EVALUATION OF ADVANCED PROGENIES FOR SEED YIELD AND QUALITY TRAITS IN SOYBEAN
(*Glycine max.* (L.) Merrill.)

By

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B.Sc. (Agri.)

DISSERTATION

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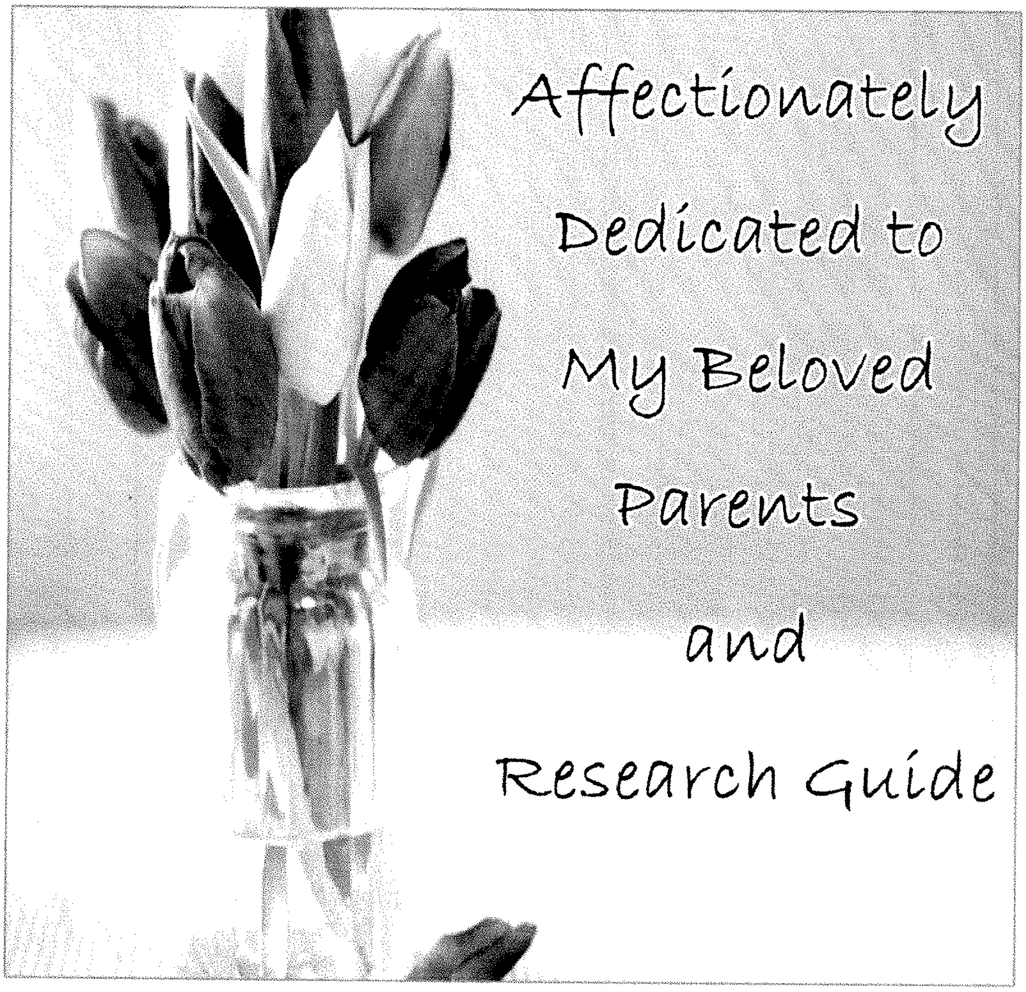

Affectionately
Dedicated to
My Beloved
Parents
and
Research Guide

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CERTIFICATE-I

This is to certify that **Anshu Ishara Tirkey** has satisfactorily prosecuted her course and research for a period of not less than four semesters and that the dissertation entitled **"EVALUATION OF ADVANCED PROGENIES FOR SEED YIELD AND QUALITY TRAITS IN SOYBEAN (*Glycine max* (L.) Merril.)"** submitted by her is the result of original research work and is of sufficiently high standard to warrant its presentation to the examination.

I also certify that the dissertation or part thereof has not been previously submitted by her for a degree of any university.

Place : PARBHANI
Date : 1 / 9 /2016

Dr.D.B. Deosarkar
Research Guide

CERTIFICATE-II

This is to certify that the dissertation entitled **"EVALUATION OF ADVANCED PROGENIES FOR SEED YIELD AND QUALITY TRAITS IN SOYBEAN (*Glycine max* (L.) Merril.)"** submitted by **Anshu Ishara Tirkey** to the Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani in partial fulfillment of the requirement for the degree of **MASTER OF SCIENCE** in the discipline of **AGRICULTURAL BOTANY (GENETICS AND PLANT BREEDING)** has been approved by the student's advisory committee after oral examination in collaboration with the external examiner.

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"Arise, awake and don't stop till the goal is reached"

-Swami Vivekananda

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(Anshu Ishara Tirkey)

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ABBREVIATIONS

d.f.	-	Degrees of freedom
et al.,	-	and other co-workers
G	-	gram
GCV	-	Genotypic coefficient of variation
Tr M S S	-	Treatment mean sum of squares
ha	-	hectare
h^2	-	heritability
M S S	-	Mean sum of squares
No.	-	Number (s)
PCV	-	Phenotypic coefficient of variation
V_g	-	Genotypic variance
V_p	-	Phenotypic variance
V_e	-	error variance
σ^2		Variance
%	-	per cent
R	-	Correlation coefficient
viz.,	-	Namely
vs	-	Versus
Cm	-	Centimeter(s)
GM	-	General mean
GA	-	Genetic advance
GAM	-	Genetic advance as percent mean
$\overline{X}$	-	Mean
Σ	-	Summation
Fig.	-	Figures
SE$\pm$	-	Standard error
CV	-	Coefficient of variation
qt	-	quintal(s)
RBD	-	Randomised Block Design

°C - degree celsius
b.s. - broad sense
EMSS - error mean sum of square
etc. - etcera
kg - kilogram(s)
/ - per
CD - critical difference
pp - pages
r_g - genotypic correlation
r_p - phenotypic correlation
DUS - Distinctiveness, Uniformity and Stability
USDA - United State Department of Agriculture
VNMKV - Vasantrao Naik Marathawada Krishi Vidyapeeth

INTRODUCTION

Chapter I

INTRODUCTION

Soybean is important oil seed crop in the world and is called as a golden bean or miracle bean. Soybean is a legume crop, meaning that it creates an environment that is home to symbiotic bacteria that fix atmospheric nitrogen and convert it to ammonia for the growing plant to manufacture amino acids, proteins, and nucleic acids. Thus the plant does not need to have supplemental nitrogen applied like corn (*Zea maize)*, cotton (*Gossypium hirsutum* L.) or other non-legume crops. Nutritional value of soybean lies in its protein (40-42%) and oil contents (18-22%) and is free from cholesterol making it highly desirable in the human diet. It has biological value as meat and fish protein and rich in amino acids like lysine and tryptophan are present. Since the yield per unit for many conventional 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.

Taxonomically, soybean belongs to the order Fabales, the family Fabaceae, the subfamily Faboidae and the genus *Glycine*. The genus *Glycine* is divided into two subgenera, *Glycine* and *Soja*. The subgenus *Glycine* includes 16 perennial species and the subgenus *Soja* (Moench) includes the cultivated soybean, *G. max* (L.) Merril (2n=40) and the two annual species, *Glycine soja* Siebold and Zucc. The cultivated species, *G. max*, hybridizes easily with its wild annual relative and most probable progenitor *G. soja* while with the perennial relatives it has low crossability rate (Singh and Hymowitz, 1999). There are three species of soybean, viz., *G. ussuriensis* wild, *G. max* (L.) Merr. cultivated and *G. gracilis* intermediate (Salunkhe *et al.*, 1992).

Soybean is reported to have originated in Eastern Asia or China. It has been traditionally grown in the northern and north-eastern hills and in scattered packet of central India and had become essential part of the daily diet in these regions. Soybean has been known by various names in India such as Bhat, Bhatman, Bhut, Gari-kalai, Garrykalya, Kalitur, Kulthi, Ramkuthi, Soya Chikkudu, Suntha Kadalai and Teli Kulth.

The estimates of world soybean area, production and productivity for 2015-16 are 120.00 million ha, 316.10 million tons and 2.69 t/ha, respectively. In India, soybean area, production and productivity for 2015-16 are 11.54 million ha, 10.92 million tons and 0.985 t/ha respectively. India ranks 5th in area, production and productivity of soybean in the world after countries like USA, Brazil, Argentina and China. (USDA- March, 2016). During kharif 2015, the estimated area under soybean has decreased to 10.02 m ha on account of late arrival of monsoon, also the total production (11.64 mt) and productivity (1062 kg/ha) is estimated to reduce significantly.

Soybean was introduced in Maharashtra state during the year 1984-1985 and it was grown only on 5.6 million ha. In Maharashtra area under soybean during kharif- 2015 was 3.94 million ha. with total production 3.21 million tons and an average productivity of 0.842 t/ha.

Major soybean growing states in India are Madhya Pradesh, Maharashtra, Rajasthan, Andhra Pradesh, Karnataka, Chhattisgarh etc. Madhya Pradesh ranks first in production of soybean. Maharashtra, Madhya Pradesh and Rajasthan continue to be the leading states with 6.02, 3.07 and 0.56 million ha under soybean and a contribution of about 85% towards total production of the crop in the country. It is generally grown as a rainy season crop under rainfed situation.

The area under soybean cultivation is increasing as it is short duration crop and higher productivity compared to other legumes family such as black gram and green gram.

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.

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

Heritability is important because it aids the breeder in determining the amount of progress or genetic gain that can be made through certain breeding strategies. A high heritability means the offspring have a greater chance of exhibiting an expression of the trait that is similar to that of the parents; whereas a low heritability shows a lower level of resemblance. Broad sense heritability denotes the proportion of phenotypic variation that is the result of the total genetic variation including both dominance and epitasis effects. Narrow sense heritability is the proportion of phenotypic variance that is the result of additive genetic variation.

Genetic variability is the basic requirement for crop improvement as this provides wider scope for selection. Thus, effectiveness of selection is dependent upon the nature, extent and magnitude of genetic variability present in material and extent to which it is heritable. Hence, in present investigation an attempt was made to assess the variability for yield and yield contributing traits, along with indices of variability i.e. genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense (h^2_{bs}), genetic advance (GA) and genetic advance as percent of mean.

Therefore the present study on ''Evaluation of advanced progenies for seed yield and quality traits in soybean'' was undertaken with the following objectives.

1. To evaluate advanced progenies for seed yield and quality traits
2. To estimate genetic variability parameters in advanced progenies
3. To study the correlation for phenotypic characters with seed yield and quality traits

REVIEW OF LITERATURE

Chapter II

REVIEW OF LITERATURE

Soybean is considered as one of the important grain legume, because of high nutritional value and oil content. In India, it is extensively cultivated during ***kharif*** season. Soybean has witnessed increasing trends in the production and productivity over the years. So there is need to develop high yielding varieties with proper plant architecture, which are resistant to biotic and abiotic stresses. An attempt has been made in the present investigation to understand the variability, correlation and genetic diversity in the soybean genotypes. The review of literature pertaining to these aspects is presented in this chapter under the following headings:

2.1 Variability, heritability and genetic advance as per cent of mean

2.2 Correlation and Path analysis studies

2.1 Variability, heritability and genetic advance as per cent of mean

A measure of variability and understanding of genetic makeup of the crop are important constituents of any crop improvement programme. In the early part of 20th century, Johansson (1909) evaluated the genetic and environmental components of variation to both heritable and non-heritable factors and the variation in a pure line is only due to environmental factors.

The heritability (h^2) is one of the genetic parameter, which most contribute to the breeder work. It provides the proportion of total phenotypic variance that is attributed to genetic causes. Thus, it measures the reliability of the phenotypic value as an indicator of the genotypic value (Ramalho et al., 1993).

Fisher (1918) divided the genotypic variance into three components *viz.,* additive, dominance and interaction components. Hayman and Mather (1955) partitioned the epistatic component into three types *viz.,* additive x additive, additive x dominance and dominance x dominance.

Lush (1949) defined narrow sense heritability as the ratio of additive variance to the total variance while, Hanson *et al.,* (1956) proposed broad sense heritability as the ratio of genotypic variance to the total variance. The genetic gain that can be obtained for a particular trait through selection is the product of its heritability, phenotypic standard deviation and selection differential (Burton and Devane, 1953).

Jain and Ramgiry (2000) recorded high phenotypic and genotypic coefficient of variability for seed yield per plant followed by plant height, plant weight and moderate coefficient of variability for 100 seed weight, seed per pod and days to flowering. High heritability estimates accompanied by high genetic advance as a percentage of mean were noticed for seed yield, plant height and pods per plant.

Singh *et al.,* (2000) observed high estimates for genotypic coefficient of variation and phenotypic coefficient of variation for seed yield per plant, pods per plant and plant height. These traits also exhibited high estimates of heritability with high genetic advance as percentage of mean.

Vollman *et al.,* (2000) studied the soybean genotypes of early maturity groups and found average to high protein content in years with high air temperature and moderate rates of rainfall during the seed-filling period, whereas seed protein content was drastically reduced in seasons of insufficient nitrogen fixation or higher amounts of precipitation during seed filling. Despite the high degree of environmental modification, genetic variation of seed protein content was considerable and genotype environment interaction was of low magnitude. Therefore selection of early maturing soybean genotypes with increased seed protein content appears to be feasible and is only limited by the moderately negative correlation between protein content and seed yield.

Agrawal *et al.,* (2001) studied genetic variability parameters *viz.,* GCV, PCV, heritability and genetic advance for plant growth characters and observed high GCV for degree of indeterminate growth habit, plant height and branches per plant. Estimates of GCV were moderate for days to flower initiation, whereas, low for days to maturity. Heritability and genetic advance as percentage of mean were high for all the plant growth characters studied.

Das *et al.*, (2001) observed significant variability among genotypes for all of the 11 traits studied, *viz.*, days to 50% flowering, days to maturity, plant height, mean internodal length, number of branches per plant, number of pods per plant, pod length, number of seeds per pod, 100-seed weight, oil content and seed yield per plant. Grouping pattern of the genotypes suggested no parallelism between genetic divergence and geographical distribution of the genotypes. Variance of cluster means revealed that pods per plant and plant height had the maximum contribution towards divergence.

Filho *et al.*, (2001) evaluated characters *viz.*, Weight of a hundred seeds, Oil Content and Protein Content, expressed in %. Oil content ranged from 12 to 20.37 % and protein content from 35.66 to 41.75% in the experiment carried out in the field, while in the experiment carried out in the greenhouse oil content ranged from 12.26 to 21.79 % and protein content from 32.95 to 41.56 %.

Mimura (2001) analyzed the genetic variability in 131 accessions of edamame soybeans using phenotypic traits e.g. maturity information, testa color, and 100-seed weight. The obtained results indicated that Edamame genetic diversity was generally clustered around maturity groups and testa color. It was also reported that the genetic diversity among the Japanese edamame cultivars was narrow, compared to Chinese maodou; Japanese edamame and Chinese maodou soybeans may have different genetic pools.

Sudaric *et al.*, (2001) calculated phenotypic variability, wide-sense heritability, genetic gain and relative genetic gain from selection for seed yield, protein and oil contents. Results of biometrical analyses indicated that advances in yield and quality had been achieved through the soybean breeding programme.

Chandankar *et al.*, (2002) recorded considerable variability among the genotypes for 11 characters *viz.*, number of days to 50% flowering, plant height, number of branches per plant, number of pods per plant, number of seeds per pod, biological yield per plant, yield per plant, oil content, harvest index, protein content and chlorophyll content. The 25 genotypes were grouped into 9 clusters. Canonical analysis indicated genetic divergence for number of days to 50% flowering, number of branches per plant, number of pods per plant, biological yield per plant, and oil content.

Dixit *et al.,* (2002) studied 38 newly developed genotypes of soybean and observed that seed yield per plant, harvest index and biological yield per plant showed comparatively high estimates of genetic variation and heritability. Hence direct selection for these traits would be effective for yield improvement.

Gawande *et al.,* (2002) observed significant variability among soybean genotypes for 10 characters (days to maturity, plant height, number of branches per plant, number of pods per plant, 100-seed weight, pod shattering percentage, oil content, protein content, pod blight, and seed yield per plant). Based on D^2 values, genotypes were grouped into ten clusters, of which only one was monogenotypic. Variances of cluster means revealed that plant height, number of pods per plant, pod shattering and days to maturity had maximum contribution towards divergence.

Bangar *et al.,* (2003) observed higher values for phenotypic coefficient of variation than genotypic coefficient of variation. The GCV and PCV estimates were highest for number of branches per plant and plant height among the characters studied. The GCV and PCV were of moderate magnitude for the traits *viz.,* number of pods per plant, 100 seed weight and seed yield per plant. Days to 50 per cent flowering and days to maturity had very low GCV and PCV estimates. Days to maturity, number of branches per plant and plant height showed the highest magnitude of heritability. Genetic advance was high for number of branches per plant, plant height and seed yield.

Ganeshamurthy and Seshadri (2004) studied the influence of additive gene action for seed yield and dry matter production. Number of pods and 100 seed weight were found to be governed by both additive and non-additive gene action.

Chettri *et al.,* (2005) reported wide range of variation for the trait 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 values. Days to maturity followed by days to 50 per cent flowering recorded the lowest genotypic and phenotypic variances and coefficient of genotypic and phenotypic variation. The number of grains per pod and 100 seed 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 material.

Dhillon *et al.*, (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 the expression of this character. Non additive heritability was observed in the expression of days to 50 per cent flowering. He also observed the non-additive gene action for protein content and palmitic acid as these traits had high heritability estimates accompanied by low genetic advance.

Karad *et al.*, (2005) revealed high phenotypic coefficient of variation than genotypic coefficient of variation for all the characters indicating the role of environment on expression of characters studied. The estimates of GCV were high for yield per plot, plant height and number of pods per plant, while they were moderate for number of seeds per pod, number of branches per plant indicating that these yield contributing characters have scope for improvement by selection.

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

Vart *et al.*, (2005) reported slight higher phenotypic coefficient of variation than genotypic coefficient of variation. Heritability estimates was high for all the characters, whereas, expected genetic gain in terms of percentage of mean was highest for clusters per plant and lowest for days to maturity. All the traits with high heritability and high genetic advance also expressed moderate to high genotypic and phenotypic coefficient of variation.

Vrataric *et al.*, (2005) evaluated genetic advance in the quantitative traits (grain yield, protein and oil content of grains and oil quality) of recently developed soybean elite breeding lines. Statistical analysis showed that most of the elite breeding lines had significantly higher grain yield, and protein and oil contents of grain relative to the control (maturity groups OO, MG O and MG I) and good stability for these traits. A significant genetic variability was observed in terms of triacylglycerols. Generally, the results indicated that genetic advance in the grain yield and grain quality of domestic soyabean lines from maturity groups OO, O and I.

Bhairav *et al.*, (2006a) observed low estimates of variability for oil content in soybean genotypes.

Faisal *et al.*, (2006) studied highly significant differences among genotypes for all the characters. High heritability was recorded for 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 content respectively indicating for source of additive type of gene action. They also reported high heritability for oil content and other morphological and quantitative characters in soybean indicating the role of additive gene action for these traits.

Gohil *et al.*, (2006) studied genetic variability, broad sense heritability and expected genetic advance for seed yield and its component traits. The highest GCV was observed for number of pods per plant followed by seed yield per plant. Plant height, number of clusters per plant, number of pods per plant and seed yield per plant had 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 procedures.

Ramana and Satyanarayana (2006) studied 70 soybean genotypes for genetic divergence using Mahalanobis' D2 statistic. The genotypes were grouped into 9 clusters and revealed that there is no linear relationship between geographic and genetic divergence, further plant height, plant dry weight, 1000-seed weight contributed maximum to the total genetic divergence.

Truong *et al.,* (2006) studied the genetic diversity for reproductive growth characters in exotic germplasm resources in soybean and revealed wide range of phenotypic variation for the traits *viz.,* number of pods per plant and seed yield per plant. Korean cultivar showed greater diversity than the exotic cultivars.

Yadav and 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.

Gupta and Punetha (2007) studied genotypic and phenotypic variability, heritability and genetic advance for 12 quantitative traits including seed yield per plant and seed vigour. The trait pods per plant exhibited the highest amount of genetic variability followed by seed vigour, seed yield per plot, seeds per pod and 100 seed weight. Pods per plant also expressed highest heritability and expected genetic advance.

Sharma *et al.,* (2007) observed the range for PCV was 3.19 per cent and GCV was minimum for protein content among the characters studied in soybean.

Sirohi *et al.,* (2007) studied eight quantitative traits in soybean *viz.,* days to 50 per cent flowering, days to maturity, plant height, number of primary branches, number of pods per plant, seed yield per plant, seed weight and harvest index. The estimates of genotypic coefficient of variation were ranged from 3.33 for pod width to 38.13 for number of pods per plant. High estimates of GCV were observed for number of pods per plant, number of clusters per plant, seed yield per plant, plant height and biological yield per plant.

Yadav (2007) revealed that seed yield per plant, number of pods per plant and plant height exhibited maximum genotypic coefficient of variation. High heritability coupled with high genetic advance as percentage of mean was noted for plant height, plant height, number of pods/plant and 100-seed weight indicating the additive type of gene action which could be improved by simple selection.

Aditya *et al.,* (2011) estimated highest PCV and GCV for dry matter weight per plant and number of nodes per plant. Grain yield per plant exhibited highly significant and positive genetic correlation with dry matter weight per plant, number of primary branches per plant, number of pods per plant and harvest index.

Patil *et al.,* (2011) observed the highest genotypic and phenotypic coefficient of variances for plant height followed by seed yield per plant and pods per plant and it was lowest for days to 50% flowering, days to maturity and pod length. High heritability and genetic advance were observed for plant height, seed yield per plant and pods per plant. He also observed the low values of genotypic and phenotypic coefficient of variances for protein content in soybean.

Saleem *et al.,* (2011) conducted to estimate the genetic variability in 20 different soybean genotypes. The results of analysis revealed that all the characters like days to flowering, days to pod formation, days to maturity, plant height (cm), branches/plant, pods/plant, pod length (cm), seeds/pod, 100 grain wt (g) and yield (g/plant) were significantly affected due to various soybean genotypes. The days to flowering ranged from 34.33 to 62.00, pod formation from 46.00-75.00 days, maturity from 91.33-116.00 days, plant height from 56.51 to 106.00 cm, branches from 4.33 to 13.33 per plant, pods from 47.33 to 165.30 per plant, pod length from 2.00 to 6.66 cm, seeds/pod from 3.33 to 1.00, 100 grain wt from 3.80 g to 17.16 g and grain yield from 3.24 to 39.42 g/plant. The genotypes Zane, Black hack, Bragg and Menlin remained the best among 20 lines studied in term of bearing pods, high grain wt and yield production.

Athoni and Basavaraja (2012) observed the prevalence of significant difference among the genotypes for all the eleven characters studied. Plant height was the only character which showed high phenotypic and genotypic co-efficient of variation while days to maturity, number of nodes per plant and oil content recorded a low phenotypic and genotypic coefficient of variation and rest of characters recorded moderate phenotypic and genotypic coefficient of variation.

