“GENETIC EVALUATION OF ELITE LINES OF SOYBEAN [*Glycine max* (L.) Merrill]”

by

Miss. Tanya Barpanda
(Reg. No. 019/050)

A Thesis submitted to the
MAHATMA PHULE KRISHI VIDYAPEETH,
RAHURI-413 722, DIST- AHMEDNAGAR,
MAHARASHTRA, INDIA

In partial fulfillment of the requirements for the degree

of

MASTER OF SCIENCE (AGRICULTURE)

in

AGRICULTURAL BOTANY (GENETICS AND PLANT BREEDING)

DIVISION OF AGRICULTURAL BOTANY
COLLEGE OF AGRICULTURE, PUNE-411 005

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2021

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APPROVED BY

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2021

CANDIDATE'S DECLARATION

I hereby declare that this thesis or part there of has not been submitted by me or other person to any other University or Institute for a Degree or Diploma

Place: Pune – 411 005

(Tanya Barpanda)

Date: / / 2021

Prof. B. H. Chavan
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Maharashtra State, India.

CERTIFICATE

This is to certify that the thesis entitled, **"GENETIC EVALUATION OF ELITE LINES OF SOYBEAN [*Glycine max* (L.) Merrill]"**, submitted to the Faculty of Agriculture, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar (Maharashtra) in partial fulfilment of the requirement for the award of the degree of **MASTER OF SCIENCE (AGRICULTURE)** in **GENETICS AND PLANT BREEDING**, embodies the result of a piece of bonafide research work carried out by **MISS. TANYA BARPANDA** under my guidance and supervision and that no part of the thesis has been submitted for any other degree or diploma.

The assistance and help received during the course of this investigation have been duly acknowledged.

Place: Pune- 411 005
Date: / / 2021

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Place: Pune- 411 005 (R. D. Nimbalkar)

Date: / / 2021

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Place: Pune- 411 005 (S. D. Masalkar)
Date: / / 2021

ABSTRACT

“GENETIC EVALUATION OF ELITE LINES OF SOYBEAN [*Glycine max* (L.) Merrill]”

By

MISS. TANYA BARPANDA

A candidate for the degree of

MASTER OF SCIENCE (AGRICULTURE)

in

GENETICS AND PLANT BREEDING

2021

Research Guide: Prof. B. H. Chavan

Department: Agricultural Botany

The present investigation entitled, “Genetic evaluation of elite lines of soybean [*Glycine max* (L.) Merrill]” was conducted at Botany Farm, Division of Agril. Botany, College of Agriculture, Pune during *Kharif,* 2020.

The experiment was conducted with the objectives to study yield and yield contributing characters of soybean and to screen genotypes for pod blight resistance under natural inoculum pressure.

The thirty genotypes of soybean were sown in a randomized block design with three replications and observations were recorded for eleven characters *viz.*, days to 50% flowering, nodulation count per plant at 50% flowering, days to maturity, plant height, branches per plant, pods per plant, pod blight incidence, seed yield per plant, 100 seed weight, protein content and oil content.

High amount of variability among the genotypes for all the characters were observed. The genotypic and phenotypic coefficient of variation was highest for pod blight incidence followed by nodulation count per plant at 50% flowering and seed yield per plant. High heritability (broad sense) was observed for nodulation count per plant at 50% flowering (99.96%), followed by pods per plant (98.80%), seed yield per plant (98.50%) and days to maturity (98.40%). High genetic advance was recorded for nodulation count per plant at 50% flowering (45.68), followed by pods per plant (37.84) and pod blight incidence (18.81).

The correlation analysis revealed that seed yield per plant showed highly significant positive correlation with pods per plant (0.8471), followed by 100 seed weight (0.4087) and branches per plant (0.2836). The characters protein content (-0.1600) and days to maturity (-0.1566) showed negative and non-significant association with seed yield per plant. Days to 50% flowering, days to maturity, plant height and branches per plant showed highly positive correlation among themselves.

Path coefficient analysis showed that the characters pods per plant (0.8612), 100 seed weight (0.2476) and days to 50% flowering (0.2333) had high to moderate positive direct effect on seed yield per plant. Days to maturity (-0.0758) had negative direct effect on seed yield per plant. The characters number of pods per plant and days to 50% flowering had indirect effect on seed yield per plant *via* other characters studied.

Divergence analysis was carried out by using Mahalanobis (1936) D^2 analysis which indicated the presence of high amount of genetic diversity among the genotypes. The D^2 values of 30 genotypes ranged from 15.27 to 81.08. The genotypes were grouped into six clusters by following Tocher's method as described by Rao (1952). Cluster IV was the largest with 10 genotypes followed by clusters II, III, and I with 8, 6 and 4 genotypes respectively. While remaining all other clusters *viz.*, V and VI were monogenotypic. The maximum inter cluster distance was found between cluster III and IV. While, cluster IV had the maximum intra cluster distance.

Variance of cluster means revealed that nodulation count per plant at 50% flowering showed maximum contribution to divergence, followed by pods per plant, days to maturity, pod blight incidence and seed yield per plant.

The genotypes *viz.*, JS 93 05, JS-335, GBIC-18758, AMS-353, DSb-33, NRC-168 and KDS-992 were observed to be superior in *per se* performance for grain yield and its components and can be used for further breeding programme.

Most of the genotypes were found to be moderately resistant to pod blight and none were found to be resistant or immune. The genotype showing least pod blight incidence was DSb-33.

Tanya Barpanda **1 to 70**

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1. INTRODUCTION

Soybean [*Glycine max* (L.) Merrill] (2n=40) is one of the most important legume crop widely grown for its various uses and versatile nutritional composition. It belongs to the family Leguminosae syn. Fabaceae and subfamily Papilionaceae with chromosome number 2n=40. Linnaeous (1737) proposed the name *Glycine* and described the soybean plant as *Phaseolus max* in his book *Genera Plantarum*. The botanical name presently used for cultivated species of soybean is *Glycine max* which was proposed by Merrill in 1917.

Soybean is a relatively new crop of twentieth century. The origin of soybean crop as cultivated form is unknown (Norman, 1963) but China has been suggested to be the origin. Cultivation of soybean was long confined chiefly to China but gradually it spread to other countries. During World War II, soybean became important in both North America and Europe chiefly as substitute for other protein-rich foods and as a source of edible oil. In the United States soybean is now a leading crop. Brazil, Argentina and Paraguay are significant soybean-exporting nations.

Soybean is an erect, spreading or semi spreading annual plant. Leaves, stem and pods are soft and hairy. It is basically a temperate origin crop and most of the varieties need a temperature range of 30-38°C.

Soybean is a highly self-pollinated crop having perfect flowers consisting of calyx, corolla, pistil and stamens. There are five petals, one standard, two wings and two keels. The keels enclose the stamens and pistils. Stamens are ten in number and diadelphous. Pistil has a single ovary with generally two or three ovules, a long style and a stigma. Fruit of soybean is a legume.

Soybean is often referred to as “wonder crop” or ‘miracle crop” or “Cow of the field”. It has the highest protein (40%) and oil (18-20%) content among grain legumes and is the world’s major source of vegetable oil. The soy protein is well balanced and is rich in lysine and tryptophan which are generally deficient in cereals. Therefore, soybean protein is considered equivalent to meat and fish protein. Soybean also contains plenty of vitamins (thiamine and riboflavin) and minerals. The edible oil from soybean is approximately 85 percent unsaturated and contains essential fatty acids containing no cholesterol.

Several products can be prepared from soybean such as milk, cheese, yogurt, ice-cream, soy nuts, bread, sweets and pastries. Soybean oil is used to manufacture *vanaspati ghee* and even to produce antibiotics. Consumption of soybean has been found useful in weight loss, and for prevention of diabetes and cardiac arrests. It also has a chemical role to play in the manufacture of varnishes, paints, lubricants, pharmaceuticals and soaps. Tofu, soy milk, soy sauce are among the popular commodities manufactured from soybean.

In addition to these uses for human consumption, soybean serves as an excellent source of fodder, hay and silage. Soybean cake is very nutritive for livestock and poultry.

Soybean crop increases fertility of soil by fixing large amounts of atmospheric nitrogen through root nodules at the rate of 65-100 kg/ha. with the help of *Rhizobium japonicum* and also by decomposition of leaves that fall from the plant at maturity.

In India, which is predominantly a vegetarian society, fats and proteins of vegetable origin acquire special significance (Bisaliah, 1986). Under such circumstances, the importance of soybean as a crop increase manifold which has led to a big rise in area under cultivation and production over the years.

Soybean was introduced in India as a non-traditional crop during the late 1970s. Initially it was grown mostly in Madhya Pradesh. It is now also cultivated in many other states like Uttar Pradesh, Bihar and Maharashtra. Production of soybean in India is presently dominated by Maharashtra and Madhya Pradesh which contribute 89 percent of the total soybean production in the country.

Due to availability of high yielding varieties, irrigation facilities, improved cultivation practices and increasing demands the area, yield and production of soybean has been increasing in both India and Maharashtra in the recent years as can be seen from Table No. 1.1.

Table 1.1: Area, yield and production of soybean in India and Maharashtra

	India			**Maharashtra**		
Year (*Kharif*)	**2018**	**2019**	**2020**	**2018**	**2019**	**2020**
Area (lakh ha.)	108.395	107.615	118.385	36.390	37.365	40.398
Yield (kg/ha.)	1009	865	883	944	1055	1125
Production (lakh Mt.)	109.336	93.061	104.559	34.343	39.415	45.446

Source: SOPA, Databank

More than 100 plant pathogens have been reported to affect soybean but one of the most important diseases reported to cause economic losses in soybean is anthracnose (Pod Bight) by *Colletotrichum truncatum* (Schw) Andrus and Moore, which can cause a yield loss of 16-100 percent. This disease is widely distributed especially in tropics under warm and humid conditions and was first reported in India by Verma and Upadhyay (1973).

Symptoms of anthracnose appear at early reproductive stages on stem, pods and petiole as irregularly shaped brown lesions, but pod blight phase is the most damaging. Reddish brown spots appear on pods and later turn black. Fruiting bodies on infected pods resemble small pin cushions surrounded by minute blackish brown setae and infected pods finally get dried out prematurely with shrivelled and mouldy seeds. The disease causes considerable damage by reducing plant stand, seed quality, seed germination and yield and affected plants are significantly shorter with fewer pods and seeds with reduced seed weight. Pod blight of soybean is thus a major constraint in the production of soybean crop.

