high heritability estimates accompanied by low genetic advance.

Correlation studies indicated significant and positive correlation of grain yield with days to maturity, plant height, 50% flowering, 100 seed weight, number of pods per plant, number of nodules per plant and nodule dry weight. Path coefficient revealed direct effect of trait days to maturity on grain yield.

Seven genotypes viz., MACS 1188, MAUS 282, MAUS 417, DSb 11, DS 2614, PS 1450 and RKS 54 exhibited better performance for days to maturity, number of branches per plant, number of pods per plant, plant height and oil content. These characters also exhibited positive correlation with grain yield per plant through direct and indirect effect.