Bekele *et al.,* (2012) observed relatively high broad sense heritability for plant height (0.42), days to flower (0.6) and days to maturity (0.45) indicating the existence of possibility for selection of varieties which are early with short height to resist lodging. Heritability estimates of branches/plant, protein content and seed yield were low (<10%). Relatively high heritability (>40%) with high genetic advance (>10%) and genetic advance in percentage of mean (>20%) was exhibited for only plant height. Days to flowering, days to maturity and oil content revealed high heritability (>40) with low genetic advance (<10).

Sudaric *et al.,* (2012) determined the variability and genetic parameters for protein content and oil content in soybean grain. The obtained results indicated achieved genetic advance in grain quality within maturity groups 00, 0 and I. This genetic advance in grain protein and oil content in domestic soybean germplasm contributes improvement and profitability of soybean production and processing.

Sujata *et al.,* (2012) reported very narrow differences between phenotypic and genotypic coefficient of variation in all the four leaflet types (oval, ovate, lanceolate and linear) for the characters *viz.,* plant height, days to flowering, days to maturity, specific leaf weight, number of pods per plant, harvest index and 100-seed weight. High heritability coupled with high genetic advance as per cent of mean was observed for traits *viz.,* number of pods per plant, specific leaf weight in oval, ovate and lanceolate leaflet types.

Abady *et al.* (2013) observed that high heritability coupled with high genetic advance as percent of mean recorded for Number of nodules per plant, dry weight of nodules per plant , hundred seed weight, above ground biomass yield, harvest index, number of clusters per plant, number of seeds per pod, number of pods per plant, and seed yield per plot. They reported that PCV were higher than the GCV and the differences were small suggesting that these characters were relatively less influenced by the environment. High broad sense heritability and genetic advance were found for plant stand count at emergence (69.09, 61.71) and plant height (73.49, 40.76) whereas, high heritability and moderate genetic advance for days to 50% flowering (78.24, 10.65).

Ghodrati (2013) observed that high broad sense heritability (81%, 76%, 74%) and genetic advance (0.35 0.20, 0.40) were obtained for the number of nodes per plant, days to flowering and plant height respectively, and strong positive correlation (r = 0.61*) was observed between seed yield and plant height. High heritability and medium genetic advance was found for days to flowering; while medium heritability and low genetic advance were observed for days to maturity and oil content. Heritability and genetic advance were the lowest for seed yield, 100 seed weight, number of branches per plant, number of pods per plant, protein content and seed yield. The highest GCV, PCV and GA were observed for number of branches per plant, followed by plant height. However, the lowest values were obtained for protein content, oil content, days to maturity, 1000 seed weight and seed yield.

Rauji *et al.*, (2013) observed that the genotypic coefficient of variance was observed higher for the characters like number of pods per plant, plant height and number of seeds per pod indicating that phenotypic selection would be effective for genetic improvement in these traits.

Okonkwo and Idahosa (2013) evaluated the parameters *viz.*, plant height, leaf area index, days to 50% flowering, 50% maturity, number of branches/plant, number of nodes/plant, nodes/branch, pods/node, pods/plant, pod length, seeds/pod, 100-seed weight, grain yield and dry matter. Significant differences ($P<0.05$) were observed among the genotypes for the characters studied. Means of agronomic characters varied considerably. High heritability for yield-related and some morphological characters were observed.

Osekita and Ajayi (2013) studied the inter-relationship among quantitative characters *viz.*, days to 50% flowering, plant height, seed dry weight, number of pods per plant, number of branches per plant, days to maturity, seed yield, number of seed per plant and 100-seed weight. Seed yield per plant had highest estimate of PCV (215.41) and GCV (213.97) followed by seed dry weight PCV (204.68) and GCV (201.76), then, number of seed per plant PCV (73.10) and GCV (57.02). Heritability was highest in five characters, *viz.*, days to maturity, days to 50% flowering, seed yield, seed dry weight and 100-seed weight.

Pushpa and Rao (2013) observed highly significant differences among the genotypes for the all the characters. High PCV coupled with high GCV observed for the traits *viz.*, branches per plant, pods per plant and yield per plant indicating the presence of wider adaptability for these traits in the genotypes studied. High heritability coupled with high genetic advance as percent of mean was observed for days to 50% flowering, plant height, branches per plant, pods per plant, 100 seed weight and seed yield per plant indicating operation of additive gene action and the ample scope for improvement in these traits through simple selection.

Badkul *et al.* (2014) observed that highest genetic advance as percentage of mean were recorded for number of branches per plant, followed by number of seeds per plant, seed yield per pod, biological yield per plant, moderate for plant height and 100 seed weight. The highest heritability was obtained for vegetative phase followed by 100 seed weight, plant height, number of pods per pant, number of branches per pant, seed yield per plant, biological yield per plant, number of seeds per plant and harvest index. Moderate heritability was recorded for reproductive phase and number of seeds per pod. Number of branches per plant, number of pods per plant, number of seeds per plant and seed yield per plant showed high heritability and high genetic advance whereas, high heritability with moderate genetic advance was found for plant height and 100 seed weight. Vegetative phase, reproductive phase and number of seeds per pod recorded high or moderate heritability with low genetic advance. It interpreted that number of branches per plant recorded the highest PCV and GCV followed by number of seed per plant, seed yield per plant, number of pods per plant and moderate PCV and GCV were recorded for plant height and 100 seed weight.

Baraskar *et al.* (2014) evaluated 61 genotypes of germplasm and estimated the Phenotypic coefficient of variation was higher than genotypic coefficients of variation, this indicated that expression of characters under study was influenced due to environmental factors. The high values of GCV and PCV were observed for number of clusters per plant, seed yield per plant, biological yield per plant, number of pods per plant and plant height indicating presence of sufficient genetic variability for selection in these traits. He also observed that high heritability accompanied by high genetic advance for plant height, number of clusters per plant, number of primary branches per plant, seed yield per plant, biological yield per plant and number of pods per plant suggested selection could be effective for these traits. High magnitude of heritability and low to moderate magnitude of genetic advance was observed for days to 50% flowering, days to maturity, number of seeds per pod, protein content and oil content may due to lack of genetic variability.

Barh *et al.,* (2014) considered thirteen characters to be most important for the genetic diversity. Lowest contribution was made by days to maturity (1.29%) and maximum contribution was through number of pods per plant (14.703%) in genetic diversity. The variability studies suggests that trait like number of pods per plant consists of fair heritability and genetic advance which can be worked out for mass selection in future but yield governing traits like number of primary branches and number of seed per pod are having very low. These results suggests that the Bhat genotypes taken under investigation having a most diverse range of pods followed by variable dry matter per plant, seed yield per plant, harvest plant height, 100- seed weight which contribute most towards diversity.

Hwang *et al.,* (2014) found that the heritability of seed protein and seed oil concentrations was 77.9% and 78.33%, respectively.

Sawale *et al.,* (2014) recorded highest Phenotypic Coefficient of Variation (PCV) for seed yield per hectare, seed yield per plant and number of pods per plant and highest Genotypic Coefficient of Variation (GCV) for number of pods per plant, seed yield per hectare and seed yield per plant indicating that these characters could be used as selection for crop improvement.

Baruah *et al.,* (2015) observed high genotypic as well as phenotypic coefficient of variance for 100-seed weight followed by seed yield per plant and seed per plant revealing a high level of diversity among the genotypes for these traits.

Jain *et al.*, (2015) observed that PCV were higher than the GCV values for all the characters i.e. days to 50 % flowering, 100 seed weight and seed yield/plant. The broad sense heritability estimates were high for all characters. High heritability estimates for days to 50 % flowering, 100 seed weight and seed yield/plant showed that selection for these characters will be effective.

Mahbub *et al.,* (2015) evaluated twenty eight genotypes and found that genotypic coefficient of variation was the highest for seed yield per plant (31.45%) followed by number of branches per plant (29.9%) and plant height (27.42%). Days to maturity (99.93%) had the highest heritability. Plant height, pod length, number of seeds per pod, number of pods per plant, hundred seed weight, branches per plant and number of seeds per pod showed significant positive genotypic and phenotypic correlation with seed yield. In path analysis, seeds per pod, hundred seed weight, pod length, days to maturity and plant height showed positive direct effect on yield. Heritability was higher for all traits. High genetic advance was found for plant height and seed per plant. Genetic advance was moderate for days to first flowering, days to 50% flowering, days to maturity and number of pods per plant and low for branches per plant, plant height, number of seeds per pod, hundred seed weight and seed yield per plant. Genetic Advance (GA) in percent of mean for seed yield per plant, branches per plant, plant height, seeds per pod, number of pods per plant and hundred seed weight were high.

Malek *et al.,* (2015) evaluated eighteen mutants to perform superiority to their mothers in respect to seed yield and some morphological traits including yield attributes. Narrow differences between phenotypic and genotypic coefficients of variation (PCV and GCV) for most of the characters revealed less environmental influence on their expression. High values of heritability and genetic advance with high GCV for branch number, plant height, pod number, and seed weight can be considered as favorable attributes for soybean improvement through phenotypic selection and high expected genetic gain can be achieved. Pod and seed number and maturity period appeared to be the first order traits for higher yield and priority should be given in selection due to their strong associations and high magnitudes of direct effects on yield.

Pagde *et al.,* (2015) estimated genetic variability in 30 soybean strains. Pods per plant exhibited highest genetic variability, followed by plant height, seed yield per plant, test weight, seeds per pod. Pods per plant also expressed highest heritability and genetic advance.

2.2 Correlation and path analysis

The correlation is a measure of intensity of linear association between two variables or a measure of joint variation degree, which can be positive or negative. Information on correlation between characters is extremely important, because they permit the breeder to know what happens with a character when another, to which the first is correlated, is selected (Ramalho et al., 1993).

Path coefficient analysis was originally reported by Wright (1921b). This technique has been used widely by animal breeders and geneticists. Deway and Lu (1959) and Frakes *et al.* (1961) demonstrated the usefulness of path coefficient analysis in plant selection. This type of analysis gives information on the direct and indirect effects of major attributes one on another and permit the separation of the correlation coefficients into components of direct and indirect effects on the major attribute. The use of this method was subsequently demonstrated by various workers in various agricultural crops but in soybean little information was available till recently and thus utilization of path coefficient analysis has not been fully exploited for developing superior varieties with high yield. However, information generated on this parameter by soybean researchers is reviewed here:

Dewey and Lu (1959) used the method of path coefficient into their components which showed that fertility and plant size were the factors existing the greatest influence both direct and indirect on seed yield.

Rajanna *et al.,* (2000) revealed significant and positive correlation for number of pods per plant and 100 seed weight with seed 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 pods per plant.

Singh *et al.,* (2000) reported significant positive correlation and high magnitude of correlated response along with relative selection efficiency for pods per plant, seeds per pod and 100 seed weight and revealed that these are major yield components in early generation of soybean.

Filho *et al.,* (2001) found the correlation between oil and protein was negative and significant. The relationship among weight of a hundred seeds with oil content and protein content was low and higly affected by the time effect.

Raut *et al.,* (2001) studied the correlation and path analysis in soybean for ten quantitative traits *viz.,* days to 50 per cent flowering, days to maturity, plant height, number of branches per plant, number of clusters per plant, number of pods per plant, 100 seed weight, oil content, harvest index and seed yield per plant. Seed yield showed positive and significant association with number of pods per plant, 100 seed weight, oil content and harvest index both at genotypic and phenotypic level.

Rezaizad *et al.,* (2001) studied the correlation analysis and observed that number of seeds per plant and seed yield per plant had the highest significant correlation coefficient. Other significant correlation coefficients were found between biomass per plant and yield and between number of pods and yield. He also studied path analysis which showed that number of seeds per plant and seed weights were important for soybean selections programme.

Bangar *et al.,* (2003) observed positive and significant correlation coefficient for seed yield with 100 seed weight followed by days to maturity, plant height and days to 50 per cent flowering. Days to maturity, plant height, pod number per plant and 100 seed weight among themselves were positively significant.

Chettri *et al.,* (2003) reported that grain yield was significantly correlated with days to maturity and number of grains per pod at the genotypic level. Days to maturity was significantly correlated with plant height and days to 50 per cent flowering at both the phenotypic and genotypic levels. The trait number of days to 50 per cent flowering was positively and significantly correlated with days to 50 per cent flowering but negatively with number of pods per plant and 100 grain weight at the genotypic level. The character 100 grain weight did not show any correlation with grain yield.

Iqbal *et al.,* (2003) determined the interrelationship between yield and its components by genotypic correlation and path coefficient analysis in ten soybean varieties. The results indicated that seed yield per plant was positively and significantly associated with all parameters studied. The result also showed that pods per plant has maximum positive direct on yield per plant followed by 100 seed weight and seeds per pod. Plant height had negative direct effect on yield per plant. It was concluded that pods per plant, seeds per pod and 100 seed weight were the main yield components.

Oneml (2003) observed that plant yield had positive and significant correlation with number of pods, number of branches, pod length and 1000 seed weight. The correlations between seed yield per plant and lowest pod height were significantly negative. The number of pods maintained positive and significant correlations with plant height, number of branches and 1000 seed weight while negative correlations with lowest pod length.

Bizeti *et al.,* (2004) studied the correlation and path analysis in soybean and showed that the seed size was not important for increase in grain yield. The number of nodes and plant height at maturity showed significant correlation with grain yield.

Ganeshamurthy and Seshadri (2004) studied number of pods, seed yield, plant height and dry matter production showed high genotypic coefficient of variation. Correlation studies indicated that seed yield per plant showed significant positive correlation with dry matter production, number of branches, days to flowering, days to maturity and plant height.

Mukhekar *et al.,* (2004) observed that the 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.

Vart *et al.,* (2005) reported that magnitude of correlation coefficients at the genotypic level was higher than the corresponding phenotypic level, thereby indicating the strong inherent association between these characters. The overall results indicated that significant positive correlations with seed yield were due to relationship between biological yield and pods per plant and hence referred as the most important component of yield.

Bhairav *et al.*, (2006b) carried out correlation and path analysis using 198 germplasm lines of soybean for eight component characters including seed yield both at genotypic and phenotypic level. Pods per plant, branches per plant, 100 seed weight and plant height had positive and significant correlation with seed yield. They 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 effect of biological yield per plant on seed yield per plant.

Faisal *et al.*, (2006) reported 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.

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% 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.

Muhammad *et al.*, (2006) reported that grain yield had positive and significant correlation with days to maturity, number of branches, number of pods and 100 seed weight.

Ngon *et al.,* (2006) evaluated the genetic diversity of genotypes of soybean based on the yield-related traits and concluded that differences among genotypes for all the characters were highly significant and the grain yield was positively and significantly correlated with number of pods per plant.

Saharan *et al.,* (2006) revealed that seed yield per plant was positively correlated with number of pods per plant, number of branches per plant, 100 seed weight and protein content. Oil content did not show any correlation with seed yield.

Truong *et al.,* (2006) estimated the correlation analysis and showed that days to flowering and days to maturity had close association with agronomic traits as well as yield and yield components. Both days to flowering and days to maturity had positive correlation with the other characters except one hundred seed weight.

Gaikwad *et al.,* (2007) observed higher values for genotypic correlation 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.

Narjesi *et al.,* (2007) revealed that number of pods per plant, number of seeds per plant and 100 seed weight had highest genotypic correlation with seed yield.

Sirohi *et al.,* (2007) observed that seed yield showed positive and significant association with days to 50 per cent flowering, number of pods per plant, days to maturity, plant height and biological yield per plant.

Yadav (2007) studied ten quantitative traits *viz.,* days to 50 per cent flowering, days to maturity, plant height, and pod bearing length, pod number per plant, seed number per plant, 100 seed weight, protein percentage, oil percentage and genetic correlation for seed yield. Results indicated that seed yield was significantly correlated with height, pod bearing length, number of pods per plant and number of seeds per plant.

Karnwal and Singh (2009) observed that seed yield showed significant positive correlations with total dry matter weight/plant, primary branches/plant, pods/plant, seed yield efficiency, 100-seed weight and harvest index while, protein and oil contents showed significant and negative association with each other. Path coefficient analysis indicated major role of pods/plant, total dry matter weight/plant, primary branches/plant, seed yield efficiency and 100-seed weight both directly and indirectly influenced seed yield. Therefore, main emphasis should be given on these traits during phenotypic selection for developing high yielding genotypes of soybean.

Cober and Voldeng (2010) looked to estimate heritability of protein, oil, andd seed yield based on backcrosses. They found an inverse relationship between seed protein and oil (-0.84 for RIL, and -0.86 for the back cross population, $P< 0.0001$).

Iqbal *et al.,* (2010) indicated that .the grain yield was positively and significantly correlated with all studied traits except plant height, which showed non-significant association during both years. Oil content showed significant and positive correlation with grain yield, 100-seed weight, and harvest index while significantly negative correlation were observed with days to maturity, plant height and number of branches per plant.

Rajkumar Ramteke *et al.,* (2010) reported significantly negative correlation coefficient of yield with days to flowering and maturity. Seed weight was negatively correlated with days to flowering, maturity, plant height, nodes but positively with oil content. Protein content, however, was positively correlated with number of branches and days to 50% flowering but negative with oil content.

Showkat and Tyagi (2010) analyzed correlation and path coefficient analysis for seed yield and its components in 40 genotypes of soybean. The studies indicated that out of 16 characters, seed yield showed positive and significant association with biological yield, days to maturity, branches per plant, harvest index, pod filling period, pods per plant, 100-seed weight and clusters per plant indicating that an intense selection for these characters improve seed yield in soybean. They analyzed path coefficient analysis and revealed that biological yield and harvest index were major characters influencing seed yield directly and indirectly. The results indicated that biological yield is responsible for manipulation of seed yield in soybean.

Aditya *et al.,* (2011) observed highly significant and positive genetic correlation for grain yield per plant with dry matter weight per plant (rg=0.491), number of primary branches per plant (rg=0.403), number of pods per plant (0.631) and harvest index (0.487).

Kobraee and Shamsi (2011) observed the results of path analysis showed that in normal condition, direct effect on yield were greatest for number of pod per plant (0.763**), while, in stress site this value belonged to number of seed per plant (0.664**). In addition, in normal site, indirect effect of pod/ plant on yield via the number of node per plant (0.648) and number of seed per plant (0.708) was greater than the other yield components. Also, for stress site seed/plant had indirect effect on yield via number of node per plant (0.588), number of pod per plant (0.579) and 100-seed weight (0.479). Number of node per plant in normal conditions had direct and negative effect on soybean yield.

Machikowa and Laosuwan (2011) investigated eight characters of soybean and verified direct and indirect effects for the selection for seed yield. Significantly positive phenotypic correlation was observed between seed yield and days to flowering. Further-more, genotypic correlation showed that seed yield was positively correlated with all characters except 100 seed weight. They observed pods per plant gave the highest positive direct effect on seed yield, followed by branches per plant. In addition, the indirect effects of most characters were high through pods per plant.

Patil *et al.,* (2011) observed that seed yield per plant was positively and significantly correlated with plant height, pods per plant, and days to 50 per cent flowering and days to maturity. They observed pods per plant had highest positive direct effect on seed yield per plant followed by plant height. The studies suggest that selection for pods per plant, seed yield and plant height to evolve high yielding varieties of soybean.

Athoni and Basavaraja (2012) found that number of pods per plant, pod weight per plant, 100 seed weight and oil content showed positive and significant correlation with seed yield per plant. The studies show that path coefficient analysis revealed maximum positive direct effect of pod weight on seed yield per plant followed by 100 seed weight and its indirect effect through other characters were also considerably high.

Abady *et al.,* (2013) studied path coefficient analysis for various quantitative and morphological traits and found that number of pods per plant, days to maturity and harvest index had positive direct effect on seed yield per plot. Number of branches per plant and plant height exerted positive and significant indirect effect on seed yield per plot through number of pods per plant; and plant height also exert positive and significant indirect effect on seed yield per plot through days to flowering and days to maturity.

Ghodrati (2013) observed a strong positive correlation (r = 0.61*) between seed yield and plant height and concluded that simultaneous selection for improving seed yield through increasing the number of nodes plant per plant, number of pods plant per plant and plant height would be an effective approach to increase seed yield as well as protein yield. They indicated that the total dry matter gave the greatest direct positive effect (0.718) on seed yield, followed by harvest index (0.589). He indicated that seed yield had significant correlations with 100 seed weight, number of pods per plant, days to maturity, harvest index, oil percentage and protein percentage.

Moe and Girdthai (2013) evaluated the diversity of soybean accessions at morpho-physiological traits and identified the correlations among the traits. Positive and significant correlations were observed between yield and other traits, except seeds/pod. In physiological traits, negative and significant correlations was found between specific leaf area (SLA) and yield while, association with SPAD chlorophyll meter reading (SCMR) values was non-significance.

Okonkwo and Idahosa (2013) observed significant positive correlation between grain yield and seeds/pod, 100-seed weight, pods/plant, pod length, days to flowering and plant height, nodes/plant; seeds/pod and plant height, LAI, flowering, pod length, 1000-seed weight and flowering, maturity, pods/node seeds/pod.

Salimi and Abdola (2013) reported significant difference among the studied soybean genotypes in the majority of traits, correlation analysis showed that grain yield per plant had significant and positive correlation with all studied traits. The highest positive correlation were observed between day to 50% flowering and day to maturity (r = 0.966**) and between fresh & dry weight of plant (r = 0.939**). The results compare means showed between genotypes significant difference were exists and data recorded in showed that Grain yield increased across the soybean genotypes. They observed that the numbers of seeds per plant have highest positive direct effect on grain yield under normal and moisture stress condition.

Amit Kumar *et al.*, (2014) evaluated 40 genotypes for agro-morphological traits and genetic parameters. Correlation was found significant with yield and its component characters. Path analysis indicated that the 100 seed weight had highest effect on yield.

Barh *et al.*, (2014) observed that number of pods per plant, number of seed per pod, 100 seed weight, number of primary branches and seed per plant were significantly correlated with yield of bhat.

Hwang *et al.*, (2014) the analysis of variance indicated that the accessions differed significantly ($P < 0.0001$) in seed protein content, and no significant interaction between accessions and locations was detected. The correlation coefficient (r) of seed protein concentration between the MD and NE experiments was quite high, $r = 0.98$ (P <

0.0001). The analysis of variance for seed oil revealed that accessions were significantly different ($P < 0.0001$) and as was the case with protein, there was no significant accession × location interaction for oil. The correlation between mean seed protein and oil contents in the MD experiment and in the NE experiment were $r = -0.64$ and $r = -0.66$, respectively.

Jain *et al.*, (2015) observed that path coefficient analysis revealed that biological yield, number of pods per plant and 100 seed weight were major characters influencing seed yield directly and indirectly.

Mahbub *et al.,* (2015) evaluated variance for plant height, seed yield per plant, branches per plant, number of seeds per pod, number of pods per plant controlled by additive gene action. Plant height, pod length, number of seeds per pod, number of pods per plant, 100 seed weight, branches per plant and number of seeds per pod showed significant positive genotypic and phenotypic correlation with seed yield.

MATERIAL AND METHODS

CHAPTER III

MATERIAL AND METHODS

The present studies have been done to know the genetic variability of soybean germplasm lines based on various morphological and qualitative traits. Advanced progenies were developed by crossing of the elite parents by emasculation and pollination programme. Developed F1 were evaluated for seed yield and quality traits advanced to F2, F3, F4, F5 and F6 by pedigree selection.

Details of the materials and techniques adopted during the course of investigation are described below:

3.1 General Description

The present investigation on "Evaluation of Advanced progenies for seed yield and quality traits in Soybean (*Glycine max* (L.) Merrill)" was undertaken during *kharif* 2015-16. Field work was carried out at the experimental farm of "All India Coordinated Research Project on Soybean" Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani while, laboratory work for estimation of oil in soybean seeds was carried out at NMR laboratory "All India Coordinated Research Project on Safflower", VNMKV, Parbhani and protein estimation was carried out at Department of Soil Science and Agricultural Chemistry, College of Agriculture, VNMKV, Parbhani. All recommended agronomic package of practices and plant protection measures were followed for satisfactory crop growth.