New genotypes are an important source that can help to meet our national food and oil demand by the development of commercial varieties on the basis of desirable plant traits (Dong *et al*., 2001). Germplasm is a prerequisite for any breeding programme serving as a building block of current and future crop improvements and providing scope for building of genetic variability. Examination of genetic variance is very important for plant breeders, particularly in a commercial crop like soybean. Study of variability and genetic advance in the germplasm will help to ascertain the real potential value of the genotype. It is necessary to study and maintain genetic diversity to establish future genetic base.

Further, efficiency of selection in any breeding programme mainly depends upon the knowledge of association of the characters. Phenotypic correlation indicates the extent of relation between two characters, while genotypic correlation provides an estimate of inherent association between the genes controlling any two characters. For formulating selection indices for genetic improvement of yield, the cause effect of the trait is very essential and can be done by path analysis. Path co-efficient analysis measures the direct and indirect effect for one variable upon another and permits the separation of the correlation co-efficient into components of direct and indirect effect (Dewey and Lu, 1959).

Correlation analysis provides information about the degree of relationship between important plant traits and is good index to predict the yield response in relation to the change of a particular character. In soybean, grain yield, is a complex character which is dependent on a number of variables. To increase its yield, the study of direct and indirect effects of yield and its components provide the basis for its successful breeding programme and thus increase in yield can be more effectively achieved on the basis of performance of yield components and selection for closely associated traits.

Genetic diversity assessment and assigning of different genotypes into different clusters is a very fundamental practice. The genetic diversity between the genotypes is important as the genetically diverged parents are able to produce high heterotic effects (Falconer, 1960). Mahalanobis (1936) generalised distance D^2 analysis is very useful tool in studying the nature and cause of diversity prevalent in the available germplasm.

Therefore, the present investigation entitled "Genetic evaluation of elite lines of Soybean" was undertaken with thirty soybean lines along with following objectives:

1. To study yield and yield contributing characters of soybean.

2. To screen genotypes for pod blight resistance under natural inoculum pressure.

2. REVIEW OF LITERATURE

A comprehensive review of literature is an essential part of any scientific investigation. Review of literature is always necessary to compare the present findings with the previous studies undertaken by the research workers. The literature pertaining to the present investigation entitled "Genetic evaluation of elite lines of soybean [*Glycine max* (L.) Merrill]" has been reviewed under following different aspects.

2.1 Genetic variability

2.2 Heritability and genetic advance

2.3 Correlation

2.4 Path coefficient analysis

2.5 Genetic divergence

2.6 Screening for pod blight resistance

2.1 Genetic variability

The extent of genetic variability available in a crop is pre-requisite for crop improvement as the efficiency of selection depends mainly on it. Fisher (1930) first reported method to separate out genotypic and environmental effects. Hutchinson (1940) provided means to compare genetic variability present in various quantitative characters. Frankel (1947), Burton (1952) and Panse and Sukhatme (1985) emphasized the utility of genetic components of variance as a basis for predicting the response of quantitative characters for selection in different breeding programs. Selection of parents from genetically diverse germplasm is of paramount importance in any breeding programme, so as to get maximum heterosis and a wide spectrum of variability in the segregating generations (Joshi and Dhawan, 1966).

Dhillon *et al*. (2005) worked on genetic variability by using 30 soybean strains. They observed that most of the characters possessed sufficient genetic variability.

Saharan *et al*. (2006) studied genetic variability in eighteen soybean genotypes and reported significant variability for all the traits. They also noticed high genetic gain accomplished by high genotypic coefficient of variation for number of branches per plant, seed yield per plant and number of pods per plant.

Iqbal *et al*. (2010) studied the traits *viz*., days to maturity, plant height at maturity, number of branches per plant, number of pods per plant, 100 seed weight, oil content, seed yield per plant, biological yield per plant and harvest index in 139 soybean genotypes. They reported that the results of analysis of variance showed significant differences among genotypes in terms of traits under study, which indicated the existence of genetic variation.

Datt Shiv *et al.* (2011) studied variability and character relationships in different quantitative traits of 25 genotypes of soybean. The genotypes evaluated showed that both phenotypic coefficient of variation and genotypic coefficient of variation were higher for most of the traits and was a close relationship between PCV and GCV. High genetic coefficient of variation and genetic gain were recorded for days to 50 percent flowering and maturity, plant height, number of pods per plant and 100 seed weight indicating the additive type of gene action which could be improved by simple selection.

Khan *et al.* (2011) conducted an experiment to estimate the genetic variability in 20 different soybean genotypes. The results of analysis revealed that all the characters like days to 50 percent flowering, days to pod formation, days to maturity, plant height, branches per plant, pods per plant, pod length, seeds per pod, 100 seed weight and yield per plant were significantly affected due to various soybean genotypes. It was suggested that genetically variable and superior lines may be focused and involved in future breeding programme for development of new high yielding soybean varieties.

Patil *et al.* (2011) estimated genetic variability in soybean for 11 characters. The highest genotypic and phenotypic coefficient variances were observed for plant height followed by seed yield per plant and pods per plant and it was lowest for days to 50 percent flowering, days to maturity and protein content.

Kumar *et al.* (2013) studied the genetic variability and character association for yield and its component characters in soybean. Among the traits, plant height exhibited high estimate of PCV followed by seed yield per plant indicating that these traits could be used for selection for crop improvement.

Osekita *et al.* (2013) studied the inter-relationship among quantitative characters namely, days to 50 percent flowering, plant height, seed dry weight, number of pods per plant, number of branches per plant, days to maturity, seed yield per plant, number of seed per plant and 100-seed weight. Seed yield per plant had highest estimate of PCV and GCV followed by seed dry weight and number of seeds per plant.

Vachhan *et al.* (2014) evaluated sixty one genotypes of soybean were to determine genetic variability for 15 yield contributing characters. The analysis of variance revealed significant variations for all characters. 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. The high values of GCV and PCV were observed for number of pod 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.

Jain *et al.* (2015) conducted an experiment during *Kharif* 2010-2011 with 41 genotypes of soybean to study genetic variability of yield and its component characters. In general, PCV were found to be higher than the GCV values for all the characters.

Akram *et al.* (2016) conducted an experiment using a randomized complete block design to estimate genetic variability of eleven soybean genotypes. Analysis of variance for yield and yield contributing traits showed significant ($p<0.01$) variation among the genotypes. Results of genetic analyses showed a higher phenotypic coefficient of variation as compared to their corresponding genotypic coefficient of variation for all the traits measured, which indicated that the traits were influenced by environment to some extent.

Chandel *et al.* (2017) evaluated 70 diverse genotypes during *Kharif* 2012-13 in Gujrat, India and found that the highest genotypic and phenotypic coefficient of variances were observed for pods per plant, primary branches per plant and clusters per plant and it was lowest for oil content and days to maturity.

Kuswantoro *et al.* (2018) studied 16 soybean varieties arranged in a randomized block design with three replications for genetic variability. The results showed that days to flowering, number of branches per plant, number of reproductive nodes, number of unfilled pods per plant, 100 seed weight, and grain yield per plant revealed broad GCV (Genetic Coefficient of Variance), whereas the days to maturity, plant height, number of pods per plant had a narrow GCV. PCV (Phenotypic Coefficient of Variance) value was higher than the value of GCV on all the observed characters with a slight difference, except for grain yield per plant.

Jain *et al.* (2018) conducted a field experiment to study the genetic variability, genotypic, phenotypic and environmental coefficient of variation, during *Kharif* 2013. The experiment was laid out in a randomized block design (RBD) with three replications, comprising of 24 genotypes and observations on 9 traits of soybean were recorded. The experiment indicated that significant variation was present among the different genotypes of the soybean for all the traits under study. The highest genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were exhibited by the test weight, number of pods per plant, harvest index and plant height. The PCV was found higher than GCV which indicates the important role of environment in the expression of the characters.

2.2 Heritability and genetic advance

Heritability is the relative role of heredity in the expression of phenotype defined by Falconer, (1989) and Allard, (1961).

Heritability is a good index of transmission of quantitative characters from parents to their offspring given by Falconer, (1989). More especially it could also be defined as the proportionate of total variability that is due to genetic causes. Lush (1949) classified heritability into broad and narrow sense. Improvement in the mean genotypic value of selected plants over parental population is known as genetic advance. The genetic advance is the product of heritability, phenotypic standard deviation and selection differential defined by Burton and Devene, (1953).

Chamundeshwari and Aher (2003) worked out broad sense heritability in 90 soybean lines and recorded the highest heritability for plant height and number of pods per plant. Genetic advance ranged from 0.18 (harvest index) to 42.26 percent (plant height), whereas genetic gain ranged from 7.35 (days to maturity) to 63.20 percent (plant height).

Patil *et al.* (2011) reported high heritability and genetic advance for plant height, seed yield per plant and pods per plant.

Kumar *et al.* (2013) reported that high heritability was observed for biological yield per plant and seed yield per plant. Moderate values of genetic advance were observed for plant height followed by days to maturity.

Osekita *et al.* (2013) reported that heritability was highest in five characters *viz*., days to maturity, days to 50 percent flowering, seed yield, seed dry weight and 100-seed weight.

Vachhan *et al.* (2014) observed 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 in soybean which suggested selection could be effective for these traits.

Akram *et al.* (2016) found high heritability values along with high genetic advance and genetic advance as percentage of mean for plant height, yield per plant, number of pods per plant and number of seeds per plant which indicated the scope of improvement for these characters.

Chandrawat *et al.* (2017) conducted evaluation of genetic variability present in the forty-one genotypes of soybean and five checks (two local + three national checks) and recorded observations on various yield and yield contributing characters *viz.*, days to 50 percent flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, 100 seed weight, harvest index and grain yield per plant at field level and oil and protein content in the laboratory. High heritability coupled with high genetic advance was observed for the traits *viz.*, Pods per plant, plant height, yield per plant, branches per plant and 100 seed weight which indicated presence of additive gene action.

Jain *et al.* (2018) observed high heritability and high genetic advance in the test weight, number of pods per plant, harvest index and plant height. The combination of the high heritability and high genetic advance provided the clear image of the trait in the selection process for crop improvement programme.

Bairwa *et al.* (2020) worked with experimental material comprising of 276 genotypes of soybean along with 4 checks. Highest heritability was observed for number of nodes per plant (99.86%) and lowest heritability was observed for seed yield per plant (62.20%). Genetic advance as percent of mean ranged from 36.66 (plant population per plot) to 4.62 (days to maturity). High heritability coupled with high genetic advance as percent of mean was observed for plant height, number of pods per plant, dry matter weight per plant, plant population per plot and harvest index. It can be concluded that these characters may be used as selection tool in future breeding programs.