3.1.1 Experimental material

The experimental material comprised of 26 germplasm lines developed at soybean research centre and some of the lines collected from different research stations and three national checks *viz.*, JS-335, JS 93-05 and JS 95-60 and three local checks *viz.*, MAUS-71, MAUS-158 and MAUS-162. The list of germplasm lines, checks and layout plan in the experimental field is presented in Table 1.

Table 1. List of soybean germplasm genotypes

Sr. No.	Name of line	Pedigree/ Parentage
1	NRC 1	NRC 2012-F-1-18-1
2	NRC 2	NRC 2012-G-3-16-2
3	NRC 3	NRC 2012-B-1-8-1-4-1-1
4	NRC 4	NRC 2012-F-25-4
5	NRC 5	NRC 2012-C-4-13-2
6	NRC 6	NRC 2012-A-3-2-1-1
7	MAUS 745	JS 335 X RKS 39
8	MAUS 746	MAUS 47 X MAUS 1039
9	MAUS 747	MAUS 1055 X MAUS 71
10	MAUS 748	JS 99-52 X MAUS 1055
11	MAUS 749	RKS 39 X JS 97-52
12	MAUS 750	MAUS 47 X JS 99-52
13	MAUS 751	G3P20 X JS 9305
14	MAUS 752	JS 335 X G-841
15	MAUS 753	JS 335 X G3P20
16	MAUS 754	MAUS 1039 X RKS 24
17	MAUS 755	JS 9982 X MAUS 1055
18	MAUS 756	NRC 75 X P3P20
19	MAUS 757	MAUS 47 X RKS 24
20	MAUS 758	JS 99-85 X RKS 45
21	MAUS 759	JS 93-05 X P1P8
22	MAUS 760	JS 9985 X JS-335
23	MAUS 761	MAUS 1039 X MAUS 1029
24	MAUS 762	MAUS 47 X JS 9985
25	MAUS 763	JS 9985 X RKS 39
26	MAUS 764	JS 97-85 X RKS 39
	Checks	
27		JS 335
28		JS 93-05
29		JS 95-60
30		MAUS 71
31		MAUS 158
32		MAUS 162

3.1.2 Location

The experimental farm of "All India Coordinated Research Project on Soybean" is located at the campus of V.N.M.K.V., in Parbhani. The location Parbhani is located at 19.27°N to 76.78°E. It has an elevation of 347 meters.

3.1.3 Layout and sowing

Twenty six elite germplasm lines of soybean along with six checks were sown during *kharif*, 2015 at experimental farm of "All India Coordinated Research Project on Soybean", Vasantrao Naik Marathwada Agriculture University, Parbhani on 27th July 2015. Plan and layout is presented in Fig 1.

3.1.4 Details of experiment

Design : R.B.D. (Randomized Block Design)

Treatments : 32 (26 genotypes + 6 checks)

Replications : Three (3)

Plot size : 1.80 m x 4.0 m. (four rows/entry)

Spacing : Row to row distance : 45 cm

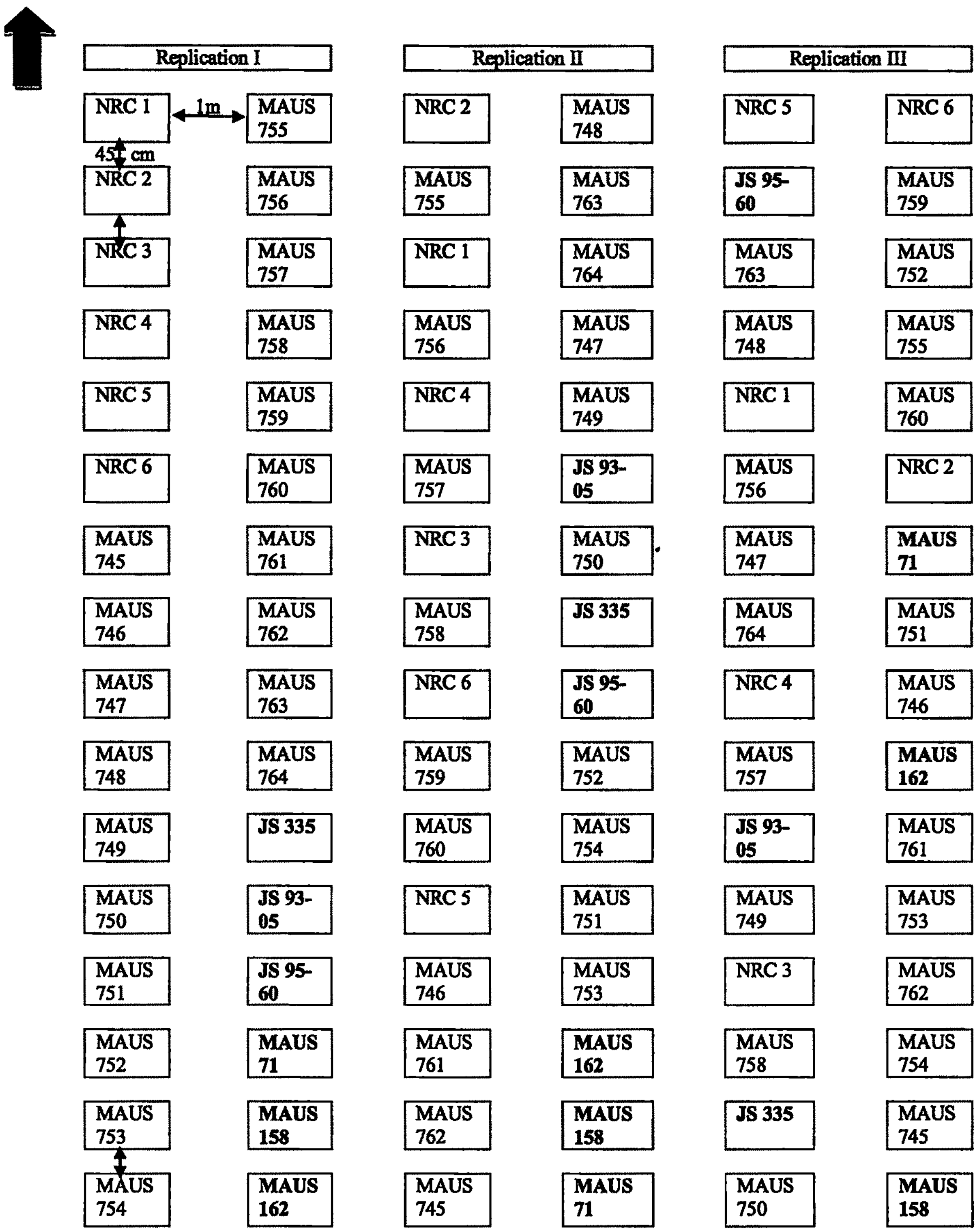
Plant to plant distance : 5 cm

Date of sowing : 27/07/2015

3.1.5 Crop Management

The crop was managed following all the agronomical practices recommended for soybean cultivation published by Vasantrao Naik Marathwada Krishi Vidyapeth, Parbhani. Each genotype was grown in four rows of 1.80 m length with a spacing of 0.45 m between rows and 0.05 m between plants. Two seeds were planted in each hill to facilitate emergence and to provide uniform stand of plants. Just before

Fig no. 1 Layout of field experiment



Replication I		Replication II		Replication III	
NRC 1	MAUS 755	NRC 2	MAUS 748	NRC 5	NRC 6
NRC 2	MAUS 756	MAUS 755	MAUS 763	JS 95-60	MAUS 759
NRC 3	MAUS 757	NRC 1	MAUS 764	MAUS 763	MAUS 752
NRC 4	MAUS 758	MAUS 756	MAUS 747	MAUS 748	MAUS 755
NRC 5	MAUS 759	NRC 4	MAUS 749	NRC 1	MAUS 760
NRC 6	MAUS 760	MAUS 757	JS 93-05	MAUS 756	NRC 2
MAUS 745	MAUS 761	NRC 3	MAUS 750	MAUS 747	MAUS 71
MAUS 746	MAUS 762	MAUS 758	JS 335	MAUS 764	MAUS 751
MAUS 747	MAUS 763	NRC 6	JS 95-60	NRC 4	MAUS 746
MAUS 748	MAUS 764	MAUS 759	MAUS 752	MAUS 757	MAUS 162
MAUS 749	JS 335	MAUS 760	MAUS 754	JS 93-05	MAUS 761
MAUS 750	JS 93-05	NRC 5	MAUS 751	MAUS 749	MAUS 753
MAUS 751	JS 95-60	MAUS 746	MAUS 753	NRC 3	MAUS 762
MAUS 752	MAUS 71	MAUS 761	MAUS 162	MAUS 758	MAUS 754
MAUS 753	MAUS 158	MAUS 762	MAUS 158	JS 335	MAUS 745
MAUS 754	MAUS 162	MAUS 745	MAUS 71	MAUS 750	MAUS 158

Plate 1. Layout of field experiment

sowing, fertilizers were applied at the rate of 30: 60: 20 and 20 kg/ha of N, P, K and S respectively.

3.1.6 Collection of Experimental Data

Five plants at random in each plot and replication were selected and labeled for recording observations and the mean of five plants was used for statistical analysis. Observations on different morphological characteristics were recorded on these plants at different stages of crop growth. The observations on the following yield and yield components and quality parameters were recorded as per the guidelines of DUS soybean.

3.2 Plant morphological characters

3.2.1 Plant height (cm)

The length of the randomly selected five plants were measured in centimeters from the base of the plant at the ground level to the tip of the main shoot at maturity and grouped as follows:

Short : < 40cm

Medium : 41-60 cm

Tall : > 60 cm

3.2.2 Number of branches per plant

At maturity five plants were selected in each plot and total numbers of effective branches were recorded in each treatment.

Less branches : < 4

Medium branches : 4-6

More branches : > 6

3.3 Flower Morphological characters

3.31 Days to initial flowering

Number of days taken from sowing to anthesis in plants in plot was recorded as days to initial flowering.

Early Flowering : ≤32 days

Medium Flowering : 33-42 days

Late Flowering : > 42 days

3.3.2 Days to 50 per cent flowering

Days required from sowing to flowering of approximately 50 percent plants in each entry was recorded and average number of days to 50 percent flowering was worked out.

Early Flowering : ≤35 days

Medium Flowering : 36-45 days

Late Flowering : > 45 days

3.3.3 Flower colour

The flower colour of selected and tagged plants in each treatment at flowering stage under natural day light condition and grouped in two categories:

A. Purple

B. White

3.4 Pod morphology

3.4.1 Pod colour at maturity

The pod colour has been taken on the plot wise basis in each treatment at pod maturity stage and grouped in three categories:

A. Yellow
B. Brown
C. Black

3.4.2 Pod Shattering / Non-shattering

The shattering / Non-shattering habits of seed from pods were recorded at fifteen days after physiological maturity for each genotype and grouped into two categories:

A. Shattering tolerant varieties

B. Shattering susceptible varieties

3.4.3 Number of pods per plant

The total number of pods obtained from each 5 randomly selected plants were calculated and then there average is been taken from each treatment.

Less : < 25.00

Medium : 25.00-40.00

More : > 40.00

3.4.4 Number of pod clusters per plant

The total number of pod clusters was observed from each 5 randomly selected plants were taken and then there average is been taken from each treatment.

Less : < 4

Medium : 4-8

More : > 8

3.5 Seed morphological characters

3.5.1 100 seed weight

Weight of the randomly selected 100 grains from a well dried composite sample of each of the genotype was recorded in grams using an electric balance and varieties were classified as follows:

Light : ≤ 10 g

Medium : 10.1-13 g

Heavy : > 13 g

3.6 Other characters

3.6.1 Days to maturity

Days required from sowing to maturity of 80 per cent of plants in a plot were recorded as days to maturity.

Early : ≤ 95.00 days

Medium : 96.00-105.00 days

Late : > 105.00 days

3.6.2 Leaf type and colour

The leaf type i.e., lanceolate, pointed ovate and rounded ovate were recorded at the stage of pod development for each treatment. Simultaneously, leaf colour was recorded viz., dark green or light green.

3.6.3 Plant growth habit

Plant growth habit is observed at the time of maturity of the crop. On the basis of that crop is divided into erect and semi-erect. Similarly, plant growth type were categorized into determinate, semi-determinate and indeterminate.

3.6.4 Number of nodes per plant

The numbers of nodes were recorded at the time of harvest in each treatment.

Less : < 5

Medium : 5-10

More : > 10

3.6.5 Seed yield (g/plant)

Seed yield of observation plant was recorded and average was taken as seed yield per plant.

3.6.6 Seed yield (qt/ha)

Based on the plot yield, the seed yield per plot is multiplied with the hectare factor and the resultant value is seed yield (kg/ha) which is later on converted into seed yield (qt/ha).

3.3 Laboratory observations:

3.3.1 Oil content

Oil content was determined by using Nuclear Magnetic Resonance (NMR) technique at AICRP on Safflower, V.N.M.K.V. Parbhani, for determination of oil content.

Low	:	$\leq$15.0
Average	:	15.1-18.0
Medium	:	18.1-20.0
High	:	> 20.0

3.3.2 Protein content (%)

Crude protein content was computed by estimating the per cent nitrogen in samples from each replication for each genotype by using Micro-kjeldhal method and later multiplied the value obtained by the factor 6.25. This method contains three steps *viz.*, digestion, distillation and titration.

Low	:	$\leq$38.0
Medium	:	38.1-40.0
High	:	> 40.0

3.4 Statistical analysis

The mean values of five random plants selected 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 (1978).

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	$\sigma^2 e + \sigma^2 r$	$\frac{RMS}{EMS}$	
2.	Treatment	(t-1)	TRMSS	$\sigma^2 e + r\sigma^2 g$	$\frac{TRMSS}{EMS}$	
3.	Error	(r-1) (t-1)	EMS	$\sigma^2 e$		
	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.

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

where,

EMSS = error mean sum of squares

r = number of replications

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

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.

$$\text{Arithematic Mean} = \frac{\text{sum of all observations}}{\text{number of observations}}$$

$$\bar{A} = \frac{\sum_{i=1}^{n} x_i}{n}$$

where,

$\sum_{i=1}^{n} x_i$ = sum of the given observations

n = number of observations

The range is the difference between the maximum and minimum value observed for each trait.

3.4.3 Genetic variability

Various parameters of genetic variability were calculated by using appropriate formulae. The genotypic and phenotypic variances were calculated by using the respective mean squares from variance table (Johnson *et al.,* 1955).

1. Genotypic variance :

$$V_g = \frac{\text{TrMSS} - \text{EMSS}}{r}$$

2. Error variance:

$$V_e = \text{EMSS}$$

3. Phenotypic variance:

$$V_p = V_g + V_e$$

where,

TrMSS = Treatment mean sum of squares

EMSS = Error mean sum of squares

r = Number of replications

V_g = Genotypic variance

V_p = Phenotypic variance

V_e = Environmental variance

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

4. Genotypic coefficient of variance

$$\text{GCV} = \frac{\sqrt{V_g}}{\bar{A}} \text{ X } 100$$

5. Phenotypic coefficient of variance

$$\text{PCV} = \frac{\sqrt{V_p}}{\bar{A}} \text{ X } 100$$

where,

V_g = Genotypic variance

V_p = Phenotypic variance

$\bar{A}$= General mean of character

3.4.4 Heritability and genetic advance

1. Heritability

Heritability (broad sense) was calculated according to the method suggested by Allard (1960).

$$\text{Heritability (H)} = \frac{V_g}{V_p}$$

$$\text{Heritability \%} = \frac{V_g}{V_p} X\ 100$$

where,

V_g= Genotypic variance

V_p = Phenotypic variance

2. Genetic advance

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

$$\text{Genetic advance (GA)} = \delta P * H * K$$

where,

K = selection intensity 2.06 when 5% of the population is selected.

P = phenotypic standard deviation of the character in the population.

H = heritability in broadsense.

3. Expected genetic advance

The expected genetic advance in percentage of mean was calculated as,

$$\text{Expected genetic advance (EGA)} = \frac{GA}{\bar{A}} X\ 100$$

where,

EGA = Expected genetic advance

GA = Genetic advance

$\bar{A}$ = General 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.

$$\text{Environmental covariance (Cov. ex.y)} = \text{EMSP}$$

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

$$\text{Phenotypic covariance (Cov. px.y)} = \text{(Cov. gx.y)} + \text{(Cov. ex.y)}$$

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 (rg_{xy})

$$rg_{xy} = \frac{Cov\ (g_x g_y)}{\sqrt{\sigma 2 g_x \cdot \sigma 2 g_y}}$$

where,

Cov ($g_X . g_Y$) = 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 (rP_{xy})

$$rp_{xy} = \frac{Cov\ (P_x P_y)}{\sqrt{\sigma 2 P_x . \sigma 2 P_y}}$$

where,

$Cov\ (P_x . P_y)$ = 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.

3.3.7 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 (1921b) 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 x1, x2, x3 and these components show following type of association with each other.

In path diagram, the grain soybean yield is the result of x1, x2, x3 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}).

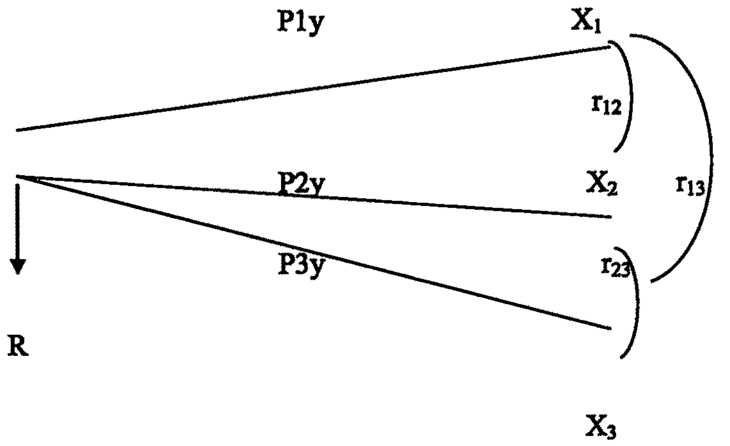


Fig. 2. Path diagram showing the factors influencing yield

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).

rny = pny + rn2p2y + rn3p3y+.....

where,

Rny = represents correction coefficient between one component and seed cotton yield

rn2 = represents correlation coefficient between that character and each of other components

pny = represents path coefficient between that characters and seed cotton yield.

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

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

The coefficients P1, P2 ....Pn 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 $r_{ij}P_{ij}$

$$\begin{array}{cccc} \textbf{Matrix-A} & & & \textbf{Matrix-B} \\ \begin{pmatrix} r1,y \\ r2,y \\ \cdot \\ \cdot \\ \cdot \\ \cdot \\ \cdot \\ rn.y \end{pmatrix} & = & \begin{pmatrix} P1 \\ P2 \\ \cdot \\ \cdot \\ \cdot \\ \cdot \\ \cdot \\ Pn \end{pmatrix} & \begin{pmatrix} r1,1 & r1,2 \ldots\ldots & r1,n \\ r2,1 & r2,2 \ldots\ldots & r2,n \\ \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot \\ rn,1 & rn,2 \ldots\ldots & 1 \end{pmatrix} \end{array}$$

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

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

where,

R^2 = (P1y, r1y + P2y, r2y +..........+ Pny, rny)

where,

P1y, P2y ....Pny = path values

r1y, r2y ....rny = correlation coefficients

RESULTS

CHAPTER IV

RESULT

The present study was conducted with 26 soybean germplasm lines collected from V.N.M.K.V., Parbhani along with three national checks i.e., JS 335, JS 93-05 and JS 95-60 and three local checks, viz., MAUS 71, MAUS 158 and MAUS 162. The main objective of this study was to approach the extent of variability in the yield of soybean germplasm lines along with morphological, oil and protein content of each germplasm lines of soybean.

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

4.1 **Analysis of variance**

4.2 **Mean performance**

4.3 **Genetic variability**

4.4 **Correlation**

4.5 **Path coefficient**

4.1 Analysis of variance

The mean sum of squares due to various sources of variation for 13 characters *viz.,* days to initial flowering, days to 50% flowering, days to maturity, plant height, number of branches per plant, number of nodes per plant, number of pod clusters per plant, number of pods per plant, test weight, seed yield per plant, seed yield (qt/ha), oil content and protein content are presented in Table 2. The variation due to replication was non-significant for all the character studied while; the variation due to genotypes was significant for all the characters under study both at 5 and 1 per cent probability level.

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

Analysis of Variance for thirteen yield and yield contributing characters														
Sr. N.	**d.f.**	**Morphological**					**Yield contributing traits**							
		Days of initial flowering	**Days of 50% flowering**	**Days to maturity**	**Plant height (cm)**	**Number of branches per plant**	**Number of nodes per plant**	**Number of pod clusters per plant**	**Number of pods per plant**	**100 seed wt. (g)**	**Oil content (%)**	**Protein content (%)**	**Seed yield (g /plant)**	**Seed yield (qt /ha)**
Replication	2	1.34	2.38	3.17	0.65	0.22	0.20	0.04	1.09	1.16	4.67	0.83	0.29	18.12
Treatment	31	24.38**	27.18**	89.13**	110.28**	2.02**	5.27**	5.83**	87.43**	4.32**	7.37**	11.54**	4.16**	34.89**
Error	62	0.44	0.47	0.46	0.79	0.07	0.31	0.09	0.77	0.27	0.19	0.56	0.07	2.59

*, ** Significance at 5% and 1%, respectively.

4.2 Mean Performance

The only legally recognized method in our country for varietal identification and genetic purity assessment practices by seed certification is based on field-plot grow out test, which include the morphological characteristics of a cultivar and also helpful to know the genetic variability for the crop.

4.2.1 Plant morphological characters

4.2.1.1 Plant Height (cm)

The plant height varied among different soybean genotypes (Table 3). The mean plant height of the genotypes was 33.33 cm. The highest plant height was observed in NRC 3 (38.40 cm), followed by MAUS 748 (38.33 cm) and NRC 4 (36.33 cm) while, the lowest plant height was observed in NRC 6 and MAUS 756 (23.63 cm) followed by MAUS 761 (26.53cm) and MAUS 754 (27.33cm). Based on the plant height, the studied twenty six genotypes were grouped into three categories as short (≤40.00 cm), medium (41.00-60.00 cm) and tall (>60.00 cm) which contain 26, 0 and 0 genotypes, respectively whereas among checks, JS 335, JS 93-05, JS 95-60 and MAUS 158 falls in the category of short plant height; MAUS 71 and MAUS 162 falls in the category of medium plant height category and the height difference can be clearly seen in plate 2.

Short: NRC 1, NRC 2, NRC 3, NRC 4, NRC 5, NRC 6, MAUS 745, MAUS 746, MAUS 747, MAUS 748, MAUS 749, MAUS 750, MAUS 751, MAUS 752, MAUS 753, MAUS 754, MAUS 755, MAUS 756, MAUS 757, MAUS 758, MAUS 759, MAUS 760, MAUS 761, MAUS 762, MAUS 763, MAUS 764, JS 335 (Check), JS 93-05 (Check), JS 95-60 (Check) and MAUS 71 (Check).

Medium: MAUS 158 (Check) and MAUS 162 (Check).

Tall: none.

Plate 2. Variation for plant height in soybean genotypes

Table 3. Mean performances of soybean genotypes for morphological, physiological and yield and yield contributing traits in soybean

Sr. No.	Genotype	Days to initial flowering		Days to 50% flowering		Days to maturity	
		Mean	Group	Mean	Group	Mean	Group
1	NRC 1	35	Medium	38	Medium	98	Medium
2	NRC 2	35	Medium	38	Medium	93	Medium
3	NRC 3	38	Medium	42	Medium	102	Medium
4	NRC 4	31	Early	34	Early	92	Medium
5	NRC 5	36	Medium	39	Medium	94	Medium
6	NRC 6	30	Early	33	Early	87	Early
7	MAUS 745	34	Medium	37	Medium	96	Medium
8	MAUS 746	32	Early	35	Early	90	Medium
9	MAUS 747	35	Medium	38	Medium	90	Medium
10	MAUS 748	33	Medium	36	Medium	91	Medium
11	MAUS 749	35	Medium	38	Medium	90	Medium
12	MAUS 750	34	Medium	37	Medium	92	Medium
13	MAUS 751	33	Medium	36	Medium	90	Medium
14	MAUS 752	35	Medium	38	Medium	93	Medium
15	MAUS 753	32	Early	35	Early	90	Medium
16	MAUS 754	33	Medium	39	Medium	90	Medium
17	MAUS 755	33	Medium	36	Medium	90	Medium
18	MAUS 756	28	Early	31	Early	87	Early
19	MAUS 757	34	Medium	37	Medium	92	Medium
20	MAUS 758	36	Medium	39	Medium	94	Medium
21	MAUS 759	35	Medium	38	Medium	90	Medium
22	MAUS 760	37	Medium	40	Medium	99	Medium
23	MAUS 761	41	Medium	44	Medium	108	Late
24	MAUS 762	40	Medium	44	Medium	106	Late
25	MAUS 763	32	Early	35	Early	89	Early
26	MAUS 764	36	Medium	39	Medium	93	Medium
Checks							
1	JS 335	35	Medium	38	Medium	90	Medium
2	JS 93-05	35	Medium	38	Medium	92	Medium
3	JS 95-60	28	Early	30	Early	85	Early
4	MAUS 71	37	Medium	39	Medium	100	Medium
5	MAUS 158	35	Medium	38	Medium	91	Medium
6	MAUS 162	39	Medium	42	Medium	102	Medium
Mean		34.56		37.69		93.29	
S.E. ±		0.38		0.40		0.39	
C.D. at 5%		1.08		1.21		1.10	
C.V. (%)		1.92		1.82		0.72	

Table 3 Contd...

Sr. No.	Genotype	Plant height (cm)		Number of branches per plant		Number of nodes per plant	
		Mean	Group	Mean	Group	Mean	Group
1	NRC 1	36.0	Short	2.5	Less	8.40	Medium
2	NRC 2	35.3	Short	3.5	Less	8.53	Medium
3	NRC 3	38.4	Short	1.7	Less	10.47	More
4	NRC 4	36.3	Short	2.1	Less	8.47	Medium
5	NRC 5	35.3	Short	0.6	Less	9.07	Medium
6	NRC 6	23.6	Short	2.4	Less	8.53	Medium
7	MAUS 745	33.4	Short	2.0	Less	8.60	Medium
8	MAUS 746	33.8	Short	1.4	Less	7.40	Medium
9	MAUS 747	32.8	Short	2.5	Less	6.53	Medium
10	MAUS 748	38.3	Short	2.4	Less	7.47	Medium
11	MAUS 749	31.9	Short	1.4	Less	6.53	Medium
12	MAUS 750	35.5	Short	1.2	Less	8.47	Medium
13	MAUS 751	30.8	Short	2.3	Less	7.47	Medium
14	MAUS 752	34.0	Short	2.5	Less	7.27	Medium
15	MAUS 753	34.1	Short	1.5	Less	6.93	Medium
16	MAUS 754	27.3	Short	2.1	Less	6.93	Medium
17	MAUS 755	34.7	Short	2.8	Less	6.47	Medium
18	MAUS 756	23.6	Short	2.5	Less	7.33	Medium
19	MAUS 757	31.3	Short	0.7	Less	7.80	Medium
20	MAUS 758	33.4	Short	3.2	Less	8.53	Medium
21	MAUS 759	29.3	Short	1.5	Less	6.33	Medium
22	MAUS 760	28.0	Short	1.3	Less	8.47	Medium
23	MAUS 761	26.5	Short	0.5	Less	11.33	More
24	MAUS 762	31.8	Short	1.5	Less	10.80	More
25	MAUS 763	34.2	Short	1.5	Less	6.27	Medium
26	MAUS 764	35.2	Short	3.5	Less	7.80	Medium
Checks							
1	JS 335	27.8	Short	3.5	Less	5.60	Medium
2	JS 93-05	32.7	Short	1.6	Less	6.47	Medium
3	JS 95-60	25.3	Short	1.7	Less	7.53	Medium
4	MAUS 71	55.3	Medium	2.5	Less	7.40	Medium
5	MAUS 158	35.4	Short	3.2	Less	7.73	Medium
6	MAUS 162	45.1	Medium	2.2	Less	6.53	Medium
Mean		33.33		2.06		7.80	
S.E. ±		0.51		0.15		0.32	
C.D. at 5%		1.45		0.42		0.91	
C.V. (%)		2.66		12.36		7.11	

Table 3 Contd...

Sr. No.	Genotypes	Number of pod clusters per plant		Number of pods per plant		100 seed wt. (g)	
		Mean	Group	Mean	Group	Mean	Group
1	NRC 1	5.00	Medium	23.40	Less	8.81	Light
2	NRC 2	5.40	Medium	24.93	Less	9.34	Light
3	NRC 3	6.13	Medium	27.87	Medium	11.86	Medium
4	NRC 4	4.93	Medium	23.33	Less	9.99	Light
5	NRC 5	5.07	Medium	23.53	Less	9.81	Light
6	NRC 6	5.13	Medium	23.60	Less	8.39	Light
7	MAUS 745	5.80	Medium	26.53	Medium	9.49	Light
8	MAUS 746	3.40	Less	16.93	Less	8.03	Light
9	MAUS 747	3.20	Less	16.47	Less	7.33	Light
10	MAUS 748	4.33	Medium	20.93	Less	8.65	Light
11	MAUS 749	1.73	Less	10.80	Less	7.17	Light
12	MAUS 750	5.67	Medium	25.33	Medium	7.93	Light
13	MAUS 751	3.73	Less	17.60	Less	7.96	Light
14	MAUS 752	4.40	Medium	21.00	Less	10.56	Medium
15	MAUS 753	2.87	Less	15.47	Less	7.83	Light
16	MAUS 754	2.60	Less	13.73	Less	7.34	Light
17	MAUS 755	3.47	Less	17.20	Less	8.73	Light
18	MAUS 756	4.73	Medium	22.27	Less	7.31	Light
19	MAUS 757	4.47	Medium	21.20	Less	7.56	Light
20	MAUS 758	4.80	Medium	23.20	Less	7.24	Light
21	MAUS 759	2.53	Less	13.47	Less	6.59	Light
22	MAUS 760	5.33	Medium	24.67	Less	8.38	Light
23	MAUS 761	6.60	Medium	29.73	Medium	8.61	Light
24	MAUS 762	6.27	Medium	28.40	Medium	8.11	Light
25	MAUS 763	2.67	Less	14.07	Less	7.73	Light
26	MAUS 764	3.73	Less	18.60	Less	7.03	Light
Checks							
1	JS 335	1.33	Less	9.67	Less	7.61	Light
2	JS 93-05	3.40	Less	16.87	Less	8.70	Light
3	JS 95-60	1.87	Less	11.60	Less	10.70	Medium
4	MAUS 71	2.60	Less	17.60	Less	8.75	Light
5	MAUS 158	4.67	Medium	22.00	Less	8.21	Light
6	MAUS 162	3.47	Less	14.00	Less	7.23	Light
Mean		4.10		19.88		8.41	
S.E. ±		0.17		0.50		0.30	
C.D. at 5%		0.49		1.43		0.85	
C.V. (%)		7.32		4.40		6.18	

Table 3 Contd...

Sr. No.	Genotype	Seed yield (g/plant)	Seed yield (qt/ha)
		Mean	Mean
1	NRC 1	4.53	16.60
2	NRC 2	4.76	18.17
3	NRC 3	5.01	19.17
4	NRC 4	4.26	16.07
5	NRC 5	4.56	17.47
6	NRC 6	4.62	17.63
7	MAUS 745	4.92	18.77
8	MAUS 746	2.85	11.60
9	MAUS 747	2.60	11.13
10	MAUS 748	3.28	13.10
11	MAUS 749	2.02	10.07
12	MAUS 750	4.90	18.47
13	MAUS 751	3.22	12.73
14	MAUS 752	3.32	13.17
15	MAUS 753	2.58	11.00
16	MAUS 754	2.35	10.60
17	MAUS 755	2.94	12.13
18	MAUS 756	3.95	14.90
19	MAUS 757	3.67	13.63
20	MAUS 758	4.15	13.53
21	MAUS 759	2.34	10.13
22	MAUS 760	4.75	17.97
23	MAUS 761	6.68	20.20
24	MAUS 762	5.67	19.60
25	MAUS 763	2.46	10.73
26	MAUS 764	3.23	13.00
Checks			
1	JS 335	1.93	8.30
2	JS 93-05	2.67	11.50
3	JS 95-60	2.32	10.10
4	MAUS 71	3.10	12.40
5	MAUS 158	3.76	14.50
6	MAUS 162	2.43	10.70
Mean		3.6	14.03
S.E. ±		0.17	0.93
C.D. at 5%		0.47	2.63
C.V. (%)		7.93	11.47

Table 3 Contd...

Sr. No.	Genotypes	Oil content (%)		Protein content (%)	
		Mean	Group	Mean	Group
1	NRC 1	21.42	High	35.81	Low
2	NRC 2	19.18	Medium	33.27	Low
3	NRC 3	21.44	High	36.39	Low
4	NRC 4	22.28	High	33.23	Low
5	NRC 5	19.03	Medium	30.43	Low
6	NRC 6	18.57	Medium	34.24	Low
7	MAUS 745	21.72	High	35.46	Low
8	MAUS 746	19.02	Medium	28.93	Low
9	MAUS 747	16.32	Average	37.40	Low
10	MAUS 748	19.21	Medium	33.22	Low
11	MAUS 749	21.62	High	35.56	Low
12	MAUS 750	20.52	High	33.59	Low
13	MAUS 751	19.00	Medium	33.47	Low
14	MAUS 752	20.07	High	33.93	Low
15	MAUS 753	17.74	Average	36.83	Low
16	MAUS 754	18.94	Medium	33.93	Low
17	MAUS 755	19.35	Medium	33.36	Low
18	MAUS 756	21.63	High	35.62	Low
19	MAUS 757	17.68	Average	37.03	Low
20	MAUS 758	18.62	Medium	34.05	Low
21	MAUS 759	19.69	Medium	34.59	Low
22	MAUS 760	22.09	High	33.20	Low
23	MAUS 761	22.07	High	33.30	Low
24	MAUS 762	22.04	High	34.01	Low
25	MAUS 763	19.81	Medium	34.33	Low
26	MAUS 764	16.98	Average	33.04	Low
Checks					
1	JS 335	19.27	Medium	36.40	Low
2	JS 93-05	19.67	Medium	36.32	Low
3	JS 95-60	19.38	Medium	38.02	Medium
4	MAUS 71	19.27	Medium	36.76	Low
5	MAUS 158	21.22	High	36.43	Low
6	MAUS 162	18.64	Medium	35.31	Low
Mean		19.8		34.6	
S.E. ±		0.25		0.43	
C.D. at 5%		0.71		1.22	
C.V. (%)		2.19		2.16	

4.2.1.2 Number of branches per plant

The number of branches per plant varied among the soybean genotypes (Table 3). The mean number of branches per plant was 2.06. Significantly higher number of branches was recorded in NRC 2 and MAUS 764 (3.47) while lower number of branches observed in MAUS 761 (0.53) followed by NRC 5 (0.60) and MAUS 757 (0.67). Based on the number of branches, among the studied all the twenty six genotypes were categorized into less number of branches as all are having branches below 4.00. Among the six checks all the genotypes were characterized into less branching type.

Less: NRC 1, NRC 2, NRC 3, NRC 4, NRC 5, NRC 6, MAUS 745, MAUS 746, MAUS 747, MAUS 748, MAUS 749, MAUS 750, MAUS 751, MAUS 752, MAUS 753, MAUS 754, MAUS 755, MAUS 756, MAUS 757, MAUS 758, MAUS 759, MAUS 760, MAUS 761, MAUS 762, MAUS 763, MAUS 764, JS 335 (Check), JS 93-05 (Check), JS 95-60 (Check), MAUS 71 (Check), MAUS 158 (Check) and MAUS 162 (Check).

Medium: none.

More: none.

4.2.2 Flower morphological characters

4.2.2.1 Days to initial flowering

The days to initial flowering varied significantly among the genotypes (Table 3). The average days taken by the genotypes for initial flowering were 34.56. The genotypes like MAUS 756 (28 days), NRC 6 (30 days) and NRC 4 (31 days) were observed earliness in days to initial flowering, while NRC 6, MAUS 758 and MAUS 754 (36 days) were late to initial flowering.

The genotypes were grouped in to three categories as early (<33.00 days), medium (33.00-42.00 days) and late (>42.00 days). Among the 26 genotypes, five had early, twenty one had medium and none of them shown late flowering type while, among checks one (JS 95-60) checks had early and five (JS 335, JS 93-05, MAUS 71, MAUS 158 and MAUS 162) had medium flowering type.

Early: NRC 4, NRC 6, MAUS 746, MAUS 753, MAUS 756, MAUS 762 and JS 95-60 (Check).

Medium: NRC 1, NRC 2, NRC 3, NRC 5, MAUS 745, MAUS 747, MAUS 748, MAUS 749, MAUS 750, MAUS 751, MAUS 752, MAUS 754, MAUS 755, MAUS 757, MAUS 758, MAUS 759, MAUS 760, MAUS 761, MAUS 762, MAUS 764, JS 335 (Check), JS 93-05 (Check), MAUS 71 (Check), MAUS 158 (Check) and MAUS 162 (Check).

Late: none.

4.2.2.2 Days to 50% flowering

The days to 50 per cent flowering varied among the genotypes (Table 3). The average days taken by the genotypes for fifty per cent flowering were 37.69. The genotypes like MAUS 756 (31 days), NRC 6 (33 days) and NRC 4 (34 days) were observed earliness in days to fifty percent flowering, while MAUS 761 and MAUS 762 (44 days) followed by NRC 3 (42 days) and MAUS 760 (40 days) were late to fifty percent flowering.

The genotypes were grouped in to three categories as early (<36.00 days), medium (36.00-45.00 days) and late (>45.00 days). Among the 26 genotypes, five had early, twenty one had medium and none of them were late flowering type while, among checks one (JS 95-60) checks had early and five (JS 335, JS 93-05, MAUS 71, MAUS 158 and MAUS 162) had medium 50% flowering type.

Early: NRC 4, NRC 6, MAUS 746, MAUS 753, MAUS 756, MAUS 762 and JS 95-60 (Check).

Medium: NRC 1, NRC 2, NRC 3, NRC 5, MAUS 745, MAUS 747, MAUS 748, MAUS 749, MAUS 750, MAUS 751, MAUS 752, MAUS 754, MAUS 755, MAUS 757, MAUS 758, MAUS 759, MAUS 760, MAUS 761, MAUS 762, MAUS 764, JS 335 (Check), JS 93-05 (Check), MAUS 71 (Check), MAUS 158 (Check) and MAUS 162 (Check).

Late: none.

4.2.2.3 Flower colour

Based on flower colour at flowering the varieties were classified into two groups. Those varieties with violate flower and other group with white flowers as shown in plate 3 and table 4. All of the six checks *viz.,* JS 335, JS 93-05, JS 95-60, MAUS 71, MAUS 158 and MAUS 162 shown purple flower colour.

Purple: NRC 1, NRC 3, NRC 4, NRC 5, NRC 6, MAUS 747, MAUS 748, MAUS 749, MAUS 750, MAUS 751, MAUS 752, MAUS 754, MAUS 757, MAUS 758, MAUS 759, MAUS 764, JS 335 (Check), JS 93-05 (Check), JS 95-60 (Check), MAUS 71 (Check), MAUS 158 (Check) and MAUS 162 (Check).

White: NRC 2, MAUS 745, MAUS 746, MAUS 753, MAUS 755, MAUS 756, MAUS 760, MAUS 761, MAUS 762 and MAUS 763.

4.2.3 Pod morphology

4.2.3.1 Pod colour at maturity

All the soybean germplasm lines were divided in three categories *viz.,* brown, black and yellow according to their pod colour (Table 4). Among germplasm lines eighteen genotypes found with brown pod colour, three with black pod colour and five with yellow pod colour at the time of maturity. Among checks JS 93-05 and JS 95-60 are having black pod at the time of maturity; JS 335 is brown pod at the time of

A. Purple

B. White

Plate 3. Variability for flower colour in soybean genotypes
A: Purple B: White

maturity and MAUS 71, MAUS 158 and MAUS 162 are yellow colour pod at the time of maturity.

Black: NRC 2, NRC 5, MAUS 750, JS 93-05 (Check) and JS 95-60 (Check).

Brown: NRC 1, NRC 3, NRC 4, NRC 6, MAUS 745, MAUS 746, MAUS 748, MAUS 752, MAUS 753, MAUS 754, MAUS 755, MAUS 756, MAUS 759, MAUS 760, MAUS 761, MAUS 762, MAUS 763, MAUS 764 and JS 335 (Check).

Yellow: MAUS 747, MAUS 749, MAUS 751, MAUS 757, MAUS 758, MAUS 71 (Check), MAUS 158 (Check) and MAUS 162 (Check).

4.2.3.2 Pod shattering/ non-shattering

Soybean genotypes behaves differently with regard to pod shattering character and were grouped in to two groups as pod shattering tolerant and pod shattering susceptible plate 4 and table 4.

Pod shattering tolerant: NRC 1, NRC 2, NRC 4, NRC 5, MAUS 745, MAUS 746, MAUS 747, MAUS 748, MAUS 749, MAUS 750, MAUS 752, MAUS 754, MAUS 758, MAUS 759, MAUS 764, JS 93-05 (Check), JS 95-60 (Check), MAUS 71 (Check) and MAUS 162 (Check).

Pod shattering susceptible: NRC 3, NRC 6, MAUS 751, MAUS 753, MAUS 755, MAUS 756, MAUS 757, MAUS 760, MAUS 761, MAUS 762, MAUS 763, JS 335 (Check) and MAUS 158 (Check).

Non-shattering

Shattering

Plate 4. Shattering/ non-shattering soybean genotypes

Table 4. Qualitative characteristics of soybean genotypes

Sr. No.	Genotype	Flower colour	Pod colour at maturity	Shattering/ Non shattering habit
1	NRC 1	Purple	Brown	Shattering tolerant
2	NRC 2	White	Black	Shattering tolerant
3	NRC 3	Purple	Brown	Shattering
4	NRC 4	Purple	Brown	Shattering tolerant
5	NRC 5	Purple	Black	Shattering tolerant
6	NRC 6	Purple	Brown	Shattering
7	MAUS 745	White	Brown	Shattering tolerant
8	MAUS 746	White	Brown	Shattering tolerant
9	MAUS 747	Purple	Yellow	Shattering tolerant
10	MAUS 748	Purple	Brown	Shattering tolerant
11	MAUS 749	Purple	Yellow	Shattering tolerant
12	MAUS 750	Purple	Black	Shattering tolerant
13	MAUS 751	Purple	Yellow	Shattering
14	MAUS 752	Purple	Brown	Shattering tolerant
15	MAUS 753	White	Brown	Shattering
16	MAUS 754	Purple	Brown	Shattering tolerant
17	MAUS 755	White	Brown	Shattering
18	MAUS 756	White	Yellow	Shattering
19	MAUS 757	Purple	Yellow	Shattering
20	MAUS 758	Purple	Brown	Shattering tolerant
21	MAUS 759	Purple	Brown	Shattering tolerant
22	MAUS 760	White	Brown	Shattering
23	MAUS 761	White	Brown	Shattering
24	MAUS 762	White	Brown	Shattering
25	MAUS 763	White	Brown	Shattering
26	MAUS 764	Purple	Brown	Shattering tolerant
27	JS 335	Purple	Brown	Shattering
28	JS 93-05	Purple	Black	Shattering tolerant
29	JS 95-60	Purple	Black	Shattering tolerant
30	MAUS 71	Purple	Yellow	Shattering tolerant
31	MAUS 158	Purple	Yellow	Shattering
32	MAUS 162	Purple	Yellow	Shattering tolerant

Table 4 Contd...

Sr. No.	Genotype	Leaf type	Leaf colour	Plant growth habit	Plant growth type
1	NRC 1	Rounded ovate	Dark green	Erect	Determinate
2	NRC 2	Pointed ovate	Dark green	Erect	Determinate
3	NRC 3	Pointed ovate	Dark green	Erect	Determinate
4	NRC 4	Rounded ovate	Dark green	Erect	Determinate
5	NRC 5	Lanceolate	Dark green	Erect	Determinate
6	NRC 6	Pointed ovate	Dark green	Semi-erect	Semi-determinate
7	MAUS 745	Pointed ovate	Dark green	Semi-erect	Semi-determinate
8	MAUS 746	Rounded ovate	Dark green	Erect	Determinate
9	MAUS 747	Pointed ovate	Light green	Erect	Determinate
10	MAUS 748	Pointed ovate	Light green	Semi-erect	Semi-determinate
11	MAUS 749	Rounded ovate	Dark green	Semi-erect	Semi-determinate
12	MAUS 750	Lanceolate	Dark green	Erect	Determinate
13	MAUS 751	Rounded ovate	Light green	Erect	Determinate
14	MAUS 752	Rounded ovate	Dark green	Erect	Determinate
15	MAUS 753	Rounded ovate	Light green	Erect	Determinate
16	MAUS 754	Rounded ovate	Dark green	Semi-erect	Semi-determinate
17	MAUS 755	Rounded ovate	Dark green	Erect	Determinate
18	MAUS 756	Pointed ovate	Dark green	Semi-erect	Semi-determinate
19	MAUS 757	Rounded ovate	Dark green	Erect	Determinate
20	MAUS 758	Rounded ovate	Dark green	Semi-erect	Semi-determinate
21	MAUS 759	Pointed ovate	Dark green	Erect	Determinate
22	MAUS 760	Pointed ovate	Dark green	Semi-erect	Semi-determinate
23	MAUS 761	Rounded ovate	Dark green	Erect	Determinate
24	MAUS 762	Pointed ovate	Dark green	Semi-erect	Semi-determinate
25	MAUS 763	Pointed ovate	Dark green	Semi-erect	Semi-determinate
26	MAUS 764	Rounded ovate	Dark green	Erect	Determinate
27	JS 335	Pointed ovate	Dark green	Erect	Determinate
28	JS 93-05	Lanceolate	Dark green	Erect	Determinate
29	JS 95-60	Lanceolate	Dark green	Erect	Determinate
30	MAUS 71	Pointed ovate	Light green	Erect	Determinate
31	MAUS 158	Rounded ovate	Dark green	Erect	Determinate
32	MAUS 162	Pointed ovate	Light green	Erect	Determinate

4.2.3.3 Number of pods per plant

The number of pods varied among the different soybean genotypes (Table 3) and clearly be seen in plate 5. The highest number of pods was recorded in the genotype MAUS 761 (29.73) followed by MAUS 762 (28.40), NRC 3 (27.87), MAUS 745 (26.53) and MAUS 750 (25.33) while, the lowest number of pods reported by MAUS 749 (10.80), MAUS 759 (13.47), MAUS 754 (13.73), MAUS 763 (14.07) and MAUS 753 (15.47).