2.3 Correlation

In the improvement of any crop, the knowledge of association of one or more characters associated with yield is useful in selecting the individual with high yield, on the basis of their phenotypic values. Such associations between plant characters are statistically elaborated by correlation coefficients.

Correlation coefficient merely describes the extent of association among the characters. Such correlations can be resolved into direct and indirect effects by the method of path coefficient analysis developed by Wright (1921).

Seed yield is a complex character dependent on many other attributes of the plant. The correlation studies are generally used to understand the association between yield and components of yield. The major genetic cause of correlation is pleiotropy and linkage (Falconer, 1960) which makes difficult to get the actual idea about positive or negative effect of genes.

Dewey and Lu (1959) used correlation coefficients first time in plants for path analysis by following Wright (1921). Learner (1958) found use of correlation values in construction of selection indices and predicting correlated response.

Shrivastava *et al.* (1998) reported that in soybean, days to 50 percent flowering had a positive association with pods per plant. Inherent existence of positive association between the eight plant traits studied except between seed yield per plant and days to maturity in both the seasons and between seed yield per plant and days to flowering, pods per plant and plant height.

Mukhekar *et al.* (2004) conducted a study in soybean and revealed positive correlations of seed yield with number of pods per plant, days to 50 percent flowering, mean inter-nodal length, days to maturity and number of branches per plant.

Chandel *et al.* (2005) evaluated 24 genotypes of soybean in randomized block design for 15 characters. Correlation studies indicated that biological yield, 100-seed weight, oil content, harvest index, plant height and leaf area showed positive significant correlation with yield.

Kumar *et al.* (2005) observed that seed yield was positively correlated with total biomass per plant, pods per plant, plant height, harvest index, days to maturity, days to 50 percent flowering, branches per plant and seeds per pod.

Faisal *et al.* (2006) reported significant correlation coefficient of yield with number of pods per plant. Increase in this trait will ultimately increase the seed yield.

Ngon *et al.* (2006) reported that the soybean developing stages had close association with agronomic traits as well as yield and yield components; however, maturity gave better relationship with plant characteristics than flowering time. Days to 50 percent flowering and maturity had positive correlation with other characteristics except 100 seed weight. Among which, flowering time and maturity were highest correlated with plant height.

While studying yield components in eighteen varieties of soybean, Saharan *et al.* (2006) observed positive and significant association between seed yield and number of pods per plant, biological yield per plant, number of branches per plant, harvest index, 100-seed weight and protein content.

A study to ascertain correlation in soybean was conducted by Sonwane *et al.* (2006) revealed that grain yield was significantly and positively correlated with harvest index, number of pods per plant, number of seeds per pod, 100 seed weight and duration of seed filling period.

Malik *et al*. (2007) studied 27 genotypes of soybean to determine the correlation and path analysis of yield and its components. Genotypic correlations were higher than the phenotypic and environmental ones for most of the characters exhibiting high degrees of genetic association among traits under consideration. Correlation coefficient for bean yield was positive with leaf area, first pod height, days to flowering, days to maturity, plant height and number of branches per plant. Therefore, it was indicated that such traits would ultimately increase the grain yield.

Nag *et al*. (2007) studied genotypic and phenotypic correlations and path analysis among twelve quantitative traits in thirty genotypes of soybean. Seed yield per plant had significant and positive correlation with its components characters like plant height, pods per plant and seed per plant.

Seventy four genotypes were analysed for physicochemical and cooking quality by Sharma *et al*. (2008). They revealed that oil correlates negatively with protein and protein correlates negatively with seed yield per plant.

Iqbal *et al.* (2010) observed that the seed yield was positively and significantly correlated with all studied traits except plant height, showed non-significant association during both years. Oil content showed significant and positive correlation with seed 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.

Datt Shiv *et al*. (2011) generated information on the character relationships in different quantitative traits of 25 genotypes of soybean grown under complete randomized block design. The genetic correlation was higher than corresponding phenotypic ones for most of the traits implying inherent relationship among them. Oil content expressed highest positive and significant phenotypic and genotypic association with days to 50 percent flowering, days to maturity, plant height, primary branches per plant, seed yield and positive correlation with primary branches and seeds per pod.

Machikowa and Laosuwan (2011) observed significant positive phenotypic correlation between seed yield and days to 50 percent flowering. Genotypic correlation showed that seed yield was positively correlated with all character except 100 seed weight.

Kumar *et al.* (2013) observed that genotypic correlation analysis indicated that number of pods per plant, biological yield per plant, harvest index and seed index showed positive significant correlation with seed yield per plant. Phenotypic correlation analysis indicates that number of pods per plant, biological yield per plant, harvest index and seed index showed positive significant correlation with seed yield per plant.

Osetika *et al.* (2013) observed that plant height showed significant and positive correlation with number of branches per plant, number of pods per plant, number of seeds per plant, seed dry weight and seed yield per plant.

Mahbub *et al.* (2015) found that in soybean 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 per plant.

Shree *et al.* (2017) evaluated ninety genotypes of soybean including five checks to find out the correlation between yield and yield attributing traits in soybean during *Kharif* 2014. Grain yield was found to be positively and highly significantly associated with number of pods per plant, seeds per pod, 100 seed weight, both at genotypic and phenotypic levels. Protein content showed positive and significant association with number of pods per plant, while oil content showed negative and significant association with plant height at both genotypic and phenotypic level.

Shekar *et al.* (2018) studied correlation in soybean variety PK 1092 treated with three doses of gamma rays (20 kR 30 kR and 40 kR) and three concentrations of ethyl methane sulphonate (EMS) (0.05%, 0.10% and 0.15%) and their combinations in M_2 generation for twelve quantitative characters. The seed yield per plant had strong positive association with number of pods per plant, number of seeds per pod, total dry matter weight per plant, harvest index, seed yield efficiency, oil content and protein content at both genotypic and phenotypic level.

Parihar *et al.* (2020) conducted multilocational trial on soybean during 2016-17 at Chhattisgarh, India to evaluate fifteen variable genotypes for 16 yield and quality characters for inter-relationship. Days to 50 percent flowering had a positive association with days to maturity, 100 seed weight and unfilled pods. Plant population had a positive correlation with pod bearing length and seed yield per plant. Plant height had a positive correlation with pod bearing length, seeds per pod, whereas highly negative correlation with 100 seed weight. Branches per plant had positive association with seed yield. Pod bearing nodes was highly significant and positive associations with filled pods, pod length and non-significant positive association with seed yield. Filled pods had significant association with unfilled pods, and highly significant association with pod length. Pod bearing length had a highly significant positive correlation with qualitative feature volume weight. Biological yield had a significant positive association with seed yield per plant.

2.4 Path coefficient analysis

Path coefficient analysis is simply a standardized partial regression coefficient which splits the genotypic correlation coefficient into direct and indirect effect. Yield is a complex entity and is observed to be associated with a number of component characters. These characters are inter-related. Such inter dependence of the contributory factors often affects their direct relationship with yield, thereby, making correlation coefficient less reliable in selection indices. The failure of correlation to explain cause and effect of relationship between the characters concerned emphasized that the use of path coefficient analysis was inevitable. The method of path coefficient analysis was first proposed by Wright (1921) and further elaborated by Dewey and Lu (1959).

Gohil *et al.* (2003) studied path analysis in soybean indicated that number of pods per plant had maximum positive direct effect on seed yield followed by 100-seed weight and number of clusters per plant. They also observed that the indirect effects of all the traits except oil and protein content through number of pods per plant were positive and higher in magnitude than rest of the traits.

Mukhekar *et al.* (2004) studied characters association and path analysis in soybean and revealed that number of pods per plant exerted the highest direct effect on grain yield followed by days to 50 percent flowering. They also observed that the characters like mean inter-node length, number of branches per plant and days to maturity exhibited negative direct and indirect effects *via* one or more characters.

Kumar *et al.* (2005) evaluated 84 genotypes of soybean using path analysis and revealed that selection for character *viz*., plant height, pods per plant, total biomass per plant and harvest index had positive influence on seed yield per plant.

Vart *et al.* (2005) revealed that harvest index had highest positive direct effect on seed yield followed by biological yield and 100-seed weight. They also observed that clusters per plant had highest negative direct effect followed by seeds per pod.

While studying path coefficient in soybean, Malik *et al.* (2006) revealed that leaf area, pod length, days to 50 percent flowering, days to flowering completion, days to maturity, plant height, oil content and protein content had negative direct effects on yield. This suggested that selection on the basis of these traits might lead to the loss in terms of grain yield.

Gaikwad *et al.* (2007) evaluated 50 genotypes of soybean and indicated that harvest index, number of pods per plant and pod length exerted maximum direct effect on seed yield per plant.

They also suggested that such traits had positive association with seed yield, indicating importance of direct selection for these traits.

Malik *et al.* (2007) revealed that days to flowering completion had maximum direct contribution to yield followed by days to pod initiation, chlorophyll content, number of pods per plant and plant height. They concluded that, these characters could be considered as selection criteria in improving the yield of soybean genotypes.

Nag *et al.* (2007) studied path coefficient analysis which revealed that the number of seeds per plant had the highest positive direct effect on seed yield per plant, followed by oil percent and 100 seed weight.

Kamwal *et al.* (2009) observed that seed yield showed significant positive correlations with primary branches per plant, number of pods per plant, 100 seed weight. Protein and oil showed significant and association with each other. Path coefficient analysis indicated major role of number of pods per plant, primary branches per plant and 100 seed weight both directly and indirectly influenced seed yield.

Shaikh *et al.* (2010) studied path analysis in soybean for thirty genotypes of soybean and revealed that number of pods per plant, number of seeds per pod had direct effect on seed yield per plant in soybean.

Machikowa and Laosuwan (2011) observed that pods per plant had highest positive direct effect on seed yield, followed by branches per plant. In addition, the indirect effect of most characters was 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, days to 50 percent flowering and days to maturity. Number of pods per plant recorded highest positive direct effect on seed yield per plant followed by plant height.

Ghodrati *et al.* (2013) conducted path coefficient analysis for 32 cultivars of soybean which indicated that the total dry matter gave the greatest direct positive effect (0.718) on seed yield, followed by harvest index (0.589). Direct effects on seed yield were 0.312 and 0.250 for number of pods per main stem and days to maturity, respectively. Based on the results of this experiment, the importance of high total dry matter and harvest index with moderate maturity (115-130 days), medium height (110 cm) and high seed weight can be seen for selection, in breeding program, with the goal of improved soybean seed yield.