Based on the number of pods per plant, the genotypes were grouped into three categories as less (< 25.00), medium (25.00-40.00) and more (> 40.00) pods per plant. Among the 26 genotypes, 21 had less, 5 had medium and 0 had more pod numbers per plant whereas, among 6 check all had less number of pods per plant.

Less: NRC 1, NRC 2, NRC 4, NRC 5, NRC 6, MAUS 746, MAUS 747, MAUS 748, MAUS 749, MAUS 751, MAUS 752, MAUS 753, MAUS 754, MAUS 755, MAUS 756, MAUS 757, MAUS 758, MAUS 759, MAUS 760, MAUS 763, MAUS 764, JS 335 (Check), JS 93-05 (Check), JS 95-60 (Check), MAUS 71 (Check), MAUS 158 (Check) and MAUS 162 (Check).

Medium: NRC 3, MAUS 745, MAUS 750, MAUS 761 and MAUS 762.

More: none.

4.2.3.4 Number of pod clusters per plant

The number of pod clusters per plant varied among different soybean genotypes (Table 3) and seen in plate 5.The mean number of pod clusters per plant of the genotypes was 4.10. Highest number of pod clusters per plant was observed in the germplasm MAUS 761 (6.60), followed by MAUS 762 (6.27), NRC 3 (6.13), MAUS 745 (5.80) and MAUS 750 (5.67) while the lowest pod clusters was observed in MAUS 749 (1.73), followed by MAUS 759 (2.53) and MAUS 754 (2.60).

Plate 5. Variability for pod cluster in soybean

Based on the number of pod clusters per plant, the genotypes were grouped into three categories as less number of pod clusters with less than 4.00 pod clusters, medium number of pod clusters with 4.00 to 8.00 pod clusters and more number of pod clusters with more than 8.00 number of pod clusters. Among the 26 genotypes, ten genotypes were grouped into less, sixteen genotypes into medium and none of genotypes into more number of pod clusters per plant. Among checks, MAUS 158 was medium number of pod clusters per plant and rests five were less number of pod clusters per plant.

Less: MAUS 746, MAUS 747, MAUS 749, MAUS 751, MAUS 753, MAUS 754, MAUS 755, MAUS 759, MAUS 763, MAUS 764, JS 335 (Check), JS 93-05 (Check), JS 95-60 (Check), MAUS 71 (Check) and MAUS 162 (Check).

Medium: NRC 1, NRC 2, NRC 3, NRC 4, NRC 5, NRC 6, MAUS 745, MAUS 748, MAUS 750, MAUS 752, MAUS 756, MAUS 757, MAUS 758, MAUS 760, MAUS 761, MAUS 762 and MAUS 158 (Check).

More: none.

4.2.4 Seed morphological characters

4.2.4.1 100 seed weight (g)

The hundred seed weight varied among different soybean genotypes (Table 3). The mean hundred seed weight of the genotypes was 8.41 g. The highest hundred seed weight was observed in the variety NRC 3 (11.86 g), followed by MAUS 752 (10.56 g), NRC 4 (9.99 g), NRC 5 (9.81 g) and MAUS 745 (9.49 g) while the lowest test weight was observed in MAUS 759 (6.59 g), followed by MAUS 764 (7.03 g) and MAUS 749 (7.17 g).

Based on the hundred seed weight, the genotypes were grouped into three categories as light weight with the hundred seed weight less than 10.00 g, medium weight with the hundred seed weight 10.00-13.00 g and heavy weight with the hundred seed weight more than 13.00 g. Among the twenty six germplasm, twenty four genotypes were grouped into light, two genotypes into medium and none of genotypes into heavy for hundred seed weight. Except check JS 95-60 (10.70g) which is medium weight and rest all are categorized into light weight seed on the basis of 100 seed weight.

Light: NRC 1, NRC 2,NRC 4, NRC 5, NRC 6, MAUS 745, MAUS 746, MAUS 747, MAUS 748, MAUS 749, MAUS 750, MAUS 751, MAUS 753, MAUS 754, MAUS 755, MAUS 756, MAUS 757, MAUS 758, MAUS 759, MAUS 760, MAUS 761, MAUS 762, MAUS 763, MAUS 764, JS 335 (Check), JS 93-05 (Check), MAUS 71 (Check), MAUS 158 (Check) and MAUS 162 (Check).

Medium: NRC 3, MAUS 752 and JS 95-60 (Check).

Heavy: none.

4.2.5 Other characters

4.2.5.1 Days to maturity

The days to harvesting varied significantly among the genotypes (Table 3). The average days required by the genotypes for harvesting were 93.29. The genotype MAUS 760 (108 days) and MAUS 761 (106 days) took more days for harvesting while, the genotype NRC 6 and MAUS 765 took less days for harvesting (87.00 days) Plate 6.

Based on the days to harvesting, the genotypes were grouped into three categories as early (< 90.00 days), medium (90.00-105.00 days) and late (>105.00 days). Among the genotypes, three genotypes had earliness, twenty one showed medium and two shown late harvesting times while, among the check only JS 96-50 has shown the earliness and rest other have shown medium maturity time period.

Early: NRC 6, MAUS 756, MAUS 762 and JS 95-60 (Check).

Medium: NRC 1, NRC 2, NRC 3, NRC 5, MAUS 745, MAUS 747, MAUS 748, MAUS 749, MAUS 750, MAUS 751, MAUS 752,

JS 95-60

NRC 6

Plate 6. Early maturity soybean genotypes

MAUS 754, MAUS 755, MAUS 757, MAUS 758, MAUS 759, MAUS 763, MAUS 764, JS 335 (Check), JS 95-06 (Check), MAUS 71 (Check), MAUS 158 (Check) and MAUS 162 (Check).

Late: MAUS 760 and MAUS 761.

4.2.5.2 Leaf type and colour

On the basis of the leaf type, germplasm lines were divided in three groups' *viz.,* lanceolate, pointed ovate and rounded ovate (Table 4) and plate7. The genotypes with the lanceolate leaf types were NRC 5 and MAUS 750; while the genotypes with pointed ovate were NRC 2, NRC 3, NRC 6, MAUS 745, MAUS 747, MAUS 748, MAUS 756, MAUS 759, MAUS 760, MAUS 762 and MAUS 763 and the genotypes which shown the rounded ovate type of genotypes were NRC 1, NRC 4, MAUS 746, MAUS 749, MAUS 751, MAUS 752, MAUS 753, MAUS 754, MAUS 755, MAUS 757, MAUS 758, MAUS 761 and MAUS 764. Among the checks, JS 93-05 and JS 95-60 had lanceolate leaf type; JS 335, MAUS 71 and MAUS 162 had pointed ovate leaf type; and MAUS 158 had shown rounded ovate leaf type.

Lanceolate: NRC 5, MAUS 750, JS 93-05 (Check) and JS 95-60 (Check).

Pointed ovate: NRC 2, NRC 3, NRC 6, MAUS 745, MAUS 747, MAUS 748, MAUS 756, MAUS 759, MAUS 760, MAUS 762, MAUS 763, JS 335 (Check), MAUS 71 (Check) and MAUS 162 (Check).

Rounded ovate: NRC 1, NRC 4, MAUS 746, MAUS 749, MAUS 751, MAUS 752, MAUS 753, MAUS 754, MAUS 755, MAUS 757, MAUS 758, MAUS 761, MAUS 764 and MAUS 158 (Check).

For leaf colour, the twenty six germplasm lines were divided into categories *viz.,* light green and dark green according to the colour of the leaf. The genotypes with dark green colour leaf were NRC 1, NRC 2, NRC 3, NRC 4, NRC 5, NRC 6, MAUS 745, MAUS 746, MAUS 749, MAUS 750, MAUS 752, MAUS 754,

Lanceolate

Pointed ovate

Rounded ovate

Plate 7. Genetic variability for leaf shapes of soybean

MAUS 755, MAUS 756, MAUS 757, MAUS 758, MAUS 759, MAUS 760, MAUS 761, MAUS 762, MAUS 763 and MAUS 764 while, genotypes with light green colour of leaf were MAUS 747, MAUS 748, MAUS 751 and MAUS 753. Among checks, MAUS 71 and MAUS 162 had light green colour of leaf while all the other checks had dark green colour of leaf. The above both features of leaf shape and colour are shown in plate 7.

Light green: MAUS 747, MAUS 748, MAUS 751, MAUS 753, MAUS 71 (Check) and MAUS 162 (Check).

Dark green: NRC 1, NRC 2, NRC 3, NRC 4, NRC 5, NRC 6, MAUS 745, MAUS 746, MAUS 749, MAUS 750, MAUS 752, MAUS 754, MAUS 755, MAUS 756, MAUS 757, MAUS 758, MAUS 759, MAUS 760, MAUS 761, MAUS 762, MAUS 763, MAUS 764, JS 335 (Check), JS 93-05 (Check), JS 95-60 (Check) and MAUS 158 (Check).

4.2.5.3 Plant growth habit

All the soybean germplasm lines were divided in two categories *viz.*, erect and semi-erect according to their plant growth habit (Table 4). Among germplasm lines majority of them were found with erect plant growth habit seen in plate 8. Among checks, all the checks were found to be erect plant growth habit type.

Erect: NRC 1, NRC 2, NRC 3, NRC 4, NRC 5, MAUS 746, MAUS 747, MAUS 750, MAUS 751, MAUS 752, MAUS 753, MAUS 755, MAUS 757, MAUS 759, MAUS 761, MAUS 764, JS 335 (Check), JS 93-05 (Check), JS 95-60 (Check), MAUS 71 (Check), MAUS 158 (Check) and MAUS 162 (Check).

Semi-erect: NRC 6, MAUS 745, MAUS 748, MAUS 749, MAUS 754, MAUS 756, MAUS 758, MAUS 760, MAUS 762 and MAUS 763.

The genotypes were also been categorized into three category based on their plant growth type *viz.*, determinate, semi-determinate and indeterminate. Sixteen

Erect

Erect

Semi-erect

Semi-erect

Plate 8. Genetic variability for plant growth habit

germplasm among twenty six germplasm were found to be determinate type and remaining ten with semi-determinate growth type. None of the genotype was found to be semi-determinate or indeterminate in checks.

Determinate: NRC 1, NRC 2, NRC 3, NRC 4, NRC 5, MAUS 746, MAUS 747, MAUS 750, MAUS 751, MAUS 752, MAUS 753, MAUS 755, MAUS 757, MAUS 759, MAUS 761, MAUS 764, JS 335 (Check), JS 93-05 (Check), JS 95-60 (Check), MAUS 71 (Check), MAUS 158 (Check) and MAUS 162 (Check).

Semi-determinate: NRC 6, MAUS 745, MAUS 748, MAUS 749, MAUS 754, MAUS 756, MAUS 758, MAUS 760, MAUS 762 and MAUS 763.

Indeterminate: none.

4.2.5.4 Number of nodes per plant

The number of nodes per plant showed a wide range of variation among the genotypes, ranged from 6.27 (MAUS 763) to 11.33 (MAUS 761) while, this range was from 5.60 (JS 335) to 7.73 (MAUS 158) among checks (Table 3). The genotypes *viz.,* MAUS 763 (6.27), MAUS 759 (6.33) and MAUS 755 (6.47) were identified with lower number of nodes per plant. The high node genotypes were MAUS 761 (11.33), MAUS 762 (10.8) and NRC 3 (10.47).

JS 335 (5.60) showed the lowest and MAUS-158 (7.73) showed the highest number of nodes per plant among checks included in the present investigation. Depending upon node number the genotypes were categorized as

Less: none.

Medium: NRC 1 NRC 2, NRC 4, NRC 5, NRC 6, MAUS 745, MAUS 746, MAUS 747 MAUS 748, MAUS 749, MAUS 750, MAUS 751, MAUS 752, MAUS 753, MAUS 754, MAUS 755, MAUS 756, MAUS 757, MAUS 758, MAUS 759, MAUS 760,MAUS

763, MAUS 764, JS 335 (Check), JS 93-05 (Check), JS 95-60 (Check), MAUS 71 (Check), MAUS 158 (Check) and MAUS 162 (Check).

More: NRC 3, MAUS 761 and MAUS 762.

4.2.5.5 Seed yield (g/plant)

The seed yield/plant varied among different soybean genotypes (Table 3). The mean seed yield per plant was 3.62 g. The highest seed yield was observed in MAUS 761 (6.68 g) followed by MAUS 762 (5.67 g), NRC 3 (5.01 g), MAUS 745 (4.92 g) and MAUS 750 (4.90 g) while the lowest seed yield per plant was observe in MAUS 749 (2.02 g), followed by MAUS 759 (2.34 g), MAUS 754 (2.35 g), MAUS 763 (2.46 g) and MAUS 753 (2.58 g).

4.2.5.6 Seed yield (qt/ha)

The seed yield (qt/ha) is different for different genotypes (Table 3 and Fig. 6). The mean value for seed yield (qt/ha) was 14.03 q/ha. Among the twenty six germplasm line, the highest seed yield was given by MAUS 761 (20.20 qt/ha), followed by MAUS 762 (19.60 qt/ha), NRC 3 (19.17 qt/ha), MAUS 745 (18.77 qt/ha) and MAUS 750 (18.47 qt/ha), while the lowest seed yield were observed in MAUS 749 (10.07 qt/ha), followed by MAUS 759(10.13 qt/ha), MAUS 754 (10.6 qt/ha), MAUS 763 (10.73 qt/ha) and MAUS 753 (11.0 qt/ha). Regarding checks, the highest seed yield was observed in MAUS 158 (14.5 qt/ha) and the lowest in JS 335 (8.30 qt/ha).

4.2.6 Laboratory observation

4.2.6.1 Oil Content (%)

The oil content varied among different soybean genotypes (Table 3 and Fig. 4). The average oil content among all soybean genotypes was MAUS 747 (16.32%) to NRC 4 (22.28%). The highest oil content observed in genotype NRC 4 (22.28%) followed by MAUS 760 (22.09%) and MAUS 761 (22.07%) while the lowest in

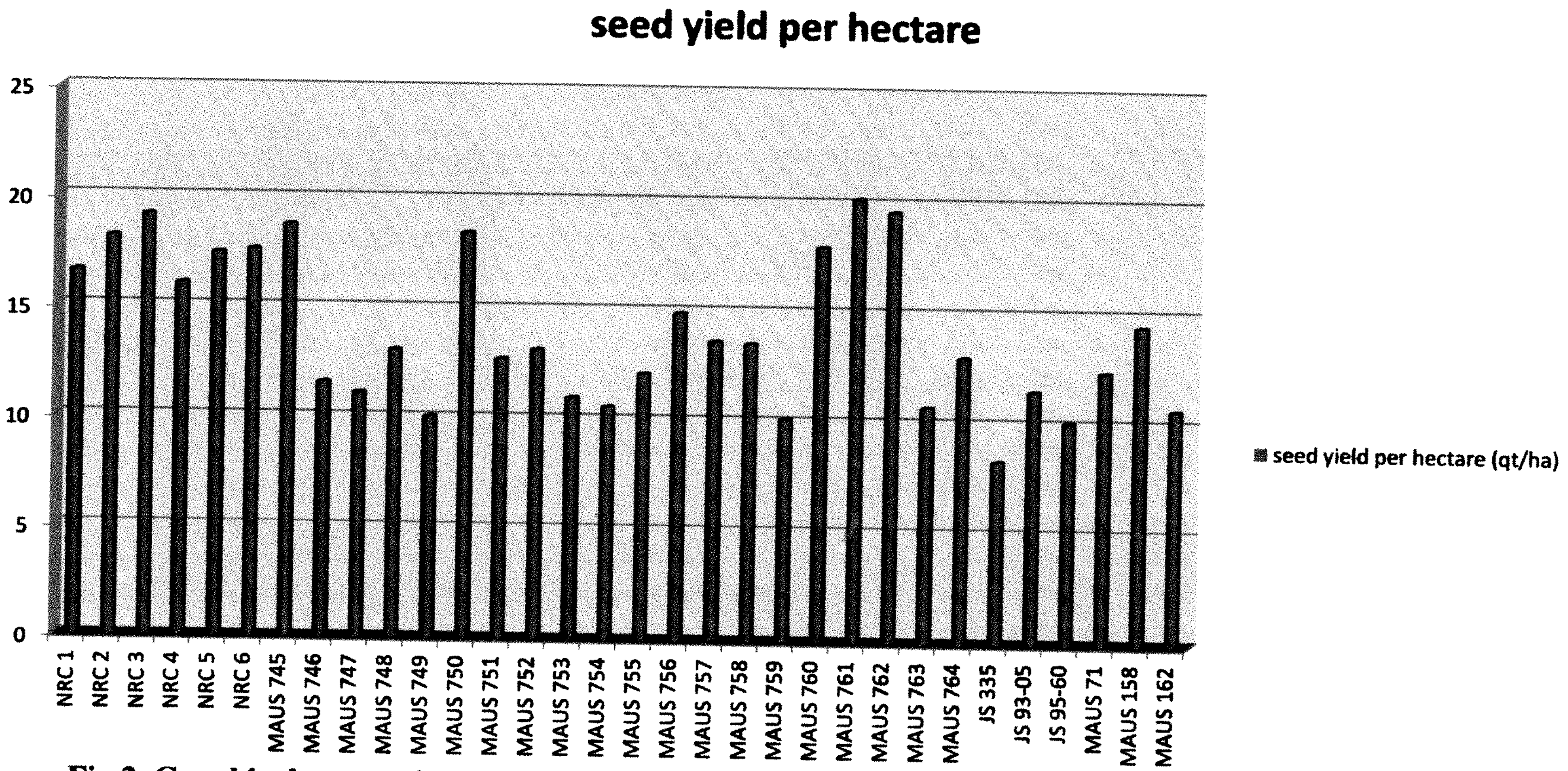


Fig 3. Graphical comparison of seed yield per hectare for soybean germplasm

genotype MAUS 747 (16.32%) followed by MAUS 764 (16.98%) and MAUS 757 (17.68%).

Among check, the lowest oil content observed in MAUS 162 (18.64%) and the highest in MAUS 158 (21.22%).

Based on the oil content, the genotypes were grouped into four categories as low oil content less than ≤ 15.0%, average oil content with 15.1-18.0% oil content, medium oil content with 18.1-20.0% and high oil content with >20.0% oil content. Among the twenty six germplasm, none of the genotype was grouped in low oil content category, four were grouped in average oil content, eleven were grouped in medium oil and eleven were grouped under high oil content.

Low: none.

Average: MAUS 747, MAUS 753, MAUS 757 and MAUS 764.

Medium: NRC 2, NRC 5, NRC 6, MAUS 746, MAUS 748, MAUS 751, MAUS 754, MAUS 755, MAUS 758, MAUS 759, MAUS 763, JS 335 (Check), JS 93-05 (Check), JS 95-60 (Check), MAUS 71 (Check) and MAUS 162 (Check).

High: NRC 1, NRC 3, NRC 4, MAUS 745, MAUS 749, MAUS 750, MAUS 752, MAUS 756, MAUS 760, MAUS 761, MAUS 762 and MAUS 158 (Check).

4.2.6.2 Protein Content (%)

The average protein content in genotypes range from MAUS 746 (28.93%) to MAUS 747 (37.40%) (Table 3 and Fig. 4). Genotypes *viz.*, MAUS 747 (37.40%), MAUS 757 (37.03%), MAUS 753 (36.83%), NRC 3 (36.39%) and NRC 1 (35.81%) showed the higher content of protein while the lower protein content showed by genotypes *viz.*, MAUS 746 (28.93%), NRC 5 (30.43%) and MAUS 764 (31.04%). Micro kjeldahl equipment given in plate 9.

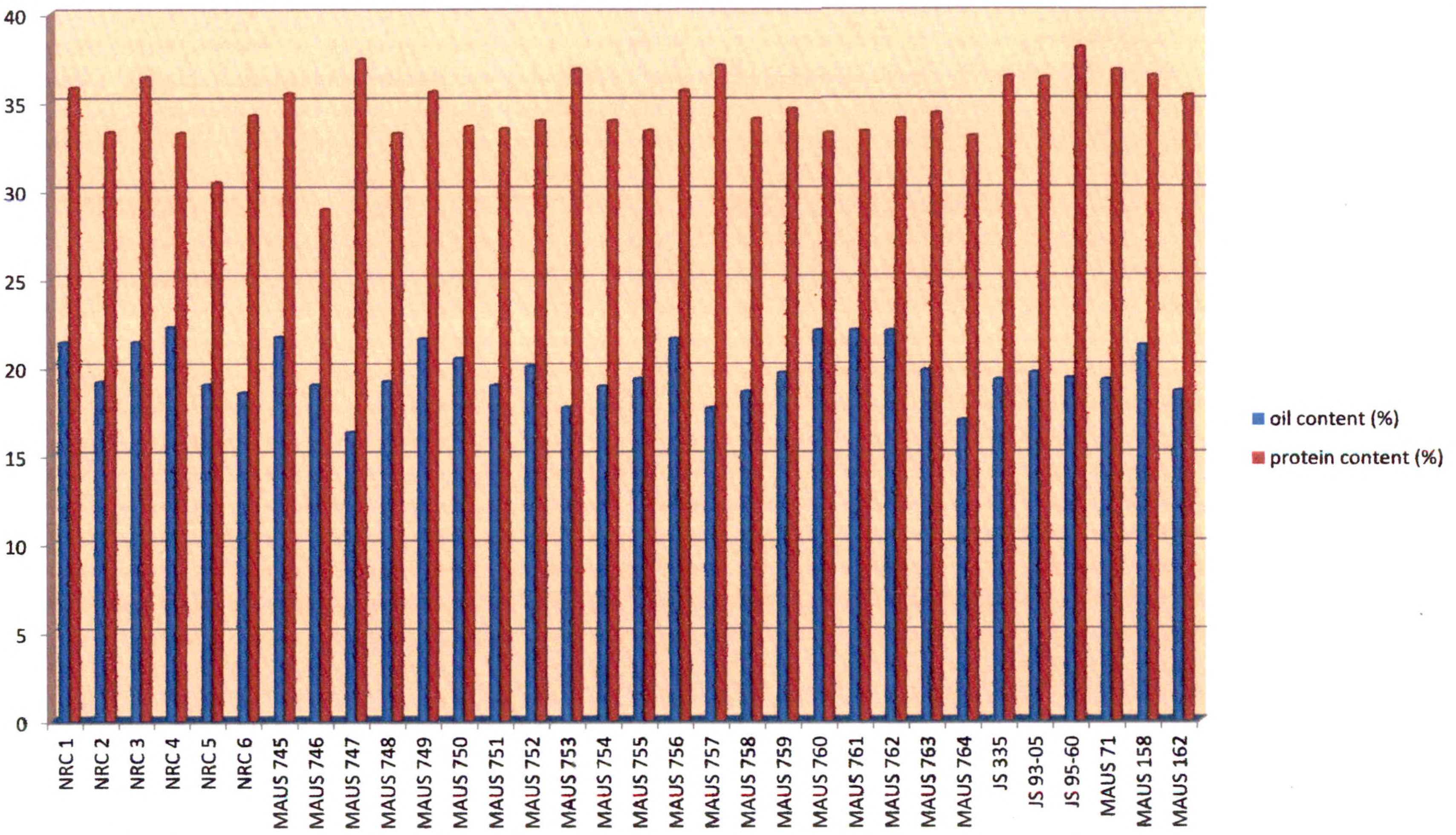
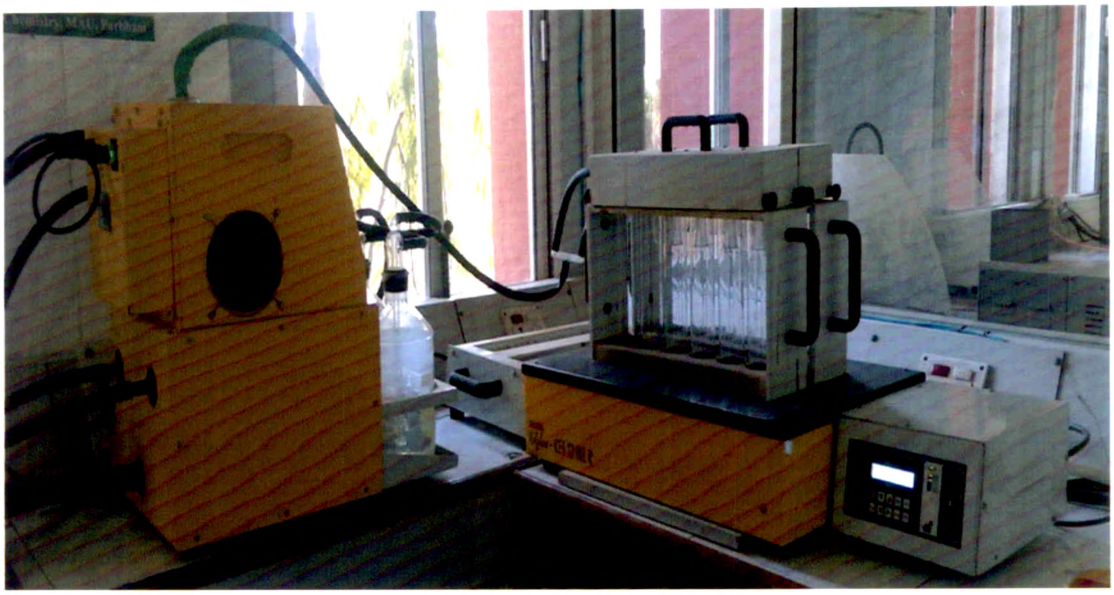


Fig 4. Graphical comparison of oil and protein content of soybean germplasm



A. Digestion unit

B. Distillation unit

C. Titration unit

Plate 9. Micro kjeldahl equipment for protein estimation

Among check, JS 95-60 was highest in protein content (38.02%) and MAUS 162 showed the lowest protein content in soybean genotypes i.e., (35.31%).

Based on the protein content, the genotypes were grouped into three categories as low protein content with ≤ 38.0% protein, medium protein content with protein value 38.1-40.0% and high protein with above 40.0%. All the genotypes along the checks categorized under low protein content.

Low: NRC 1, NRC 2, NRC 3, NRC 4, NRC 5, NRC 6, MAUS 745, MAUS 746, MAUS 747, MAUS 748, MAUS 749, MAUS 750, MAUS 751, MAUS 752, MAUS 753, MAUS 754, MAUS 755, MAUS 756, MAUS 757, MAUS 758, MAUS 759, MAUS 760, MAUS 761, MAUS 762, MAUS 763, MAUS 764, JS 335 (Check), JS 93-05 (Check), MAUS 71 (Check), MAUS 158 (Check) and MAUS 162 (Check).

Medium: JS 95-60(Check).

High: none.

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 of variation (PCV), heritability (broad sense) and expected genetic advance as percent of mean (EGA). The results are present in Table 5.

4.3.1 Days to initial Flowering

The range observed for days to initial flowering from 28.00 days (JS 95-60) to 39.00 days (MAUS 162). The mean value for days to initial flowering was 33.16. Genotypic variance observed was 7.98, which is lower than the phenotypic variance observed as 8.42. The genotypic and phenotypic coefficient of variation was 8.17 percent and 8.40 percent, respectively. High heritability (94.80) with moderate amount of genetic advance (5.66) and moderate genetic advance as percent of mean (16.39) observed for seed yield per plant.

Table 5. Parameters of genetic variability for morphological, physiological and yield contributing traits in soybean

Sr. No.	Character	Range	General mean	Genotypic variance	Phenotypic variance	GCV (%)	PCV (%)	Heritability (h^2)	Genetic advance 5% (GA)	Genetic advance as % of mean (GAM)
1	Days to initial flowering	28-41	34.56	7.98	8.42	8.17	8.40	94.77	5.66	16.39
2	Days to 50% flowering	30-44	37.69	8.90	9.38	7.92	8.12	94.97	5.99	15.89
3	Days to maturity	85-108	93.29	29.56	30.02	5.83	5.87	98.48	11.11	11.91
4	Plant ht. (cm)	23.63-55.33	33.33	36.50	37.28	18.12	18.32	97.89	12.31	36.94
5	Number of branches per plant	0.53-3.53	2.06	0.65	0.72	39.18	41.09	90.95	1.58	76.98
6	Number of nodes per plant	6.27-11.33	7.80	1.66	1.96	16.50	17.97	84.34	2.43	31.22
7	Number of pod clusters per plant	1.33-6.60	4.10	1.91	2.00	33.71	34.50	95.50	2.79	67.86
8	Number of pods per plant	9.67-29.73	19.88	28.89	29.65	27.04	27.40	97.42	10.93	54.98
9	100 seed wt. (g)	6.59-11.86	8.41	1.35	1.62	13.83	15.15	83.38	2.19	26.02
10	Seed yield (g/plant)	1.92-6.68	3.62	1.36	1.44	32.25	33.09	92.71	2.34	64.76
11	Oil content (%)	16.98-22.28	19.79	2.40	2.58	7.82	8.12	94.99	3.07	15.51
12	Protein content (%)	28.93-38.02	34.61	3.66	4.22	5.53	5.94	86.71	3.67	10.60
13	Seed yield (qt/ha)	8.3-20.2	14.03	10.77	13.36	23.38	26.04	80.61	4.89	34.86

GCV = Genotypic coefficient of variability
PCV = Phenotypic coefficient of variability

4.3.2 Days to 50% flowering

The range of days to 50 % flowering was from 30.00 days (JS 95-60) to 42.00 days (MAUS 162). Genotypic variance (8.90) was lower than phenotypic variance (9.38). The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for days to 50 % flowering were 7.92 % and 8.12 %, respectively. High heritability estimates (95.00 percent), moderate genetic advance (5.99) and moderate genetic advance as percent of mean (15.89) observed for the trait days to 5o per cent flowering.

4.3.3 Days to maturity

The character days to maturity was ranged from 85.00 days (JS 95-60) to 102.00 days (MAUS 162) while, the average mean for the character was 91.34 days. Genotypic variance (29.56) was lower than the phenotypic variance (30.02). The genotypic coefficient of variation (GCV) was (5.83) and phenotypic coefficient of variation (PCV) was (5.87) for the trait days to maturity. The high amount of heritability (98.5) coupled with high genetic advance (11.11) and low genetic advance as percent of mean (11.91) observed for days to maturity.

4.3.4 Plant height (cm)

The plant height for all the genotypes ranged from 23.63 cm (NRC 6) to 55.33 cm (MAUS 71) and average plant height observed was 33.33 cm. Genotypic coefficient of variation and phenotypic coefficient of variation was 18.12 and 18.32 percent, respectively while lower amount of genotypic variance (36.50) than phenotypic variance (37.28) observed for plant height. High heritability (97.9) along with high genetic advance (12.31) and high genetic advance as percent of mean (36.94) observed for the trait plant height.

4.3.5 Number of branches per plant

Number of branches per plant ranged from 0.53 (MAUS 761) to 3.47 (NRC 2 and MAUS 764) with the average mean of 2.06 for the respective trait. Genotypic variance (0.65) was lower than phenotypic variance (0.72). GCV and PCV

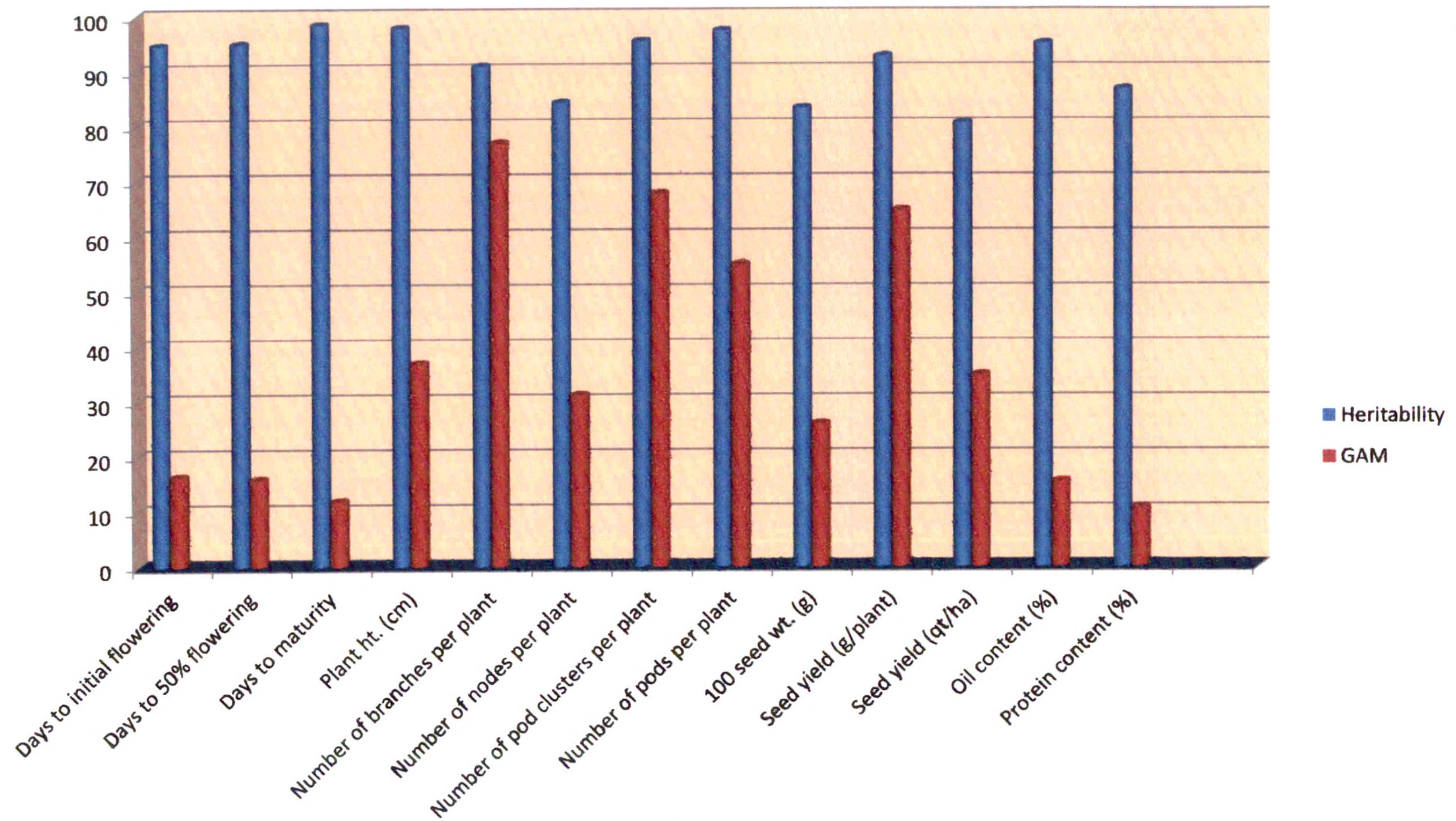


Fig 5. Graphical comparison of heritability and GAM for 13 characters of Soybean

were observed as 39.18 and 41.09 percent, respectively. High heritability estimate (91.00), low genetic advance (1.58) and high genetic advance as percent of mean (76.98) reported for number of branches per plant.

4.3.6 Number of nodes per plant

The range for number of nodes per plant was ranged from 5.33 (MAUS 761) to 11.40 (MAUS 71) with an overall mean of 8.64. The genotypic variance (1.66) observed lower than the phenotypic variance (1.96). The GCV and PCV estimates were 16.50 and 17.97, respectively. High heritability (84.30), low genetic advance (2.43) and moderate genetic advance as percent of mean (31.22) observed for the trait number of nodes per plant.

4.3.7 Number of pod clusters per plant

The number of pod clusters per plant for all the studied genotypes ranged from 1.33 (JS 335) to 6.60 (MAUS 761) and average number of pod clusters per plant observed was 4.10. Genotypic coefficient of variation and phenotypic coefficient of variation was 33.71 and 34.49 percent, respectively while lower amount of genotypic variance (1.91) than phenotypic variance (2.00) observed for number of pod clusters per plant. High heritability (95.50) along with low genetic advance (2.79) and high genetic advance as percent of mean (67.86) observed for the trait number of pod clusters per plant.

4.3.8 Number of pods per plant

The range for number of pods per plant was from 9.67 (JS 335) to 29.73 (MAUS 761), showing the wide range for mean performance of the trait. The average mean value for pods per plant was 19.88. Genotypic variance observed was 28.89 and phenotypic variance was 29.65 for number of pods per plant which showed the (σ^2g) < (σ^2p). The GCV was 27.04 percent and PCV was 27.40 percent with the high amount of heritability (97.40), medium expected genetic advance (10.93) and high genetic advance as percent of mean (54.98).

4.3.9 100 seed weight (g)

100 seed weight were ranged from 6.59 g (MAUS 759) to 11.86 g (NRC 3), with the average mean of 8.41g. Genotypic variance (1.35) was lower than phenotypic variance (1.62). The genotypic coefficient of variation (GCV) observed was 13.83 percent while the phenotypic coefficient of variation was 15.15 percent. The high heritability (83.40) coupled with low genetic advance (2.80) and high genetic advance as percent of mean (26.02) observed for 100 seed weight.

4.3.10 Seed yield (g/ plant)

The range observed for seed yield per plant from 1.92 g (JS 335) to 6.68 g (MAUS 761) per plant. The mean value for grain yield per plant was 3.62 g. Genotypic variance observed was 1.36, which is lower than the phenotypic variance observed as 1.44. The genotypic coefficient of variation and phenotypic coefficient of variation was 32.25 percent and 33.09 percent, respectively. High heritability (95.00) with low amount of genetic advance (2.34) and high genetic advance as percent of mean (64.76) observed for grain yield per plant.

4.3.11 Oil content (%)

The range for oil content was ranged from 16.32% (MAUS 747) to 22.28% (NRC 4) with an overall mean of 19.79%. The genotypic variance (2.34) observed lower than the phenotypic variance (2.58). The GCV and PCV estimates were 7.82 and 8.12, respectively. High heritability (92.70), low genetic advance (3.07) and high genetic advance as percent of mean (15.51) observed for the trait oil content.

4.3.12 Protein content (%)

Protein content showed an overall mean of 34.60% and showed the range of protein content from 28.93% (MAUS 746) to 38.02% (JS 95-60). The genotypic variance (3.66) was lower than the phenotypic variance (4.22). GCV was 5.53 percent and PCV was 5.94 while the heritability estimate was observed as high (86.70) with low genetic advance (3.67) and high genetic advance as percent of mean (10.60).

4.3.13 Seed yield (qt/ha)

Seed yield (qt/ha) ranged from 8.30 (JS 335) to 20.20 (MAUS 761) with the average mean of 14.1 qt/ha for the respective trait. Genotypic variance (10.77) was lower than phenotypic variance (13.36). GCV and PCV were observed as 23.38 and 26.04 percent, respectively. High heritability estimate (80.61), low genetic advance (4.89) and high genetic advance as percent of mean (34.86) reported for seed yield (qt/ha).

4.4 Correlation studies

The correlation study was undertaken to find out the inter relationship of different yield contributing characters with seed yield per plant at both genotypic (G) and phenotypic (P) level which is presented in Table 6 and Fig 6.

4.4.1 Association of seed yield per plant with its attributing traits

The characters initial flowering (G=0.443, P=0.417), days to 50% flowering (G=0.441, P=0.419), days to maturity (G=0.628, P=0.610), number of nodes per plant (G=0.965, P=0.865), number of pod clusters per plant (G=0.967, P=0.924), number of pods per plant (G=0.977, P=0.947), 100 seed weight (G=0.377, P=0.334) and oil content (G=0.529, P=0.493) were significantly and positively correlated with seed yield per plant at genotypic and phenotypic level. A positive and weak correlation was observed with protein content (G=0.005, P=0.013) whereas, plant height and number of branches per plant exhibited negative correlation at both the level.

4.4.2 Association among other attributing traits

4.4.2.1 Days to initial flowering

The character days to initial flowering exhibits positive and significant association with days to 50% flowering (G=0.980, P=0.969), days to maturity (G=0.856, P=0.836), plant height (G=0.324, P=0.308), number of nodes per plant (G=0.496, P=0.447), number of pod clusters per plant (G=0.400, P=0.372) and number of pods per plant (G=0.386, P=0.377) at genotypic and phenotypic level.

Table 6. Estimates of genotypic and phenotypic correlation coefficients for various yield and yield contributing characters in soybean

Sr. No.	Characters		Days to initial flowering	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of nodes per plant	Number of pod clusters per plant	Number of pods per plant	100 seed wt. (g)	Oil content (%)	Protein content (%)	Seed yield per plant (g)
1	Days to initial flowering	G	1.000	0.980**	0.856**	0.324**	-0.108	0.496**	0.400**	0.386**	-0.022	0.129	-0.012	0.443**
		P	1.000	0.969**	0.836**	0.308**	-0.099	0.447**	0.372**	0.377**	-0.034	0.122	-0.011	0.417**
2	Days to 50% flowering	G		1.000	0.823**	0.237*	-0.108	0.507**	0.412**	0.390**	-0.052	0.130	0.014	0.441**
		P		1.000	0.807**	0.228*	-0.097	0.458**	0.387**	0.382**	-0.043	0.116	0.021	0.419**
3	Days to maturity	G			1.000	0.374**	-0.231*	0.699**	0.571**	0.573**	0.195	0.404**	-0.026	0.628**
		P			1.000	0.367**	-0.241*	0.637**	0.551**	0.560**	0.185	0.390**	-0.018	0.610**
4	Plant height (cm)	G				1.000	0.164	-0.054	-0.037	0.004	0.160	-0.123	-0.121	-0.084
		P				1.000	0.152	-0.043	-0.027	0.008	0.137	-0.115	-0.095	-0.080
5	Number of branches per plant	G					1.000	-0.328**	-0.175	-0.152	-0.105	-0.237*	-0.051	-0.234*
		P					1.000	-0.256*	-0.166	-0.148	-0.079	-0.228*	-0.062	-0.202
6	Number of nodes per plant	G						1.000	0.892**	0.909**	0.473**	0.476**	-0.039	0.965**
		P						1.000	0.801**	0.830**	0.389**	0.422**	-0.006	0.865**
7	Number of pod clusters per plant	G							1.000	0.997**	0.379**	0.454**	0.084	0.967**
		P							1.000	0.963**	0.332**	0.440**	0.057	0.924**
8	Number of pods per plant	G								1.000	0.412**	0.466**	0.064	0.977**
		P								1.000	0.371**	0.445**	0.063	0.947**
9	100 seed wt.(g)	G									1.000	0.348**	-0.107	0.377**
		P									1.000	0.287**	-0.097	0.334**
10	Oil content (%)	G										1.000	-0.006	0.529**
		P										1.000	0.012	0.493**
11	Protein content (%)	G											1.000	0.005
		P											1.000	0.013

* Significant at 5% ** Significant at 1%

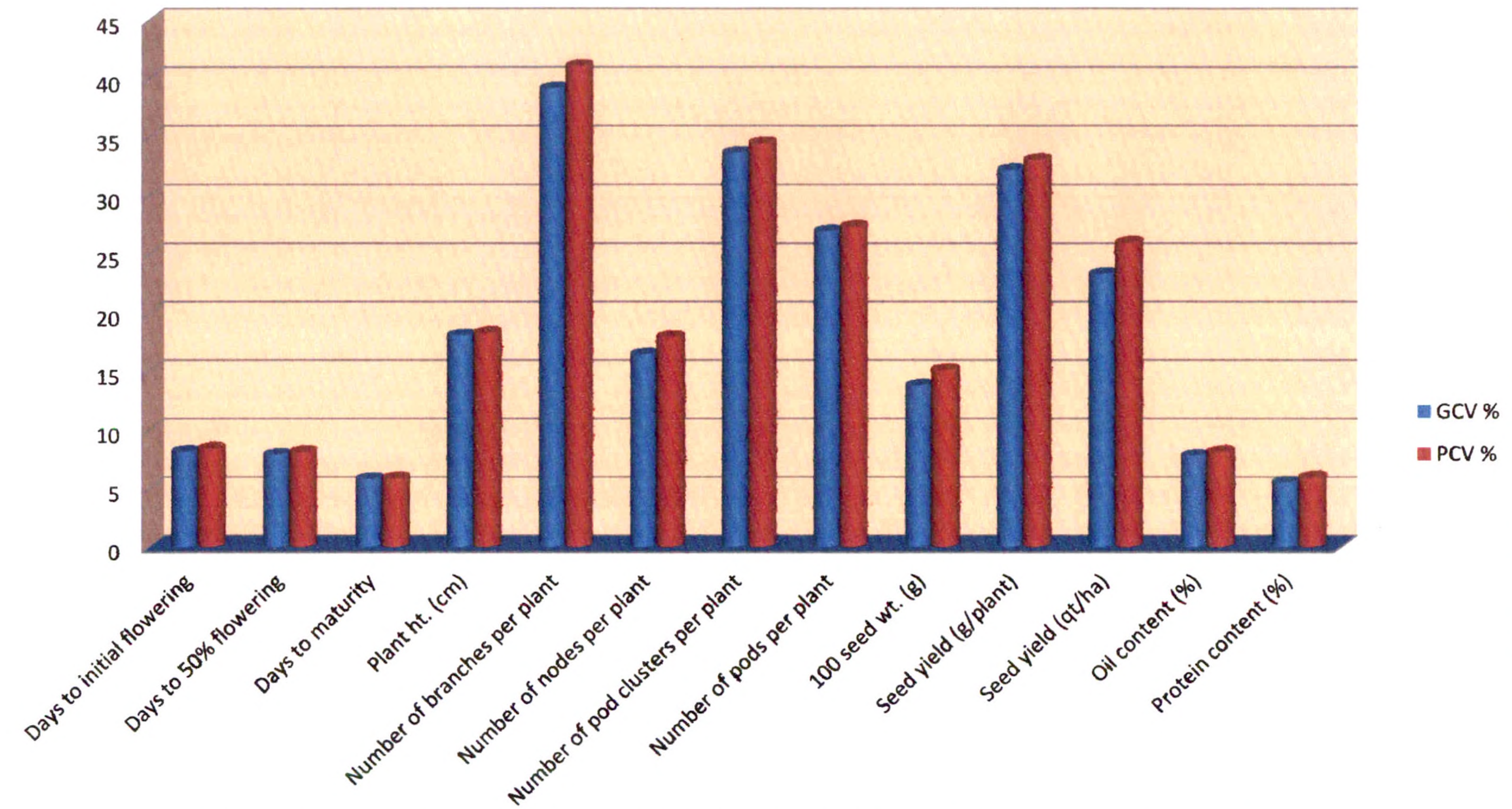


Fig 6. Graphical comparison of GCV and PCV for 13 characters of Soybean

4.4.2.2 Days to 50% flowering

A highly significant and positive association of days to 50% flowering with days to maturity (G=0.823, P=0.807), plant height (G=0.237, P=0.228), number of nodes per plant (G=0.507, P=0.458), number of pod clusters per plant (G=0.412, P=0.387) and number of pods per plant (G=0.390, P=0.382) at genotypic and phenotypic level.