Jain *et al.* (2015) revealed that biological yield, number of pods per plant and 100 seed weight were major characters influencing seed yield directly and indirectly. The results indicated that biological yield is responsible for manipulation of seed yield in soybean

Akram *et al.* (2016) in their experiment for eleven soybean genotypes also estimated path coefficient between yield and its components of eleven genotypes of soybean. Path coefficient analysis showed that the seeds per plant had the highest (2.848) positive direct effect on yield per plant, followed by pods per plant, days to first flowering, number of branches per plant, 100-seed weight, plant height, and pod length. So, the number of pods per plant and seeds per plant could be considered as important selection criteria for yield improvement in soybean.

Kumar *et al.* (2017) experimented on soybean variety *i.e.* PK 1029. Path coefficient analysis revealed that total dry matter weight per plant had highest positive direct effect on seed yield (0.9642) followed by harvest index (0.3605) and number of pods per plant (0.0844). The results indicated that total dry matter weight per plant and number of pods per plant is responsible for manipulation of seed yield per plant in soybean.

Humtsoe *et al.* (2017) laid out an experiment in randomized block design with three replications during *Kharif*, 2015 at the experimental farm of School of Agricultural Sciences and Rural Development, Nagaland to study character association and path analysis among twelve genotypes of soybean under foot hill condition of Nagaland. Studies were done on nine characters *viz.*, days to 50 percent flowering, plant height, number of primary branches, number of secondary branches, number of pods per plant, number of seeds per pod, days to 80 % maturity, 100 seed weight and seed yield per plant. The Path analysis showed that number of pods per plant has the highest positive direct effect followed by plant height at genotypic level. Thus, direct selection for number of pods per plant and plant height would likely be effective in increasing yield.

Shekar *et al.* (2018) carried out path analysis in soybean and found that the characters days to 50 percent flowering, days to maturity, number of pods per plant, number of seeds per pod, total dry matter weight per plant, harvest index, 100 seed weight, oil and protein content had positive direct effect on seed yield per plant at genotypic level. The selection based on number of pods per plant, number of seeds per pod, total dry matter per plant, harvest index, seed yield efficiency and 100 seed weight could help in genetic improvement of seed yield per plant in soybean population under study.

Parihar *et al.* (2020) path analysis revealed that seed yield is directly affected by days to 50 percent flowering, 100 seed weight, through a low magnitude of direct effect, while plant height, pod bearing length, and harvest index contributes through a moderate magnitude of direct effect on seed yield. Filled pods and biological yield contribute to seed yield by the highest magnitude of direct effect. The negligible value of residual factor value justified that characters considered in the study was justified for seed yield. Findings indicate that direct selection of significant characters will enhance the breeding efficiency for seed yield in soybean.

2.5 Genetic divergence

The development of new varieties is mainly governed by the magnitude of genetic variability in the base material and extent of variability for desired characters. Genetic variability and divergence is of greatest interest to the plant breeder as it plays a vital role in framing a successful breeding programme. The genetically diverse parents are likely to produce high heterotic effects and desirable segregants.

The concept of D^2 analysis for measuring divergence between two populations was introduced by Mahalanobis (1936). It gave results based on the magnitude of divergence independent of size sample. Murthy and Arunachalam (1966) revealed that geographical distribution and genetic diversity could not be related in any of the crops.

Mahalanobis *et al.* (1949) applied the D^2 statistic in a detailed study of anthropometric data of Uttar Pradesh, classifying it in twenty three groups into three major clusters, *i.e.* Brahmin (B-cluster) at the top of Hindu social hierarchy, comprising nine groups, the Artisans (A-cluster) in the middle consisting of four groups, and the Tribal cluster (T-cluster) at the bottom comprising of ten groups.

Genetic divergence is a result of changes in the gene frequencies of different population due to evolutionary forces. While, the frequency of given gene in turn is a function of its contribution in the total adaptation of individuals in natural populations. The individuals showing more fitness contribute more than those having less fitness to the population gene pool.

Allard (1961) studied relationship between genetic diversity and consistency of performance in different environments by using three distinct levels of genetic diversity. He concluded that genetic diversity and productivity were completely related and further stated that many factors determined the productivity of mixed populations. While, the genetic diversity and productivity are simply related irrespective of number of characteristics of the components involved.

Murthy and Arunachalam (1966) stated that the genetic drift and selection in different environments could cause greater diversity among genotypes than their geographical distance.

Chandankar *et al.* (2002) studied genetic divergence among twenty five genotypes of soybean using Mahalanobis D^2 statistics. These genotypes are grouped into 9 clusters. Canonical analysis indicated genetic divergence for number of days to 50 per cent flowering, number of branches per plant, biological yield per plant and oil content.

Dev Vart *et al.* (2002) evaluated 56 lines of soybean for genetic divergence. The lines were grouped into 11 clusters. The intra-cluster values of 0.0 (VIII, IX and XI) to 240.05 (VII) showed considerable diversity among cluster while, the intra-cluster distances for cluster I to VII (13.7 to15.5) suggested close relationship and almost parallel diversity among the genotypes included in these clusters. The inter-cluster divergence values varied from 273.1 (between II and V) to 3548.2 (between I and IX). The results revealed that geographic diversity may not be important factor in determining genetic divergence.

Hooda *et al.* (2004) studied genetic diversity among 160 soybean genotypes using Mahalanobis D^2 analysis. A wide genetic diversity was observed among the genotypes. Data were subjected to multivariate analysis and the genotypes were grouped into 8 clusters. The most divergent clusters were V and VIII, followed by VI and VIII. The clustering pattern revealed that no definite relationship existed between genetic diversity and geographical diversity.

Sharma *et al.* (2005) studied genetic divergence using Mahalanobis D^2 analysis among sixty two soybean varieties based on 17 characters led to their grouping into 15 clusters, out of which 9 were monogenotypic. Among 17 characters, protein per cent contributed maximum to the genetic divergence, followed by number of pods per plant and seed yield per plant. This indicated that these characters were mainly responsible for the genetic divergence in the parent material.

Ramana and Satyanarayana (2006) studied 70 soybean genotypes for genetic divergence using Mahalanobis' D^2 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.

An experiment was conducted by Sood *et al.* (2006) for evaluating 68 advanced lines of soybean for seed yield and its components to assess genotypic variability in relation to genetic divergence. Analysis of variance revealed significant differences among the lines for all the traits studied. On the basis of D^2 analysis, lines were grouped into 14 clusters. The pattern of distribution of genotypes in different cluster indicated that genetic divergence was not related to parentage.

An attempt was made by Gohil *et al.* (2007) to estimate the genetic distance between 55 genotypes of soybean by using D^2 analysis, the result revealed that 55 genotypes were grouped into 11 clusters (I to XI) with substantial genetic divergence between them, maximum inter-cluster distance was obtained between cluster- IX and XI followed by those between cluster-II and XI.

An experiment was conducted by Iqbal *et al.* (2008) for evaluating 139 genotypes of soybean for yield and yield associated traits. The result revealed significant differences among genotypes for all traits studied. Cluster analysis based on these traits, 139 genotypes were divided into five clusters. Cluster I showed maximum number of filled pods per plant, 100-seed weight, grain yield per plant, biological yield and harvest index. Cluster II showed least oil content, grain yield per plant and harvest index. Cluster III showed maximum plant height and number of branches per plant. Cluster IV comprised of accessions having high oil content and least number of unfilled pods per plant while early maturity was observed in cluster V.

Kayande *et al.* (2008) studied 50 genotypes of soybean from different geographical sources by using Mahalanobis D^2 statistics. These genotypes were grouped into ten clusters. Canonical analysis indicated genetic divergence for number of pods per plant, days to 50 % flowering, plant height and seed yield per plant. The clustering pattern revealed that genetic diversity was not necessarily associated with geographical diversity in soybean.

Kayande and Patil (2009) studied 50 genotypes of soybean from different geographical sources by using Mahalanobis D^2 statistics for eight characters. These genotypes were grouped into ten clusters. Canonical analysis indicated genetic divergence for number of pod per plant, days to 50 per cent flowering, plant height and seed yield per plant. The clustering pattern revealed that genetic diversity was not necessarily associated with geographical diversity in soybean.

Dhapke *et al.* (2011) studied genetic divergence among high yielding sixty six elite genotypes of soybean. These genotypes fell into 10 clusters out of which one was monogenotypic. Among seven characters, number of pods per plant contributed maximum to the genetic divergence, followed by number of branches per plant. This indicated that these characters were mainly responsible for genetic divergence.

Shadakshari *et al.* (2011) from the genetic diversity studies based on 12 morphological characters of 50 genotypes of soybean, it could be inferred that, the traits seeds per plant and seed yield per plant contributed maximum to the genetic diversity. The clustering pattern revealed that there was no correlation between the geographical diversity and genetic diversity.

The clusters IX (JS 90-29 and IC18277) and X (IC93656) were the distant clusters and clusters III (IC 39873 and IC 93751) and VIII (IC 34057 and IC 18736) were the nearest clusters. The clusters IX and I possessed the high mean values for many of the traits studied. With respect to seed yield per plant the clusters IX, VI and I were the superior clusters. The entries *viz*., JS 90-29 and IC18277 of IX cluster and IC93656 of X cluster can be used in crossing programme for development of good recombinants for seed yield.

Tyagi and Sethi (2011) estimated genetic distance between forty genotypes of soybean by using D^2 statistics. These genotypes were clustered into six clusters (I to VI). The analysis further indicated that the genotypes of common geographical origin were grouped into different clusters, suggesting a lack of relationship between genetic and geographical diversity.

Promin *et al.* (2014) evaluated 46 genotypes of soybean for morphological traits to determine the genetic divergence among the introduced lines. The clustering of genotypes based on 8 traits revealed the existence of variability among genotypes, and nine clusters were obtained. Estimates of average inter-cluster distance revealed that IV and V were most divergent (D^2 = 36.07) followed by cluster I and II (D^2 = 25.96), VI and VII (D^2 = 20.15), cluster III and IV (D^2 = 18.18).

Khedkar *et al.* (2017) carried out multivariate analysis by using Mahalanobis D^2-statistics, revealing wider genetic diversity among forty genotypes of soybean. Among the twelve characters studied, oil content (40.00% divergence), was the largest contributor in the divergence followed by seed shattering by hot air oven (HAO) method (27.82% divergence) and Seed yield per plant (23.21% divergence). The clustering pattern did not establish a clear-cut relationship between genetic diversity and geographical origin. The cultivars included in the diverse clusters can be used as promising parents for hybridization programme for obtaining high heterotic response and thus better segregants in the early as well as subsequent generations in soybean.

Neelima *et al.* (2017) conducted a trial during the year 2015-16 with 124 germplasm accessions of soybean at All India Coordinated Research Project on Soybean, Parbhani to identify the diverse genetic stocks for the use in hybridization programme through genetic diversity based on Mahalanobis D^2 statistics. The data was recorded on 11 yield contributing characters on accessions raised in Randomized Block Design in two replications. The germplasm accessions were grouped into five different clusters. Among the five clusters, the Cluster I recorded high mean performance for five characters *viz.*, Days to initial flowering, Days to 50% flowering, Days to maturity, Plant height and 100 seed weight.

Dubey *et al.* (2018) studied genetic divergence in 50 genotypes of soybean and recorded observations on 13 traits. The analysis of variance indicated that significant variation was present among the different genotypes of the soybean for all the traits under study. Genetic divergence was assessed using D^2 statistics for characters which resulted in grouping of all the genotypes in 13 clusters. Among 13 clusters, cluster I was the biggest with 24 genotypes followed by cluster III with 11 genotypes and cluster IV with five genotypes. Clusters II, V, VII, VIII, IX, X, XI, XII and XIII were solitary. Maximum differences among the genotypes within the same cluster (intra-cluster) were shown by cluster IV (76.21) followed by cluster III (62.03) and cluster I (60.32). Solitary clusters II, V, VII, VIII, IX, X, XI, XII and XIII showed zero intra-cluster distances. Diversity among the clusters varied from 38.21 to 987.90 inter-cluster distances. Clusters IV and XIII showed maximum inter-cluster distance (987.90).

Joshi *et al.* (2018) evaluated the genetic variation in soybean by means of 120 accessions of soybean received from NBPGR New Delhi and DSR Indore along with 5 checks *viz.*, SL 688, PS 1347, PS 1092, Bragg and PS 1042. The adjusted mean of genotypes were subjected to Hierarchical Cluster Analysis (HCA) and the genotypes were grouped based on 40 % dissimilarity level. The 120 genotypes of soybean including 5 checks were grouped in 9 clusters based on hierarchical cluster analysis. The distribution pattern of accessions in clusters showed that accessions from different locations were clustered together in one cluster and also accessions from the same region were grouped under different clusters. This suggested that there is no parallelism between genetic diversity and geographical diversity. Inter and intra clustering distance was also calculated to determine extent of diversity among and between the clusters. Greater intracluster distance shows greater diversity among the accessions of the same cluster whereas less intra-cluster distance shows that these accessions are closely related and less variable with respect to their mean values.

Mishra *et al.* (2018) conducted an investigation during *Kharif* 2015 with 60 advanced breeding lines of soybean, to identify the most diverse and promising lines for hybridization programme through genetic diversity analysis by Mahalanobis' D^2 statistics.

Observations on twelve yield contributing traits were recorded on lines raised with 3 replications in RBD. The results revealed significant differences among lines for all studied traits. Sixty soybean lines were grouped in 16 clusters following Tocher's method. Among twelve traits, numbers of pods per plant, number of seeds per plant and seed yield per plant were maximum contributing traits to genetic diversity.

2.6 Screening for Pod Blight Resistance

Singh (1993) evaluated 48 soybean cultivars against *Colletotrichum truncatum* in the field following inoculation at the pod initiation stage with a suspension containing 10^4 condia/ml. None of the cultivars were found to be immune, however, the degree of susceptibility varied among the cultivars. HM1 and Birsa Soybean 2 were found to be the most resistant.

Ghawde *et al.* (1996) screened 7 soybean varieties for pod blight of soybean under artificial epiphytotic conditions, and found that varieties JS-22 and PKV-1 were highly resistant and variety MACS-13 was also resistant.

Sajeesh *et al.* (2014) screened 11 entries of soybean for pod blight resistance and found that 64% genotypes showed moderately resistant reaction. Genotype Dsb 12 showed resistant reaction.

Chavan *et al.* (2018) found under artificial epiphyotics and controlled conditions, all the 40 soybean entries studied exhibited different reactions against *C. truncatum*. Sixteen test entries *viz.*, MACS-1201, VLS-76, JS-9752, MACS-1336, MAUS-2, PS-1477, SL-794, MACS-1140, MAUS-158, VLS-75, PS-1476, BAUS-40, Dsb-20, MACS-1311, MAUS-71 and SL-871 were found moderately resistant with mean percent disease intensity in the range of 12.20 to 23.10 per cent. However, five test entries *viz.*, NRC-86, PS-1466, DS-27- 11, DS-12-13, NRC-85 found moderately susceptible with mean per cent disease intensity in the range of 26.70 to 29.10 per cent. Fifteen test entries *viz.*, Dsb-18, SL-799, KBS-8, RKS-63, MACS-1039, KS-103, KDS-344, AMS-243, CSB-08-08, JS (SH)-2003-8, MAUS-449, JS-20- 29, MAUS-453, AMS-MB-5-19 and JS-93-05 were found susceptible with mean per cent disease intensity in the range of 51.20 to 54.25 per cent and four test entries *viz.*, SL-778, Bragg, AMS-MB-5-18, and JS-335 were found highly susceptible with per cent disease intensity in the range of 75.14 to 77.70 per cent. None was found highly resistant or immune to the disease.

Natraj *et al.* (2020) evaluated 225 germplasms of soybean for anthracnose resistance which resulted in the identification of five genotypes *viz.*, EC 538828, EC 34372, EC 457254, AKSS 67 and Karune as highly resistant. Genetics of anthracnose resistance in three F_2 populations derived from EC 34372 × JS 95-60, EC 457254 × JS 95-60 and AKSS 67 × JS 95-60 revealed that the resistance in all the three resistant parents was governed by two major genes interacting in complementary fashion. The χ^2 test for goodness of fit revealed that F_2 plants in each of the three populations segregated in 9 resistant: 7 susceptible ratio. This was the first report on genetics of anthracnose resistance in soybean and aided soybean breeders to develop a strategic anthracnose resistance breeding program and to map the genes governing resistance.

Research findings from this study indicated the potential role of exotic germplasm in Indian soybean improvement against anthracnose disease.

3. MATERIAL AND METHODS

The present investigation entitled, “Genetic evaluation of elite lines of soybean [*Glycine max* (L.) Merrill] was conducted at Botany Farm, Division of Botany, College of Agriculture, Pune during *Kharif* 2020. The details of the materials used, methods adopted and statistical analysis followed, during the investigation are described as below.

3.1 Experimental material

The experimental material used for the study consisted of 30 genotypes of soybean obtained from the Officer Incharge, Agriculture Research Station (ARS), Kasbe Digraj, Sangli,. The list of genotypes used in the experiment is given in Table 3.1.

Table 3.1 List of 30 genotypes of soybean used for the present study

Sr. No.	Genotype	Source	Sr. No.	Genotype	Source
1	AMS-20-19	ARS, Digraj	**16**	KDS-992	ARS, Digraj
2	AMS-353	ARS, Digraj	**17**	KDS-1045	ARS, Digraj
3	AMS-MB-5-19	ARS, Digraj	**18**	KDS-1095	ARS, Digraj
4	AMS-100-39	ARS, Digraj	**19**	KDS-1096	ARS, Digraj
5	DS-228	ARS, Digraj	**20**	KDS-1097	ARS, Digraj
6	DSb-33	ARS, Digraj	**21**	KDS-1144	ARS, Digraj
7	DSb-36	ARS, Digraj	**22**	KDS-1149	ARS, Digraj
8	GBIC-18758	ARS, Digraj	**23**	KDS-1150	ARS, Digraj
9	HIMSO-1690	ARS, Digraj	**24**	MAUS-732	ARS, Digraj
10	JS-335	ARS, Digraj	**25**	MAUS-8060	ARS, Digraj
11	JS-9305	ARS, Digraj	**26**	NRC-142	ARS, Digraj
12	KDS-344	ARS, Digraj	**27**	NRC-168	ARS, Digraj
13	KDS-726	ARS, Digraj	**28**	RSC-11-22	ARS, Digraj
14	KDS-753	ARS, Digraj	**29**	RVS-2011-76	ARS, Digraj
15	KDS-980	ARS, Digraj	**30**	TS-46	ARS, Digraj

3.2 Experimental Details

Thirty genotypes of soybean were evaluated in a Randomised Block Design (RBD) with three replications during *Kharif*, 2020. They were sown with spacing of 30 × 10 cm in a single row of 3m length.

3.3 Observations recorded

Five plants per genotype per replication were selected at random for recording observations on quantitative traits and averages were calculated.

3.3.1 Days to 50 % flowering (No.)

Number of days from date of sowing to the date of 50 percent plants flowered was recorded in each replication and the average number of days for 50 percent flowering was calculated.

3.3.2 Nodulation count per plant at 50% flowering (No.)

Nodulation count was taken at 50 percent flowering stage of each replication. The plants were carefully dug out and washed to remove the soil under tap water after which the physical count of nodules was taken.

3.3.3 Days to maturity (No.)

Numbers of days required from the date of sowing to the maturity of crop were recorded as days to maturity.

3.3.4 Plant height (cm)

Plant height was recorded in centimetre at the time of harvesting by measuring the height of the plant from ground level to the top of the main axis.

3.3.5 Branches per plant (No.)

Total number of branches on main stem was counted.

3.3.6 Pods per plant (No.)

The total number of pods was counted from five plants at maturity and the average was calculated.

3.3.7 100 seed weight (g)

It was recorded by weighing randomly selected 100 seeds for each genotype.

3.3.8 Pod blight incidence (%)

Number of pods on each plant exhibiting typical symptoms of pod blight were counted 15 days before harvesting. The plants were graded and categorized as per the following:

Table 3.2 Grading and characterization of percent pod infection for disease reaction for pod blight incidence in soybean genotypes

Percent pod infection (%)	Disease Reaction
0	Immune
< 1	Highly Resistant
2-5	Resistant
6-25	Moderately Resistant
25-50	Susceptible
>75	Highly Susceptible

$$\text{Where, percent pod infection (\%)} = \frac{\text{No. of infected pods}}{\text{Total No. of pods observed}} \times 100$$

3.3.9 Seed yield per plant (g)

The observations were recorded by recording the seed weight of selected plant and the average of five plants was estimated.