4.4.2.3 Days to maturity

The character days to maturity revealed a significant and positive association with plant height (G=0.374, P=0.367), number of nodes per plant (G=0.699, P=0.637), number of pod clusters per plant (G=0.571, P=0.551), number of pods per plant (G=0.573, P=0.560) and oil content (G=0.404, P=0.390) at genotypic and phenotypic level. This character was negative and significantly associated with number of branches per plant (G= -0.231, P= -0.241) at both the level.

4.4.2.4 Plant height (cm)

The character plant height reported positive association with the characters number of branches (G=0.164, P=0.152), number of pods per plant (G=0.004, P=0.008) and 100 seed weight (G=0.160, P=0.137). Plant height had negative association with number of nodes per plant (G= -0.054, P= -0.043), number of pod clusters per plant (G= -0.037, P= -0.027), oil content (G= -0.123, P= -0.115) and protein content (G= -0.121, P= -0.095) at both the level.

4.4.2.5 Number of branches per plant

The character number of branches per plant had negative association with number of nodes per plant (G= -0.328, P= -0.256) and oil content (G= -0.237, P= -0.228) at both level.

4.4.2.6 Number of nodes per plant

Number of nodes per plant revealed significant and positive correlation with number of pod clusters per plant (G=0.892, P=0.801), number of pods per plant

(G=0.909, P=0.830), 100 seed weight (G=0.473, P=0.389) and oil content (G=0.476, P=0.422) at genotypic and phenotypic level.

4.4.2.7 Number of pod clusters per plant

The character number of pod clusters per plant showed a positive and significant association with number of pods per plant (G=0.997, P=0.963), 100 seed weight (G=0.379, P=0.332) and oil content (G=0.454, P=0.440) at both the level.

4.4.2.8 Number of pods per plant

Number of pods per plant registered positive and significant association with 100 seed weight (G=0.412, P=0.371) and oil content (G=0.466, P=0.445) at genotypic and phenotypic level.

4.4.2.9 100 seed weight (g)

The character 100 seed weight exhibited a positive and significant association with oil content (G=0.348, P=0.287), whereas a negative association is observed for protein content (G= -0.107, P= -0.097) at both the level.

4.4.2.10 Oil content (%)

Oil content was negatively associated with protein content at genotypic level (-0.006), whereas, a positive association was observed at phenotypic level (0.012).

4.5 Path analysis

The genotypic and phenotypic correlation coefficient was further partitioned into direct and indirect path coefficient which is presented in Table 7 and Fig 7 and 8.

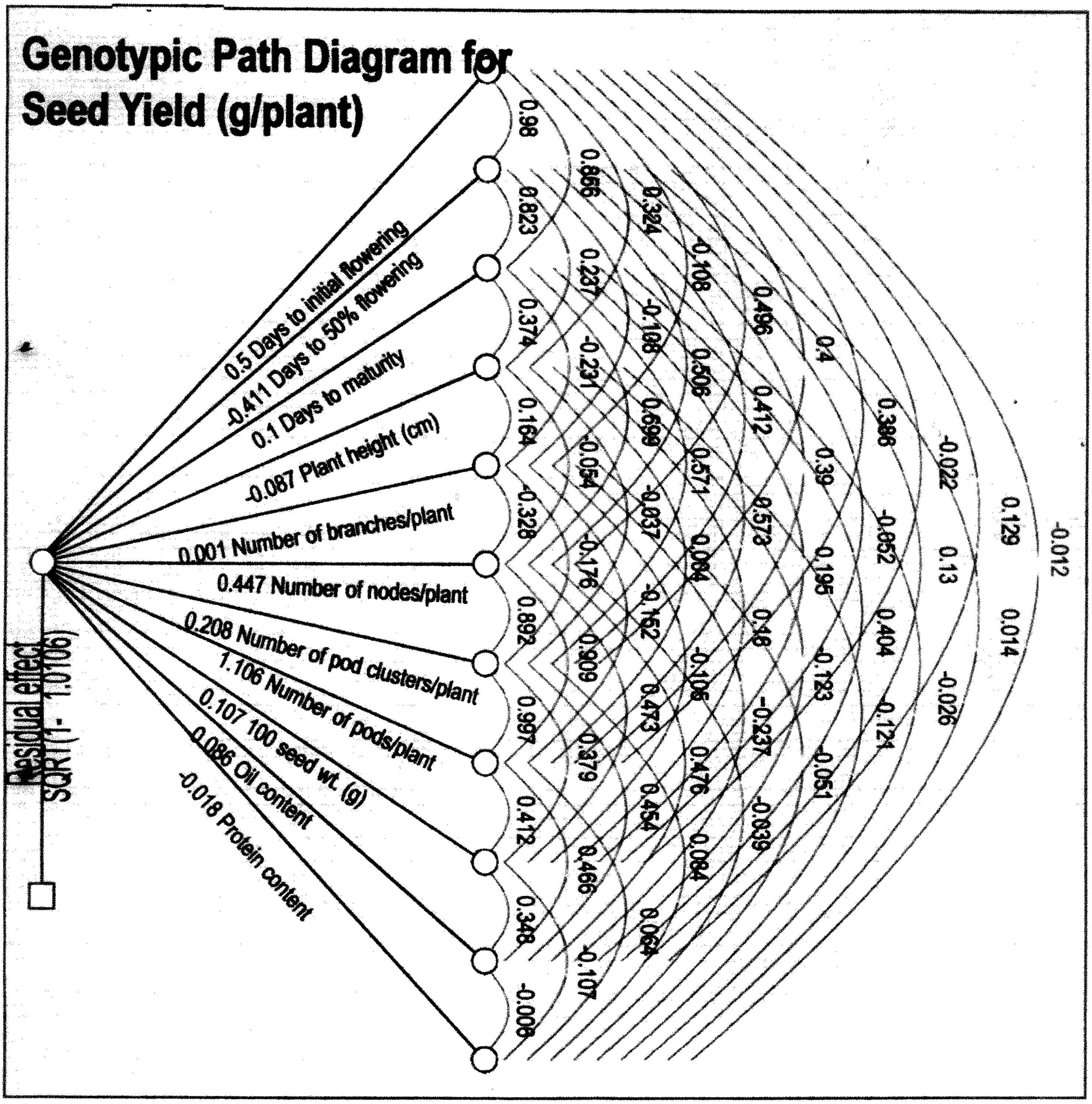
4.5.1 Direct effect

The characters number of pods per plant (G=1.106, P=0.648), days to initial flowering (G=0.499, P=0.122), number of nodes per plant (G=0.447, P=0.159), number of pod clusters per plant (G=0.208, P=0.093) and days to maturity (G=0.099,

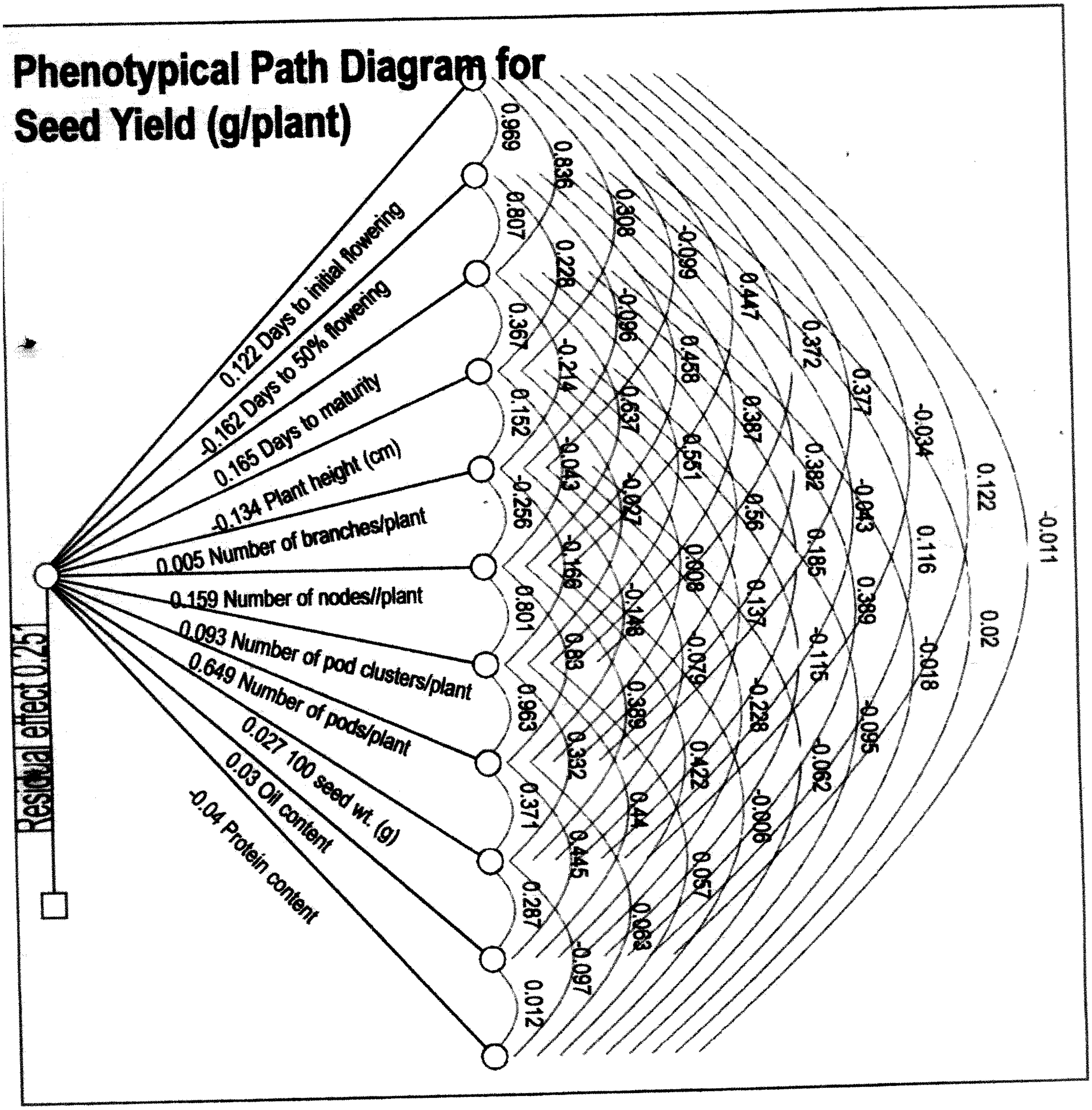
Table 7. Genotypic and phenotypic analysis for direct and indirect effects of yield component on seed yield per plant of soybean

Sr. No.	Characters		Days to initial flowering	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of nodes per plant	Number of pod clusters per plant	Number of pods per plant	100 seed wt. (g)	Oil content (%)	Protein content (%)	Correlation coefficient Seed yield per plant (g)
1	Days to initial flowering	G	**0.499**	-0.403	-0.085	-0.028	-0.0001	0.221	-0.203	0.427	0.002	0.011	0.0002	0.443**
		P	**0.122**	-0.157	0.138	-0.041	-0.0005	0.071	0.035	0.244	0.0009	0.004	0.0005	0.417**
2	Days to 50% flowering	G	0.489	**-0.411**	-0.081	-0.021	-0.0001	0.226	-0.209	0.431	0.005	0.011	-0.0002	0.441**
		P	0.118	**-0.162**	-0.133	-0.031	-0.0005	0.073	0.036	0.248	0.001	0.003	-0.0008	0.419**
3	Days to maturity	G	0.471	-0.338	**0.099**	-0.032	-0.003	0.342	-0.290	0.443	-0.021	-0.044	0.0005	0.628**
		P	0.102	-0.131	**0.165**	-0.049	-0.001	0.102	0.051	0.364	-0.005	0.012	0.0007	0.610**
4	Plant height (cm)	G	0.162	-0.098	-0.037	**-0.087**	0.0002	-0.024	0.019	0.005	-0.017	-0.011	0.002	-0.084
		P	0.037	-0.037	0.061	**-0.134**	0.0007	-0.007	-0.003	0.005	-0.004	-0.003	0.004	-0.080
5	Number of branches per plant	G	-0.054	0.044	0.023	-0.014	**0.001**	-0.146	0.089	-0.168	0.011	-0.021	0.0009	-0.234*
		P	-0.012	0.015	-0.035	-0.020	**0.005**	-0.041	-0.016	-0.096	0.002	-0.007	0.003	-0.202
6	Number of nodes per plant	G	0.248	-0.208	-0.069	0.005	-0.0004	**0.447**	-0.453	1.006	-0.051	0.041	0.0007	0.965**
		P	0.054	-0.074	0.105	0.006	-0.0012	**0.159**	0.075	0.539	-0.010	0.013	0.0002	0.865**
7	Number of pod clusters per plant	G	0.194	-0.264	-0.057	0.003	-0.0002	0.198	**0.208**	0.702	-0.041	0.039	-0.001	0.967**
		P	0.045	-0.063	0.091	0.004	-0.0008	0.128	**0.093**	0.625	-0.008	0.013	-0.002	0.924**
8	Number of pods per plant	G	0.053	-0.260	-0.057	-0.0004	-0.0002	0.146	0.006	**1.106**	-0.044	0.040	-0.001	0.977**
		P	0.045	-0.062	0.093	-0.001	-0.0007	0.132	0.089	**0.648**	-0.009	0.013	-0.003	0.947**
9	100 seed wt.(g)	G	-0.011	0.022	-0.019	-0.014	-0.0001	0.211	-0.193	0.456	**-0.107**	0.03	0.0019	0.377**
		P	-0.004	0.007	0.031	-0.018	-0.0004	0.062	0.031	0.241	**-0.026**	0.009	0.004	0.334**
10	Oil content (%)	G	0.064	-0.053	-0.040	0.011	-0.0003	0.213	-0.231	0.515	-0.037	**0.086**	0.0001	0.529**
		P	0.015	-0.019	0.064	0.015	-0.001	0.067	0.041	0.288	-0.007	**0.029**	-0.0005	0.493**
11	Protein content (%)	G	-0.006	-0.005	0.003	0.011	-0.0001	-0.017	-0.043	0.071	0.012	-0.0005	**-0.018**	0.005
		P	-0.001	-0.003	-0.003	0.013	-0.0003	-0.0009	0.005	0.041	0.003	0.0004	**-0.040**	0.013

* Significant at 5% and ** Significant at 1%. Figures in bold indicates direct effects and normal indicates indirect effects. Residual effect (G) = SQRT(1-1.0106) and Residual effect (P) = 0.2513.



Genotypic Path Diagram for Seed Yield (g/plant)



Phenotypical Path Diagram for Seed Yield (g/plant)

P=0.165) had revealed maximum positive direct effect on seed yield per plant at both the level.

4.5.2 Indirect effect

4.5.2.1 Days to initial flowering

Days to initial flowering had a positive indirect effect on seed yield per plant through characters *viz.*, number of nodes per plant (G=0.221, P=0.071), number of pods per plant (G=0.427, P=0.244), 100 seed weight (G=0.002, P=0.0009), oil content (G=0.011, P=0.004) and protein content (G=0.0002, P=0.0005), whereas, negative indirect effect was recorded via days to flowering (G= -0.403, P= -0.157) and plant height (G= -0.028, P= -0.041) at both the level. It had a positive indirect effect on seed yield per plant through days to maturity (0.138) and number of pod clusters per plant (0.035) at phenotypic level.

4.5.2.2 Days to 50% flowering

The character days to 50% flowering showed a positive indirect effect on seed yield per plant via characters days to initial flowering (G=0.489, P=0.118), number of nodes per plant (G=0.226, P=0.073), number of pods per plant (G=0.431, P=0.248), 100 seed weight (G=0.005, P=0.001) and oil content (G=0.011, P=0.003). However, it reported positive indirect effect on seed yield per plant through number of pod clusters per plant (0.036) at phenotypic level.

4.5.2.3 Days to maturity

The character days to maturity reported a positive indirect effect on seed yield per plant through days to initial flowering (G=0.471, P=0.102), number of nodes per plant (G=0.342, P=0.102), number of pods per plant (G=0.443, P=0.364) and protein content (G=0.0005, P=0.0007) while, other traits showed negative indirect effect at genotypic and phenotypic level. It showed a positive indirect effect on seed yield per plant via number of pod clusters per plant (P=0.051) and oil content (P=0.012) at phenotypic level.

4.5.2.4 Plant height (cm)

The character plant height had registered positive indirect effect on seed yield per plant through days to initial flowering (G=0.162, P=0.037), number of branches per plant (G=0.0002, P=0.0007), number of pods per plant (G=0.005, P=0.005) and protein content (G=0.002, P=0.004) at both the level. Its indirect effect was found to be positive on seed yield per plant through number of pod clusters per plant (G=0.019) at genotypic level and days to maturity (P=0.061) at phenotypic level.

4.5.2.5 Number of branches per plant

The character number of branches per plant was reported positive indirect effect on seed yield per plant via days to 50% flowering (G=0.044, P=0.015), followed by 100 seed weight (G=0.011, P=0.002) and protein content (G=0.0009, P=0.003) at both the level. Its positive indirect effect on seed yield per plant reported via days to maturity (G=0.023) and number of pod clusters per plant (G=0.019) only at genotypic level.

4.5.2.6 Number of nodes per plant

Number of nodes per plant showed positive indirect effect on seed yield per plant through days to initial flowering (G=0.248, P=0.054), plant height (G=0.005, P=0.006), number of pods per plant (G=1.006, P=0.539), oil content (G=0.041, P=0.013) and protein content (G=0.0007, P=0.0002) and the remaining traits showed negative indirect effect at both the level. Its positive indirect effect on seed yield per plant through traits days to maturity (P=0.105) and number of pod clusters per plant (P=0.075) at phenotypic level.

4.5.2.7 Number of pod clusters per plant

Number of pod clusters per plant reported positive indirect effect on seed yield per plant via days to initial flowering (G=0.194, P=0.045), plant height (G=0.003, P=0.004), number of nodes per plant (G=0.198, P=0.128), number of pods per plant (G=0.702, P=0.625) and oil content (G=0.039, P=0.013) at both the level. It exhibit positive indirect effect on days to maturity (P=0.091) only at phenotypic level.

4.5.2.8 Number of pods per plant

Number of pods per plant showed positive indirect effect on seed yield per plant through days to initial flowering (G=0.053, P=0.045), number of nodes per plant (G=0.146, P=0.132), number of pod clusters per plant (G=0.006, P=0.009) and oil content (G=0.040, P=0.013) at both the level. It reported positive indirect effect on seed yield per plant via days to maturity (P=0.093) at phenotypic level.

4.5.9 100 seed weight (g)

The character 100 seed weight expressed positive indirect effect on seed yield per plant via days to 50% flowering (G=0.022, P=0.007), number of nodes per plant (G=0.211, P=0.062), number of pods per plant (G=0.456, P=0.241), oil content (G=0.03, P=0.009) and protein content (G=0.0019, P=0.004) at both the level. It revealed positive indirect effect on days to maturity (0.031) and number of pod clusters per plant (0.031) at phenotypic level.

4.5.10 Oil content (%)

Oil content had positive indirect effect on seed yield per plant via days to initial flowering (G=0.064, P=0.015), plant height (G=0.011, P=0.015), number of nodes per plant (G=0.213, P=0.067) and number of pods per plant (G=0.515, P=0.288) at both the level. It reported positive indirect effect on seed yield per plant through days to maturity (0.064) and number of pod clusters per plant (0.041) were seen at genotypic level.

4.5.11 Protein content (%)

The character protein content reported a positive direct effect on seed yield per plant via plant height (G=0.011, P=0.013), number of pods per plant (G=0.071, P=0.041) and 100 seed weight (G=0.012, P=0.003) at both the level. It exhibit positive indirect effect on seed yield per plant through days to maturity (0.003) at genotypic level whereas, number of pod clusters per plant (0.005) and oil content (0.0004) at phenotypic level.

DISCUSSION

Chapter V

DISCUSSION

Soybean is both a legume as well as oilseed crop. Encouraging soybean as an oilseed crop would be a worthwhile approach in order to supplement the existing vegetable oil crisis in the country as well as in the Maharashtra state. Among the principal oilseed crops, groundnut plays a vital and prime role in the edible oil production, but it is an erratic and unpredictable crop causing instability to the national and state oilseed economy. So, need arises to have a crop that would be supplementary to major oilseed crops and in this context soybean may find a place as a sole and an intercrop in Maharashtra.

The knowledge of genetic variability and relationship among various quantitative characters is helpful in deciding the selection criteria to bringing out the possible improvement. Genetic variation though important can be used for crop improvement only when it is considered in relation to non genetic variation. Number of studies in soybean by several workers revealed wide variation for various traits. Yield is a polygenically controlled complex character and is determined by a number of component characters which are also quantitatively inherited. Knowledge of heritability and genetic advance of the characters indicates the scope of improvement through selection.

Though association analysis is helpful in determining the components of yield, it does not provide an exact picture of relative importance of indirect and direct influence of each of the components towards grain yield. The inclusion of large number of variables in the correlation analysis shows more complex indirect associations. In such a situation, knowledge of major yield components is of paramount significance in formulating an effective selection programme. Information is merging exclusively on genetic variation heritability, correlation and path analysis in soybean .Hence, this investigation was undertaken to find out the genetic variation and major yield components in soybean through correlation and path analysis.

5.1 Genetic variability, heritability and genetic advance

5.1.1 Variability

In the present investigation, 26 genotypes of soybean and 6 checks were evaluated for fourteen different quantitative characters. The existence of significant variation in plant characters under the study implied of that the data could be appropriately subjected to further estimation genetic parameters. Characters of economic importance had exhibited scope for selection. The analysis of variance for 13 traits in the present study revealed presence of highly significant variation among the genotypes. The high variability observed might be attributed to their genetic make up and the different geographical regions from which they have originated.

A moderate range of phenotypic variability was recorded in days to initial flowering, days to 50% flowering, days to maturity, plant height and number of pods per plant while it was low for number of branches per plant, number of nodes per plant, number of pod clusters per plant, 100 seed weight, seed yield per plant, oil content and protein content. This variation indicated the scope for selection of these traits for further breeding work. The phenotypic range of variation is not the sole criteria for judging the amount of genetic variation present in a population, but the genetic parameters such as genotypic coefficient of variation (GCV), heritability and genetic advance (GA) are important in studying the amount of genetic variability.

The phenotypic variance was, therefore, partitioned into genotypic and error variances (environmental influence), for different characters. It was observed that, for all the characters the genotypic component of variation was higher than the environmental component, indicating the phenotypic variability as a reliable measure of genotypic variability.

In the present investigation, high amount of GCV was observed for number of branches per plant, number of pod clusters per plant, number of pods per plant and seed yield (gm/plant). Gohil *et al.,* (2006), Aditya *et al.,* (2011), Pushpa and Rao (2013) and Pagde *et al.,* (2015) obtained the similar results for number of pods per plant.

For seed yield per plant Aditya *et al.,* (2011), Osekita *et al.,* (2013), Pushpa and Rao (2013) and Mahbub *et al.* (2015) observed the GCV and PCV as high and for number of branches per plant Bangar *et al.,* (2003) and Malek *et al.* (2015). Similar results were observed in case of number of pod clusters per plant Baraskar *et al.* (2014), indicating the wider adapability of these traits in the genotypes studied.

The character plant height (cm), number of nodes per plant and 100 seed weight showed moderate GCV and PCV values in the present investigation. Similar results reported by Jain and Ramgiry (2000), Bangar *et al.,* (2003) and Badkul *et al.,* (2014) observed GCV and PCV as moderate while observed as low by Basavraja (2002) and Ghodreti *et al.,* (2013) for 100 seed weight. Similar results were observed by Athoni *et al.,* (2012) and Bekele *et al.,* (2012) for number of nodes per plant, Bekele *et al.,* (2012) and Badkul *et al.,* (2014) for plant height. This suggests that there is scope to enrich the variation for these characters.

Days to initial flowering, days to 50% flowering, days to maturity, oil content and protein content showed the lowest GCV in the present investigation. Similar kinds of results were obtained by Bekele *et al.,* (2012) for days to initial flowering, Bangar *et al.* (2003), Chettri *et al.,* (2005) and Patil *et al.,* (2011) for days to 50 per cent flowering, Patil *et al.,* (2011), Athoni *et al.,* (2012), Bekele *et al.,* (2012) and Ghodreti *et al.,* (2013) for days to maturity, Athoni *et al.,* (2012), Bekele *et al.,* (2012) and Ghodreti *et al.,* (2013) for oil content, Bekele *et al.,* (2012) and Ghodreti *et al.,* (2013) for protein content. These all the studied traits also exhibited high phenotypic coefficient of variation than genotypic coefficient of variation, indicating their phenotypic expression in the environment. On the basis of their genetic capacity and ability to express in the given environment, these components may form a basis for selection.

5.1.2 Heritability (%)

The coefficient of variation indicates only the extent of variability existing for various characters, but does not give any information regarding heritable proportion of it. Hence, amount of heritability permits greater effectiveness of selection by separating out the environmental influence from the total variability and to indicate accuracy with which a genotype can be identified phenotypically. If heritability is 100 per cent, the phenotypic performance will be perfect indication of genotypic performance (σ^2ph = σ^2g). In such a hypothetical situation, heritability value itself provides known indication of the amount of genetic progress that may result by selecting superior individuals. The genetic progress will increase with the availability of wide genetic variation. The GCV along with heritability estimates would provide a better picture of the amount of genetic advance expected by phenotypic selection (Burton, 1952). In present study, broad sense heritability, which includes both additive and non-additive gene effects Hanson *et al.*, (1956), was estimated. Heritability is categorized into three groups i.e., low (< 30%), moderate (30-60%) and high (> 60%) by Johnson *et al.*, (1955).

In the present study results indicated that heritability estimates were high for the traits *viz.*, days to initial flowering, days to 50% flowering, days to maturity, plant height, number of branches per plant, number of pod clusters per plant, number of pods per plant, 100 seed weight, seed yield per plant, number of nodes per plant, oil content and protein content. Pushpa and Rao (2013) observed the similar findings for the above traits.

Similar findings were observed for days to 50% flowering by Osekita *et al.*, (2013) and Jain *et al.* (2015), days to maturity by Osekita *et al.*, (2013) and Baraskar *et al.* (2014), plant height by Bekele *et al* (2012), Dilnesaw *et al.*, (2013) and Malek *et al.* (2015), number of branches per plant by Badkul *et al.* (2014) and Malek *et al.* (2015), number of pod clusters per plant by Badkul *et al.* (2014) and Baraskar *et al.* (2014), number of pods per plant by Barh *et al.*, (2014), Malek *et al.* (2015) and Padge *et al.*, (2015), 100 seed weight by Osekita *et al.*, (2013), Jain *et al.* (2015) and Malek *et al.* (2015), seed yield per plant by Patil *et al.*, (2011), Abady *et al.*, (2013) and Osekita *et al.*, (2013) and Jain *et al.* (2015), number of nodes per plant Ghodrati (2013) and protein yield by Pushpa and Rao (2013) and Singh (2014).

5.1.3 Genetic Advance (%)

The genetic advance expressed as percentage of mean is the product of genotypic coefficient of variation, the square root of heritability ratio and selection intensity. The high heritability estimates enable plant breeder to base the selection programme on phenotypic performance. Johnson *et al.*, (1955) suggested that heritability estimates in conjunction with genetic advance were reliable in predicting the resultant effect from selecting the best individuals and categorized in three groups i.e., low (< 10%), moderate (10-20%) and high (> 20%).

Yield being a complex character is influenced by many factors. In the present study, high heritability coupled with high genetic advance as per cent mean was observed for plant height, number of branches per plant, number of nodes per plant, number of pod clusters per plant, number of pods per plant, 100 seed weight and seed yield per plant suggesting that these traits are under the control of additive gene action and can be improved through simple selection procedure, Similar results were reported by Yadav (2007), Baraskar *et al.* (2014) and Malek *et al.* (2015) for plant height, Basavaraja (2002), Bangar *et al.* (2003) and Malek *et al.* (2015) for number of branches per plant, Abady *et al.* (2013) and Baraskar *et al.* (2014) for number of pod clusters per plant , Baraskar *et al.* (2014) Barh *et al.*, (2014) and Malek *et al.* (2015) for number of pods per plant, Hina Kausar (2005), Sahay *et al.*, (2005) and Baraskar *et al.* (2014) for seed yield per plant, Abady *et.al.*,(2013) and Badkul *et.al.*, (2014) for 100 seed weight and Okonwkwo and Idahosa (2013) for number of nodes per plant. This indicates the lesser influence of environments in expression of characters and prevalence of additive gene action in their inheritance, since are amenable for simple selection.

High heritability with moderate genetic advance as per cent of mean was recorded for days to initial flowering, days to 50% flowering, days to maturity, oil content and protein content. Similar results were obtained by Ghodrati (2013), Baraskar *et al.* (2014), Badkul *et al.* (2014) and Mahbub *et al.* (2015) for days to initial flowering, Bekele *et al.*, (2012) Dilnesaw *et al.*, (2013), Badkul *et al.* (2014), Baraskar *et al.* (2014) and Mahbub *et al.* (2015) for days to 50 per cent flowering and days to maturity, for oil content Pushpa and Rao (2013) and for protein content Singh (2014). The results indicate that these characters were less influenced by environment but governed by additive and non-additive gene action.

From the above discussions, it can be concluded that high genotypic coefficient of variability and phenotypic coefficient of variability coupled with high heritability were observed for the characters number of branches per plant, number of nodes per plant, number of pod clusters per plant, number of pods per plant and seed yield per plant. This indicates that there is a lesser influence of environment in the expression of character which is amenable for selection. The character *viz.*, days to initial flowering, days to 50 per cent flowering, days to maturity, plant height, 100 seed weight, oil content and protein content showed high heritability but low level of variability. Hence, these characters are not amenable for selection in the present study.

5.2 Correlation coefficient

Correlation coefficient is an important statistical constant, which indicates the degree of association among the various characters.

The genotypic correlations were generally higher than the phenotypic correlations indicating the inherent association between various traits. Seed yield is a complex character and is dependent on number of component characters. Therefore, study of relationship of characters with each other and with seed yield become more important in crop improvement programmer. Therefore, it is essential to find out relative contribution of each of the component character in yield for giving due weightage during selection.

In present study, phenotypic and genotypic correlation of seed yield per plant was positive and significant with days to initial flowering, days to 50% flowering, days to maturity, number of nodes per plant, number of pod clusters per plant, number of pods per plant, 100 seed weight and oil content. The results obtained from this study are in confirmation with the results of Machikowa *et.al.*, (2011) and Salimi and Abola (2013) for days of initial flowering, Patil (2011) and Salimi and Abola (2013) for days of 50% flowering, Salimi and Abola (2013), Okonkwo and Idahosa (2013) and Ghodrati *et.al.*,(2013) for days to maturity, Showkat *et.al.*,(2010) for number of pod clusters per plant, Okonkwo and Idahosa (2013), Barh *et.al.*, (2014) and Mahbub *et.al.*, (2015) for number of pods per plant, Okonkwo and Idahosa (2013), Barh *et.al.*, (2014) and Mahbub *et.al.,* (2015) for 100 seed weight, Athoni *et.al.,* (2012), Bueno *et.al.,* (2013) and Ghodrati *et.al.,*(2013) for oil content and for number of nodes per plant by Ruben and Gustavo (2012), Ghodrati *et.al.,*(2013) and Okonkwo and Idahosa (2013).

However, seed yield per plant showed non-significant and negative association with protein content in both genotypic and phenotypic correlation studies. These results are in confirmation with the results of Ghodrati *et.al.,* (2013). The negatively significant association of seed yield per plant was seen in plant height and number of branches per plant. The results obtained from this study are in confirmation with the results of Iqbal *et.al.,* (2010), Udensi (2012) and Li *et.al.,* (2013) for plant height and for number of branches per plant by Ariyo (1995) and Badawy and Mehasen (2012). This showed the selection of such character will not be effective for further crop improvement.

5.3 Path coefficient analysis

The correlation coefficient measures the relationship existing between pairs of character. But, a dependent character is an interaction production of many mutually, associated component characters and change in any one component will disturb whole network of cause and effect system. The path coefficient analysis, a statistical device developed by Wright (1921b), which takes into account the cause and effect relation between the variables is unique in partitioning the association into direct and indirect effect through other independent variables. The path coefficient analysis also measures the relative importance of causal factors involved.

This is simply a standard partial regression analysis, wherein total correlation value is sub-divided into causal scheme. The importance of path diagram facilitates the understanding of the nature of cause and effect system. Path coefficient analysis helps in giving the weightage to particular character during the selection. The technique of path coefficient analysis originally developed by Wright (1921a) and first times used by Dewey and Lu (1959) in selection programme of crested wheat grass.

The genotypic and phenotypic correlation of these characters with grain yield per plant was partitioned into their direct and indirect effects through path coefficient analysis.

In the present investigation, days to 50% flowering, plant height, plant height, 100 seed weight and protein content had direct negative effect on seed yield per plant. Similar observations were found by Abady *et.al.,* (2013), Faisal *et.al.,* (2014) Mahbub *et.al.,* (2015) for days to 50% flowering, Li *et.al.,* (2013) and Jain *et.al.,* (2014) for plant height, Abady *et.al.,* (2013) and Mahbub *et.al.,* (2015) for 100 seed weight and Faisal *et.al.,* (2014) for protein content. This indicated that direct selection for these characters will reduce the breeding efficiency for grain yield in soybean.

The path analysis indicated that number of pods per plant has highest positive direct effect on seed yield per plant at genotypic and phenotypic level. Abady *et.al,* (2013) and Jain *et.al,* (2015), found the highest positive direct effect of the number of pods per plant on seed yield per plant.

Through the study of path analysis it was appearent that maximum direct effects were exerted by number of pods per plant, number of pod clusters per plant, number of nodes per plant and days to initial flowering. Similar observations were found by Badaway and Mehasen (2012), Abady *et.al.,* (2013), Jain *et.al.,* (2015) for number of pods per plant, Gohil *et.al.,* (2006) and Abady *et.al.,* (2013) for number of pod clusters per plant, Ruben and Gustavo (2012) for number of nodes per plant and Malik *et.al.,* (2007) and Abady *et.al.,* (2013) for days to initial flowering. All of these four traits exhibited positive correlation with seed yield per plant, therefore these characters may be considered as the most important yield contributing characters and due emphasis should be placed on these characters while breeding for high seed yield in soybean.

SUMMARY AND CONCLUSION

Chapter VI

SUMMARY AND CONCLUSION

The present investigation entitled "Evaluation of advanced progenies for seed yield and quality traits in soybean (*Glycine max* (L). Merill.)" was undertaken during *kharif*-2015 at experimental farm of All India Coordinated Research Project on Soybean, Soybean Research Station, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani with following objectives.

01. To evaluate advanced progenies for seed yield and quality traits.

02. To estimate genetic variability parameters in advanced progenies.

03. To study the correlation for phenotypic characters with seed yield and quality traits.

The experimental material consisted of twenty six genotypes and six checks of soybean selected from Germplasm collection maintained at Soybean Research Station, VNMKV, Parbhani, which were utilized to elucidate information on the nature and magnitude of genetic variability for qualitative and quantitative characters, heritability, genetic advance, correlation and path analysis for quantitative characters including seed yield.

The germplasm lines were planted in randomized block design with three replications. Three local checks (MAUS-71, MAUS-158 and MAUS 162) and three national checks (JS 335, JS 93-05 and JS 95-60) included in the study. The observations were recorded on five randomly selected plants for qualitative and quantitative characters from each replication. The salient features of findings are as under.

01. The analysis of variance revealed that, prevalence of significant differences among the genotypes for all the thirteen characters studied.

02. The present investigation revealed that the genotypes NRC 1, NRC 3, NRC 4, MAUS 745, MAUS 756, MAUS 760, MAUS 761 and MAUS 762 showed grain yield and quality characters especially oil content superior than the checks.

03. Phenotypic coefficient of variation was higher in magnitude than the genotypic coefficient of variation in respect of all the characters. Number of branches per plant, number of nodes per plant, number of pod clusters per plant, number of pods per plant and seed yield per plant are the characters which showed high genotypic coefficient of variation along with high heritability and high genetic advance.

04. Days to initial flowering, days to 50% flowering, days to maturity, number of nodes per plant, number of pod clusters per plant, number of pods per plant, 100 seed weight and oil content showed positive and significant correlation with seed yield per plant at both phenotypic and genotypic level.

05. Path analysis revealed that number of pods per plant had highest positive direct effect on seed yield per plant at both genotypic and phenotypic level. Other traits days to initial flowering, days to maturity, number of branches per plant, number of nodes per plant, number of pod clusters per plant and oil content directly contribute to seed yield per plant at both the levels.

06. The number of pods per plant had highest indirect effect via number of nodes per plant, days to maturity had highest indirect effect via number of pods per plant, number of nodes per plant had highest indirect effect through number of pods per plant, number of pod clusters per plant had highest indirect effect via number of pods per plant, 100 seed weight had highest indirect effect via oil content, oil content had highest indirect effect via number of pods per plant and protein content had highest effect via number of pods per plant on grain yield per plant both at genotypic and phenotypic level.

CONCLUSION

The present investigation revealed that the genotypes NRC 1, NRC 3, NRC 4, MAUS 756, MAUS 760, MAUS 761 and MAUS 762 showed significantly higher seed yield and quality characters over checks.

Based on these findings, it can be concluded that in breeding programme for improving grain yield in soybean, more emphasis should be given on the traits *viz.*, number of pods per plant, days to initial flowering, number of nodes per plant and number of pod clusters per plant as these characters are positively correlated with seed yield per plant. Being an oil rich crop some genotypes like NRC 1, NRC 3, NRC 4, MAUS 745, MAUS 749, MAUS 750, MAUS 752, MAUS 756, MAUS 760, MAUS 761, MAUS 762 and MAUS 158 (Check) can be used directly in breeding programme for improvement of oil content.

Since, most of the traits *viz.*, number of branches per plant, number of pod clusters per plant, seed yield per plant and number of pods per plant exhibited high heritability and high expected genetic advance under such situation selection can plant be effective following intermitting among promising genotypes.

A correlation study of the characters days to initial flowering, days to maturity, number of nodes per plant, number of pod clusters per plant, number of pods per plant, 100 seed weight and oil content were significantly and positively correlated with seed yield per plant were reported at both genotypic and phenotypic levels. These traits showed effective selection for future crop improvement programme.

Study of path analysis at genotypic and phenotypic level showed by characters number of pods per plant, days to initial flowering, number of nodes per plant, number of pod clusters per plant and days to maturity had received maximum direct effect on seed yield suggested effective selection for crop improvement.

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ABSTRACT

THESIS ABSTRACT

a) Title of the thesis : **EVALUATION OF ADVANCED PROGENIES FOR SEED YIELD AND QUALITY TRAITS IN SOYBEAN (*Glycine max.* (L.) Merrill.)**

b) Name of the student : **ANSHU ISHARA TIRKEY**

c) Degree to be awarded : M.Sc. (Agriculture)

d) Year of award of degree : 2016

e) Major subject : Genetics and Plant Breeding

f) Total number of pages in the thesis : 90

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h) Signature of the student :

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ABSTRACT

A soybean with both high yielding and high concentrations of desired seed quality components is an ideal cultivar. The importance of genetic variation assists the breeder to decide the proper strategy and selection criteria to be followed for improvement of the target traits. The present day study was carried out during *kharif*, 2015, at AICRP on Soybean of V.N.M.K.V., Parbhani(M.S.). Twenty six soybean germplasm lines along with six checks were evaluated for genotypic and phenotypic variation, broad sense heritability and GA for seed yield and some quality properties.

The analysis of variance revealed significant variations for all characters. The present investigation revealed that the characters *viz.*, number of pods per plant, plant height and days to maturity showed sufficient variability. The estimates of phenotypic (PCV) and genotypic (GCV) coefficients of variation indicated that the values of PCV were higher than that of GCV, but the differences were closer between these two estimates for all the traits. This indicated that expression of characters under study was less influenced due to environmental factors.

For grain yield the genotypes *viz.*, MAUS 761, MAUS 762, NRC 3, MAUS 745 and MAUS 750 were high yielding can be utilized in breeding programme for improvement of yield. Being a protein rich crop with many nutraceutical chemicals providing health benefits, the food uses of soybean in the country are showing increasing trends since last few yew years, the genotypes identified in the present investigation having high protein content *viz.*, MAUS 747, NRC 3 and MAUS 757 and high oil content genotype NRC 4, MAUS 760 and MAUS 764 may be used in breeding programme for development of high protein and oil content lines.

High heritability accompanied by high genetic advance for plant height, number of branches per plant, number of nodes per plant, number of pod clusters per plant, number of pods per plant, 100 seed weight and seed yield per plant (g) suggested selection could be effective for these traits.

A correlation study of the characters days to initial flowering, days to maturity, number of nodes per plant, number of pod clusters per plant, number of

pods per plant, 100 seed weight and oil content were significantly and positively correlated with seed yield per plant were reported at both genotypic and phenotypic levels. These traits showed effective selection for future crop improvement programme.

Study of path analysis at genotypic and phenotypic level showed by characters number of pods per plant, days to initial flowering, number of nodes per plant, number of pod clusters per plant and days to maturity had received maximum direct effect on seed yield suggested effective selection for crop improvement.

APPENDIX

WEEKLY WEATHER DATA RECORDED AT CENTRAL METEROLOGY OBSERVATRY VNMKV, PARBHANI 2015-16

WK	Period	Rainfall (mm)	R.D.	Temperature °C		Humidity (%)		EVP	BSS (Hr.)	W. V. (Kmph)
				Max.	Min.	AM	PM			
1	01-07 Jan.	9.2	1.0	27.0	15.1	89	52	3.1	5.3	3.7
2	08-14 Jan.	0.0	0.0	28.3	5.8	76	20	4.7	9.9	3.1
3	15-21 Jan	0.0	0.0	28.9	10.2	72	29	5.2	8.3	4.4
4	22-28 Jan	0.0	0.0	31.1	14.1	76	26	5.1	7.9	4.4
5	29-04 Feb.	0.0	0.0	30.8	13.0	71	27	5.9	9.1	4.3
6	05-11 Feb	0.0	0.0	32.2	14.1	65	27	6.5	8.4	5.7
7	12-18 Feb.	0.0	0.0	33.1	12.3	73	18	6.6	9.7	3.8
8	19-25 Feb.	0.0	0.0	35.0	14.6	66	18	7.7	9.7	3.9
9	26-04 Mar.	24.3	2.0	30.9	15.0	79	38	6.3	7.3	4.4
10	05-11 Mar.	16.6	1.0	33.4	16.0	77	29	6.5	9.7	5.4
11	12-18 Mar.	0.0	0.0	34.3	18.7	69	30	7.4	9.3	5.7
12	19-25 Mar.	0.0	0.0	37.6	19.6	67	20	9.5	9.4	4.9
13	26-01 Apr.	0.0	0.0	37.6	20.3	67	22	9.3	7.2	4.5
14	02-08 Apr.	0.0	0.0	39.5	19.0	72	16	10.5	10.0	4.9
15	09-15 Apr.	24.6	5.0	34.2	18.9	87	38	6.9	8.0	5.7
16	16-22 Apr.	67.2	2.0	36.8	20.6	82	29	6.4	9.2	3.5
17	23-29 Apr.	0.0	0.0	40.2	22.2	68	19	10.5	9.2	4.3
18	30-06 May	22.8	1.0	42.2	22.4	67	17	13.7	10.0	5.6
19	07-13 May	2.0	0.0	39.5	23.4	61	21	9.2	8.3	4.6
20	14-20 May	0.0	0.0	40.0	25.6	58	24	9.6	7.6	5.5
21	21-27 May	0.0	0.0	44.2	27.0	52	16	16.7	10.7	9.4
22	28-03 June	0.0	0.0	42.8	26.9	50	17	14.3	8.6	7.9
23	04-10 June	27.0	2.0	39.0	25.5	69	33	9.5	7.1	6.3
24	11-17 June	61.1	3.0	34.2	23.1	88	54	5.3	6.5	6.6
25	18-24 June	37.5	2.0	31.6	23.5	86	64	4.5	2.5	5.8
26	25-01 July	0.0	0.0	35.1	24.3	75	43	7.3	7.5	6.6
27	02-08 July	5.0	1.0	35.8	23.8	76	38	8.1	9.4	9.4
28	09-15 July	0.0	0.0	36.2	25.8	69	37	6.0	9.4	9.4
29	16-22 July	0.6	0.0	35.8	24.8	76	45	5.5	8.9	8.9
30	23-29 July	8.0	1.0	34.0	24.0	75	47	4.9	8.5	8.5
31	30-05 Aug	19.8	1.0	33.0	23.1	80	59	6.0	8.4	8.4
32	06-12 Aug	28.8	4.0	29.9	23.0	87	68	2.4	5.5	5.5
33	13-19 Aug	23.4	2.0	31.3	23.0	85	57	4.1	5.7	5.7
34	20-26 Aug	11.2	1.0	32.9	23.0	81	49	9.5	6.0	6.0
35	27-02 Sept	0.0	0.0	32.2	23.3	79	50	7.0	6.3	6.3
36	03-09 Sep	88.1	4.0	32.9	22.2	87	60	7.0	4.8	4.8
37	10-16 Sep	38.4	4.0	31.8	22.7	90	63	6.2	3.6	3.9

38	17-23 Sep	57.4	1.0	31.4	22.0	81	59	4.1	5.9	4.7
39	24-30 Sep	0.0	0.0	33.5	20.9	74	44	6.7	7.5	3.6
40	01-07 Oct.	1.8	0.0	34.3	20.9	75	44	7.1	7.3	3.6
41	08-14 Oct.	0.0	0.0	35.1	19.4	73	32	7.8	9.0	2.2
42	15-21 Oct.	0.0	0.0	35.7	18.3	70	29	7.8	9.1	3.6
43	22-28 Oct.	0.0	0.0	35.1	19.5	70	31	5.9	8.2	3.0
44	29-04 Nov.	0.0	0.0	33.0	18.9	75	36	5.6	8.1	4.4
45	05-11 Nov.	0.0	0.0	34.0	16.9	68	25	6.1	7.5	4.6
46	12-18 Nov.	0.0	0.0	33.6	14.3	75	23	6.1	8.9	5.3
47	19-25 Nov.	0.0	0.0	32.1	18.4	78	36	6.6	6.4	6.2
48	26-02 Dec.	0.0	0.0	32.9	17.0	79	33	5.6	7.6	3.0
49	03-09 Dec.	0.0	0.0	32.6	13.8	71	26	5.3	9.3	3.1
50	10-16 Dec.	0.0	0.0	33.8	17.7	72	31	5.6	8.9	3.4
51	17-23 Dec.	0.0	0.0	32.9	16.1	71	31	5.8	8.5	4.7
52	24-31 Dec.	0.0	0.0	30.3	8.5	74	24	5.2	7.7	4.8
	Total	574.8	38							