3.3.10 Protein content (%)

The protein content of each genotype was estimated by NIR (Near Infrared) spectroscopy method.

3.3.11 Oil content (%)

The oil content of each genotype was estimated by NIR (Near Infrared) spectroscopy method.

3.4 Statistical Analysis

The mean values of five randomly selected observational plants for eleven different characters were used for statistical analysis. The following statistical parameters were calculated for presentation of data on different quantitative attributes.

3.4.1 Analysis of variance (ANOVA)

The analysis of variance was done as suggested by Panse and Sukhatme (1985).

Sr. No.	**Sources of Variation**	**Degrees of Freedom**	**Expected mean sum of squares**
1	Replications	r-1	$\sigma^2 e + t\,\sigma^2 r$
2	Treatments	t-1	$\sigma^2 e + r\,\sigma^2 t$
3	Error	(r-1) (t-1)	$\sigma^2 e$
4	Total	(rt-1)	

Where,

r = Number of replications

t = Number of treatments

e = error

3.4.2 Genotypic coefficient of variation (GCV)

It was estimated by the formula suggested by Burton (1952).

$$GCV = \left(\sqrt{(\sigma^2_g) / \bar{X}}\right) \times 100$$

Where,

$\sigma^2_g = V_g$ = Genotypic variance

$\bar{X}$ = General mean of the character

3.4.3 Phenotypic coefficient of variation (PCV)

It was estimated by the formula suggested by Burton (1952).

$$PCV = \left(\sqrt{(\sigma^2_p) / \bar{X}}\right) \times 100$$

Where,

$\sigma^2_p = V_p$ = Phenotypic variance

$\bar{X}$ = General mean of the character

3.4.4 Heritability percentage

Heritability percentage in broad sense was calculated as given by Burton (1952).

h^2 (b.s.) = $V_g / V_p \times 100$

OR

h^2 (b.s.) = $\sigma^2_g / \sigma^2_p \times 100$

Where,

h^2 (b s) = Heritability percentage in broad sense

$\sigma^2_g = (V_g)$ = genotypic variance

$\sigma^2_p = (V_g)$ = phenotypic variance

3.4.5 Genetic advance

Genetic advance was calculated by the formula given by Johnson *et al*. (1955).

$GA = K \times (\sigma^2_g / \sigma^2_p) \times \sigma_p$

Or

$GA = K \times h^2 \times \sigma_p$

Where,

K= Selection differential which is 2.06 at 5 percent selection intensity.

σ^2_g (V_g) = Genotypic variance.

σ^2_p (V_p) = Phenotypic variance.

$\sqrt{V_p}$ or σ_p= Phenotypic standard deviation.

3.4.6 Correlation

To understand the association among the characters, genotypic and phenotypic correlation coefficients were worked out by adopting the method described by Singh and Chaudhary (1979).

3.4.6.1 Phenotypic correlation coefficient

r_p = covariance $(X, Y)_p / \sqrt{\text{Variance } x_{(p)} \text{ Variance} Y_{(p)}}$

Where,

r_p = Phenotypic correlation coefficient between character X and Y.

3.4.6.2 Genotypic correlation coefficient

$r_g = \text{covariance } (X, Y)_g / \sqrt{\text{Variance } x(_g) \text{ Variance} Y(_g)}$

Where,

r_g = Genotypic correlation coefficient between character X and Y.

Significance of correlation coefficients were tested by using "t" test given by Panse and Sukhatme (1985).

3.4.7 Path Coefficient Analysis

Path coefficient analysis was done according to the procedure suggested by Dewey and Lu (1959).

If "Y" is the effect and X_1 is the cause, the path coefficient for the path from cause X_1 to the effect Y is $\sigma X_1 / \sigma Y$

Direct and indirect effects were worked out by using genotypic correlations as below:

Direct effect of X_1 on y = PX_1 Y

Where,

PX_1 = Path coefficient of X_1 on Y.

Similarly, direct effects of other attributes on yield were worked out.

Indirect effect of X_1 *viz.*, X_2 or Y = PX_2 Y r X_1 X_2

Where,

PX_2Y = Path coefficient of the component character X_2 on Y.

r X_1 X_2= Genotypic correlation between X_1 and X_2.

Similarly, indirect effects in all possible combinations were calculated for all component characters.

The residual effect (R) was calculated as below;

$R = [1- (PX_1.\ rX_1Y) - (PX_2.\ rX_2Y) - \ldots\ldots(PX_n.\ rX_nY)]^{1/2}$

Where,

PX_1. PX_2,......PX_n= Direct effects of respective characters on Yield.

rX_1. rX_2,…..rX_n = Correlation coefficient between respective

characters and yield.

3.4.8. Genetic distance (D^2)

The generalized distance between two populations was defined by Mahalanobis (1936) as:

$D^2 = \Sigma\, \lambda\, i.j.di.\ dj.$

Where,

λ i. j. = Reciprocal matrix to the common dispersion matrix.

di= Difference between the mean values of two populations for ith character .

dj= difference between the mean values of two populations for jth character.

Estimation of D^2 values from the above formula is very complicated in the present study. Since, it requires the inversion of a thirteenth order determinant and then the evaluation of B (BH) / 2 terms whose sum is D^2. It was found convenient to work with a set of uncorrelated characters construed form the original measurements. D^2 with such transformed variables reduces to the evaluation of a simple sum of squares. Transformation was done by Singh and Chaudhary (1979) using pivotal condensation method.

The coefficients for the transformation were obtained by dividing the first row of the reduced matrix by the square root of the corresponding pivotal condensation elements.

3.4.9 Determination of gene constellations

Tocher's method as described by Rao (1952) was followed for cluster formation. No formal rules can be laid down for finding the clusters because a cluster is not a well-defined term. The only criterion appears to be that any two groups belonging to the same cluster should be at least on an average shows a smaller D^2 than those belonging to two different clusters. A simple device suggested by K. D. Tocher is to start with two closely associated groups and find a third group which has the smallest average D^2 from the first two. Similarly, the fourth is chosen to have the smallest D^2 from the first three and so on. If at any stage the average D^2 value of a group from those already listed appears to be high, then this group does not fit in with the former groups and is therefore taken outside the former cluster. The groups of the first cluster are then omitted and the rest are treated similarly. It is also useful to calculate the change in average D^2 within a cluster due to the inclusion of an additional group. If the changes are appreciable then the newly added group has to be considered as outside the cluster.

3.4.10 Average intra and inter cluster D^2 and D values

3.4.10.1 Average intra cluster D^2

$D^2 = \Sigma D^2 i / n$

Where,

Di is the sum of distance between all possible combinations (n) of the population included in a cluster.

3.4.10.2 Average inter cluster D^2

$D^2 = \Sigma$ distance between the population of cluster i and j. $/ n_i . n_j$

Where,

n_i = number of populations in the cluster i.

n_j = number of populations in the cluster j.

3.4.10.3 Average intra and inter-cluster distance

$D = \sqrt{D^2}$

3.4.11 Cluster means

Cluster means were calculated for individual character on the basis of mean performance of the genotype included in the cluster.

3.4.12 Cluster diagram

With the help of D^2 values between the clusters, a diagram showing the relationships between different clusters was drawn.

4. RESULTS AND DISCUSSION

The present investigation entitled, "Genetic evaluation of elite lines of soybean [*Glycine max* (L.) Merrill]" was conducted at Botany Farm, Division of Botany, College of Agriculture, Pune during *Kharif* 2020. The results obtained are presented below:

4.1 Mean performance of the genotypes

The mean performance of 30 genotypes of soybean for 11 characters is given in Table No. 4.1.

4.1.1 Days to 50% flowering (No.)

The general mean of days to 50 percent flowering was observed 39.76 days. Sixteen genotypes were found to be early and fourteen genotypes were late than the general mean. The variation in days to 50 percent flowering ranged from 36.33 to 48.00 days. Among the genotypes KDS-1097 (36.33) was earliest in flowering followed by DS-228 (36.67). While, KDS-344 (48.00) was late in flowering followed by KDS-726 (47.00).

4.1.2 Nodulation count per plant at 50% flowering (No.)

The general mean of nodulation count per plant at 50 percent flowering was observed 54.98 nodules. Fourteen genotypes were found to have lower number of nodules than the general mean, while sixteen had higher number of nodules. The variation in nodulation count per plant at 50 percent flowering ranged from 19.67-92.00 nodules. GBIC-18758 (92.00) had the highest number of nodules at 50 percent flowering followed by KDS-1096 (91.00), while MAUS-732 (19.67) had the least number of nodules at 50 percent flowering followed by TS-46 (21.00).

4.1.3 Days to maturity (No.)

The general mean of number of days to maturity was observed 105.98. Nine genotypes were early and twenty one genotypes were late as compared to general mean. The variation in days to maturity ranged from 92.00 to 115.00. JS 93 05 (92.00) and KDS-1045 (96.00) were early in maturity. RSC-11-22 (115.00) and KDS-344 (114.33) were late in maturity.

4.1.4 Plant Height (cm.)

The general mean of plant height was observed 46.20 cm. Seventeen genotypes were dwarf and thirteen were taller as compared to general mean. The plant height ranged from 31.33 to 61.45 cm. KDS-344 genotype (61.45) was the tallest genotype followed by KDS-1096 (55.66). JS-9305 genotype was dwarf followed by KDS-753 (33.55).

Table No. 4.1 Mean performance of 30 genotypes of soybean for 11 characters

	Genotypes	Days to 50% flowering (No.)	Nodulation count per plant at 50 % flowering (No.)	Days to maturity (No.)	Plant height (cm.)	Branches per plant (No.)	Pods per plant (No.)	100 seed weight (g)	Pod Blight Incidence (%)	Seed yield per plant (g)	Protein content (%)	Oil content (%)
1.	AMS-20-19	39.00	58.00	107.33	48.99	4.22	78.00	13.17	7.34	25.67	37.62	18.91
2.	AMS-353	40.33	47.33	106.00	53.51	3.44	107.33	14.06	15.39	28.94	37.68	19.61
3.	AMS-MB-5-19	37.67	40.00	101.67	52.57	5.18	86.33	13.16	32.33	28.06	37.98	18.23
4.	AMS-100-39	39.00	83.67	97.00	43.82	4.85	88.00	14.37	9.58	37.74	38.92	18.30
5.	DS-228	36.67	46.67	104.67	42.48	4.77	92.00	15.87	13.14	26.45	39.25	17.92
6.	DSb-33	37.33	24.00	97.00	47.96	5.11	82.67	15.17	6.70	32.66	38.55	18.24
7.	DSb-36	41.00	29.00	110.00	53.99	4.67	54.33	12.70	9.15	17.33	39.09	17.28
8.	GBIC-18758	37.33	92.00	107.00	45.61	4.18	71.00	12.87	12.72	21.23	37.33	19.21
9.	HIMSO-1690	40.33	78.00	107.33	43.79	2.59	45.67	12.97	28.03	16.23	40.81	17.79
10.	JS-335	37.67	82.00	103.00	44.66	4.71	91.00	12.40	39.29	27.73	38.95	18.35
11.	JS 93 05	37.00	65.00	92.00	31.33	4.66	66.33	14.43	9.39	23.66	40.72	17.88
12.	KDS-344	48.00	39.67	114.33	61.45	4.83	59.67	12.83	7.22	28.01	39.64	17.99
13.	KDS-726	47.00	80.67	107.33	42.80	4.77	73.00	19.73	14.65	36.08	38.91	18.64
14.	KDS-753	40.00	56.33	105.67	33.55	3.44	67.00	18.70	10.31	28.89	39.29	19.23
15.	KDS-980	37.67	56.67	108.33	46.77	5.54	80.67	14.87	13.69	29.90	39.94	17.32
16.	KDS-992	38.33	51.33	107.67	49.22	5.99	97.67	16.13	32.10	38.73	39.07	18.48
17.	KDS-1045	39.67	25.00	96.00	45.66	5.43	53.33	15.03	13.30	20.06	39.95	18.75

(contd…)

	Genotypes	Days to 50% flowering (No.)	Nodulation count per plant at 50 % flowering (No.)	Days to maturity (No.)	Plant height (cm.)	Branches per plant (No.)	Pods per plant (No.)	100 seed weight (g)	Pod Blight Incidence (%)	Seed yield per plant (g)	Protein content (%)	Oil content (%)
18.	KDS-1095	37.67	63.67	107.00	46.11	5.22	41.33	17.33	29.12	17.82	39.81	18.15
19.	KDS-1096	39.33	91.00	112.33	55.66	4.77	76.33	15.13	14.33	29.16	39.62	18.53
20.	KDS-1097	36.33	36.33	106.00	54.55	5.62	56.67	11.57	15.88	20.47	38.42	18.75
21.	KDS-1144	41.33	50.33	107.67	50.44	4.77	63.67	15.40	11.3	23.46	38.93	17.93
22.	KDS-1149	41.00	25.00	105.00	44.16	5.44	84.33	13.50	31.17	34.60	39.74	18.36
23.	KDS-1150	41.00	40.67	107.00	35.77	4.29	45.33	12.83	18.46	14.50	39.89	18.91
24.	MAUS-732	40.33	19.67	106.33	45.86	3.72	45.00	12.07	9.15	13.50	40.92	17.77
25.	MAUS-8060	41.00	87.00	107.00	43.12	5.81	52.33	12.23	14.72	16.00	40.72	18.35
26.	NRC-142	41.33	75.00	111.33	42.72	4.05	51.00	12.40	28.56	17.32	40.64	17.65
27.	NRC-168	39.00	56.00	109.00	45.05	4.67	94.67	13.77	13.65	38.97	41.66	16.80
28.	RSC-11-22	40.67	70.00	115.00	34.00	3.51	58.33	13.50	30.40	19.81	39.58	18.15
29.	RVS-2011-76	40.00	58.33	106.00	51.88	4.44	99.33	12.90	25.34	38.66	40.85	17.76
30.	TS-46	39.67	21.00	107.33	48.61	5.44	69.33	11.70	10.78	20.87	41.08	16.51
	Mean	39.76	54.98	105.98	46.20	4.67	71.06	14.09	17.57	25.75	39.52	18.19
	C.V. (%)	3.61	1.43	1.06	5.60	10.69	5.03	6.38	14.50	6.32	1.56	1.37
	S.E.	0.83	0.45	0.65	1.49	0.29	2.06	0.52	1.47	0.94	0.36	0.14
	C.D. 5%	2.35	1.29	1.84	4.23	0.81	5.84	1.47	4.17	2.66	1.01	0.41

4.1.5 Branches per plant (No.)

The general mean of number of branches per plant was observed 4.67. Thirteen genotypes produced less number of branches and seventeen genotypes produced more number of branches per plant when compared to the general mean. The variation in number of branches per plant ranged from 2.59 to 5.99. KDS-992 (5.99) showed highest number of branches per plant followed by MAUS-8060 (5.81). HIMSO-1690 (2.59) had least number of branches per plant followed by AMS-353 and KDS-753 (3.44).

4.1.6 Pods per plant (No.)

The general mean of number of pods per plant was observed 71.06. Sixteen genotypes produced less number of pods and fourteen genotypes produced more number of pods per plant as compared to general mean. The variation in number of pods per plant ranged from 41.33 to 107.33. AMS-353 genotype (107.33) produced highest number of pods per plant followed by RVS-2011-76 (99.33). The genotype KDS-1095 (41.33) produced least number of pods per plant followed by MAUS-732 (45.00).

4.1.7 100 seed weight (g)

The general mean of 100 seed weight was observed 14.09 g. Twelve genotypes had more weight of 100 seeds and eighteen genotypes had less weight of 100 seeds than general mean. The variation for 100 seed weight ranged from 11.57 to 19.73 g. KDS-726 genotype (19.73) had the highest 100 seed weight followed by KDS-753 (18.70). KDS-1097 genotype (11.57) had least 100 seed weight followed by TS-46 (11.70).

4.1.8 Pod blight incidence (%)

The general mean of pod blight incidence was found 17.57 percent. Twenty genotypes had less pod blight incidence and ten had more as compared to general mean. The variation in pod blight incidence ranged from 6.70 to 39.29%. DSb-33 (6.70%) infected with least pod blight followed by KDS-344 (7.22%), while JS-335 genotype (39.29%) had highest pod blight incidence followed by AMS-MB-5-19 (32.33%)

4.1.9 Seed yield per plant (g)

The general mean for seed yield per plant was observed to be 25.75 g. Fifteen genotypes produced lower and fifteen genotypes produced higher seed yield per plant than the general mean. The variation in seed yield per plant ranged from 13.50 to 38.97 g. The genotype NRC-168 (38.97) had the highest yield per plant followed by KDS-992 (38.76). MAUS-732 (13.50) had the lowest yield followed by KDS-1150 (14.50).

4.1.10 Protein content (%)

The general mean of protein content was observed 39.52 percent. Fourteen genotypes contained less protein and sixteen genotypes contained more protein percent than general mean. The protein content in genotypes ranged from 37.33 to 41.66 percent. NRC-168 (41.66%) had the highest protein content followed by TS-46 (41.08%). GBIC-18758 (37.33%) had lowest protein content followed by AMS-20-19 (37.62%).

4.1.11 Oil content (%)

The general mean of oil content was observed 18.19 percent. Sixteen genotypes had higher oil content and fourteen genotypes had lower oil content than the general mean. The variation in oil content varied from 16.51 to 19.61 percent. AMS-353 genotype (19.61%) had the highest oil content followed by KDS-753 (19.23%). TS-46 genotype (16.51%) had the lowest oil content followed by NRC-168 (16.80%).

The genotype NRC-168 recorded highest *per se* performance for seed yield per plant and protein content. AMS-353 recorded higher number of pods per plant and oil content. KDS-726 exhibited highest performance for 100 seed weight and desirable *per se* performance for nodulation count per plant at 50 percent flowering. KDS-992 performed better in terms of branches per plant and pods per plant. JS 93 05 was desirably early to flower and earliest to mature. KDS-1097 was earliest to flower. DSb-33 showed lowest pod blight incidence.

Therefore it can be concluded that genotypes *viz.* NRC-168, AMS-353, KDS-726, KDS-992, JS 93 05, KDS-1097 and DSb-33 were the best genotypes having desired *per se* performance for yield components and can be used as potential parents in future crop improvement programme.

4.2 Analysis of variance

The analysis of variance (Table No. 4.2) revealed that the mean sum of squares due to genotypes for all the characters studied were highly significant, which indicated presence of appreciable amount of genetic variability among the genotypes.

Table no. 4.2 Analysis of Variance for 11 characters in soybean

Sr. No.	Characters	Mean sum of squares		
		Replications (2)	Treatments (29)	Error (58)
1	Days to 50% flowering (No.)	3.21	20.23**	2.06
2	Nodulation count per plant at 50 % flowering (No.)	0.71	1476.44**	0.62
3	Days to maturity (No.)	7.08	78.09**	1.26
4	Plant height (cm.)	6.45	137.48**	6.71
5	Branches per plant (No.)	0.22	1.86**	0.25
6	Pods per plant (No.)	6.18	1037.75**	12.75
7	100 seed weight (g)	0.22	11.76**	0.81
8	Pod Blight Incidence (%)	3.63	262.97**	6.49
9	Seed yield per plant (g)	1.99	182.72**	2.65
10	Protein content (%)	1.29	3.66**	0.38
11	Oil content (%)	0.05	1.42**	0.06

** significant at 1 percent level.

Values in parenthesis indicate degree of freedom.

4.3 Parameters of genetic variability

Range of variability, estimates of genotypic and phenotypic coefficient of variation, heritability percentage in broad sense, genetic advance and genetic advance expressed as percentage of mean are presented in Table No. 4.3.

4.3.1 Coefficients of variation

It was observed that the estimates for genotypic coefficients of variation (GCV) were lower than the phenotypic coefficients of variation (PCV) for all the characters. This indicates the effect of environmental factors on these characters.

The protein content exhibited lowest GCV (2.65) as well as PCV (2.80), while pod blight incidence had highest GCV (52.61) as well as PCV (53.28). It was followed by nodulation count per plant at 50 percent flowering, seed yield per plant, pods per plant, branches per plant, plant height, 100 seed weight, days to 50 percent flowering, days to maturity and oil content.

The highest difference between GCV and PCV values was observed for branches per plant (1.17) followed by pod blight incidence (0.67) indicating that environment played significant role in expression of these characters. Nodulation count per plant at 50 percent flowering, days to maturity and oil content had the lowest difference between GCV and PCV estimates indicating less role of environment in the phenotypic expression of these characters. This means that one can rely on phenotype alone while carrying out selection for these traits.

The characters pod blight incidence, nodulation count per plant at 50 percent flowering, seed yield per plant, pods per plant, branches per plant and plant height showed higher estimates of GCV and PCV. This shows presence of large variation in the genotypes for these characters. Therefore, simple selection can be opted for the improvement of these characters.

The estimates of GCV and PCV were high for plant height, number of pods per plant and seed yield per plant. These results were in confirmation with the findings of Patil *et al.* (2011) and Vachhan *et al.* (2014). In addition to this, Jain *et al.* (2018) showed similar results. Similar results were obtained by Saharan *et al.* (2006), Chandel *et al.* (2017) and Kuswantoro *et al.* (2018) for branches per plant, pods per plant and seed yield per plant.

4.3.2 Heritability (b.s.)

Heritability indicates effectiveness of selection on the basis of phenotypic performance and it does not mean a high genetic gain for that character. A character with high genetic gain indicates additive gene action. Such a character can be improved by simple selection. On the other hand, high heritability with low genetic gain indicates non-additive gene action and such trait can be improved in hybridisation.

In the present study, the estimates of heritability (b.s.) ranged from 86.60 percent to 99.96 percent. The lowest heritability was observed for branches per plant (86.60%) followed by protein content (89.60%), days to 50 percent flowering (89.80%). The highest heritability was observed for nodulation count per plant at 50 percent flowering (99.96%) followed by pods per plant (98.80%), seed yield per plant (98.50%), days to maturity (98.40%), pod blight incidence (97.50%), oil content (95.60%), plant height (95.10%), 100 seed weight (93.10%) which indicates the least effect of environment on these characters.

Similar estimates of high heritability were observed for plant height, number of pods per plant, seed yield per plant, days to maturity by Chamundeshwari and Aher (2003), Patil *et al.* (2011), Osekita *et al.* (2013) and Kumar *et al.* (2013).

Table No. 4.3 Parameters of Genetic variability in 30 genotypes of soybean

Sr. No.	Character	Mean	Range	GCV (%)	PCV (%)	h^2 % (B.S.)	Genetic Advance	Gen. Adv as % of Mean
1	**Days to 50% flowering (No.)**	39.76	36.33 - 48.00	6.19	6.53	89.80	4.80	12.08
2	**Nodulation count per plant at 50 % flowering (No.)**	54.98	19.67 - 92.00	40.34	40.35	99.96	45.68	83.09
3	**Days to maturity (No.)**	105.98	92.00 - 115.00	4.77	4.81	98.40	10.34	9.76
4	**Plant height (cm.)**	46.20	31.33 – 61.45	14.29	14.65	95.10	13.26	28.71
5	**Branches per plant (No.)**	4.67	2.59 – 5.99	15.68	16.85	86.60	1.40	30.06
6	**Pods per plant (No.)**	71.06	41.33 – 107.33	26.01	26.18	98.80	37.84	53.26
7	**100 seed weight (g)**	14.09	11.57 – 19.73	13.56	14.05	93.10	3.80	26.95
8	**Pod Blight Incidence (%)**	17.57	6.70 – 39.29	52.61	53.28	97.50	18.81	107.04
9	**Seed yield per plant (g)**	25.75	13.50 – 38.97	30.09	30.31	98.50	15.84	61.53
10	**Protein content (%)**	39.52	37.33 – 41.66	2.65	2.80	89.60	2.04	5.16
11	**Oil content (%)**	18.19	16.51 – 19.61	3.70	3.78	95.60	1.36	7.45

4.3.3 Genetic Advance

The relative role of genetic factors in expression of phenotypes can be obtained from calculation of heritability (Falconer, 1989). The expected genetic gain from the selection applied in a population can be measured by genetic advance. High heritability with high genetic advance leads to the best efficiency for selection.

The nodulation count per plant at 50 percent flowering (45.68) showed highest genetic advance, followed by followed by pods per plant (37.84) and pod blight incidence (18.81). The lowest genetic advance was observed for oil content (1.36) followed by branches per plant (1.40), protein content (2.04) and 100 seed weight (3.80).

In the present investigation, high heritability with high genetic advance was observed for nodulation count per plant at 50 percent flowering, pods per plant, pod blight incidence, seed yield per plant, plant height and days to maturity indicating that these traits could be effective for genetic improvement. Similar findings were reported by Vachhan *et al.* (2014), Akram *et al.* (2016), Chandrawat *et al.* (2017), Jain *et al.* (2018) and Bairwa *et al.* (2020).

High heritability and low genetic advance for oil content, branches per plant, protein content and 100 seed weight indicate that these characters are controlled by non-additive gene action *i.e.* dominance or epistasis and thus heterosis breeding will be helpful for the improvement of these characters.

The highest genetic advance as a percentage of mean was observed for pod blight incidence (107.04) followed by nodulation count per plant at 50 percent flowering (83.09) and seed yield per plant (61.53) while, it was lowest for protein content (5.16) followed by oil content (7.45).

Therefore, considering the estimates of genetic parameters like genotypic coefficient of variation, heritability and genetic advance nodulation count per plant, pods per plant and seed yield are the most important characters in soybean for further improvement through selection.

4.4 Correlation

A large amount of variation in the characters is the basis of selection in a breeding programme. The study of correlation gives the inter-relationship among the quantitative traits which is useful in the selection of breeding method for crop improvement. The genetic correlation coefficient provides a measure of association between characters which is helpful in overall crop improvement.

Yield is a complex character and it is the result of interaction between various yield components. The success of any breeding programme depends on the efficiency of selection. This is where study of correlation becomes necessary for the selection of characters for future breeding programme.

In the present study, various quantitative characters were studied and their relation with yield as well as among themselves was examined using correlation analysis and the genotypic and phenotypic correlation coefficients between yield and its related components are presented in Table No. 4.4.

The seed yield per plant showed highly significant positive association with pods per plant (0.8471), followed by 100 seed weight (0.4087) and branches per plant (0.2836) at both genotypic and phenotypic level. The characters plant height (0.1784), nodulation count per plant at 50 percent flowering (0.0882), pod blight incidence (0.0520), days to 50 percent flowering (0.0276) and oil content (0.0194) were positively associated but non-significant at the genotypic as well as phenotypic level. The characters protein content (-0.1600) and days to maturity (-0.1566) showed non-significant association with seed yield per plant.

Similar findings of positive correlation of seed yield per plant with pods per plant were recorded by Mukhekar *et al.* (2004), Kumar *et al.* (2005), Faisal *et al.* (2006), Sonwane *et al.* (2006), Nag *et al.* (2007), Machikowa and Laosuwan (2011), Kumar *et al.* (2013), Shree *et al.* (2017) and Shekar *et al.* (2018). Chandel *et al.* (2005), Sonwane *et al.* (2006), Shree *et al.* (2017) obtained similar positive significant correlation of seed yield with 100 seed weight. Mukhekar *et al.* (2004), Kumar *et al.* (2005), Malik *et al.* (2007), Machikowa and Laosuwan (2011) showed positive and significant correlation of seed yield with branches per plant.

Saharan *et al.* (2006), Iqbal *et al.* (2010), Mahbub *et al.* (2015) also reported similar results.

Shrivastava *et al.* (1998) and Sharma *et al.* (2008) also obtained similar negative correlation of seed yield per plant with days to maturity and protein content with seed yield per plant respectively.

The inter relationship between component characters at genotypic and phenotypic level is presented below.

Days to 50% flowering was highly significantly and positively correlated with days to maturity (0.4664). It showed positive and non-significant correlation with plant height (0.1822), protein content (0.1687), 100 seed weight (0.1448), seed yield per plant (0.0276) and nodulation count per plant at 50 percent flowering (0.0056).It showed negative and significant correlation with pods per plant (-0.2518). It showed negative but non-significant correlation with branches per plant (-0.1662), pod blight incidence (-0.1565) and oil content (-0.0169).

Nodulation count per plant at 50 percent flowering was significantly and positively correlated with pod blight incidence (0.2233) and oil content (0.2169). It showed positive and non-significant correlation with 100 seed weight (0.1781), days to maturity (0.1568), seed yield per plant (0.0882) and pods per plant (0.0488). It showed negative and significant correlation with plant height (-0.2505) and branches per plant (-0.2446). It showed negative but non-significant correlation with protein content (-0.0621).

Days to maturity was positively and significantly correlated with plant height (0.3011). It showed positive but non-significant correlation with pod blight incidence (0.1480) and protein content (0.0885). Days to maturity was significantly and negatively correlated with branches per plant (-0.2364) and negatively and non-significantly correlated with 100 seed weight (-0.1311).

Plant height showed positive and significant correlation with number of branches per plant (0.3078) and pods per plant (0.2221). It showed positive and non-significant correlation with seed yield per plant (0.1784). Plant height showed negative and significant correlation with protein content (-0.2948) and 100 seed weight (-0.2624). It showed negative and non-significant correlation with protein content (-0.2624) and pod blight incidence (-0.1092).

Branches per plant showed positive and significant correlation with seed yield per plant (0.2836) whereas it showed positive but non-significant correlation with pods per plant (0.1784), 100 seed weight (0.0478) and pod blight incidence (0.0008). It showed negative but non-significant correlation with oil content (-0.1771) and protein content (-0.0468).

Pods per plant showed highly positive significant correlation with seed yield per plant (0.8471). It showed positive and non-significant correlation with 100 seed weight (0.1645), pod blight incidence (0.1080) and oil content (0.0803), whereas it showed negative and significant correlation with protein content (-0.3281).

100 seed weight had highly positive and significant association with seed yield per plant (0.4078) and oil content (0.2956). It showed negative and non-significant correlation with protein content (-0.1820).

Table 4.4 Genotypic correlation (above diagonal) and phenotypic correlation (below diagonal) of 11 characters in 30 genotypes of soybean

Observations	Days to 50% flowering (No.)	Nodulation count per plant at 50 % flowering (No.)	Days to maturity (No.)	Plant height (cm.)	Branches per plant (No.)	Pods per plant (No.)	100 seed weight (g)	Pod Blight Incidence (%)	Protein content (%)	Oil content (%)	Seed yield per plant (g)
Days to 50% flowering (No.)	1	0.0056	0.4664**	0.1822	-0.1662	-0.2518*	0.1448	-0.1565	0.1687	-0.0169	0.0276
Nodulation count per plant at 50 % flowering(No.)	0.0067	1	0.1568	-0.2505*	-0.2446*	0.0488	0.1781	0.2233*	-0.0621	0.2169*	0.0882
Days to maturity (No.)	0.4539**	0.1559	1	0.3011**	-0.2364*	-0.1906	-0.1311	0.1480	0.0885	-0.1585	-0.1566
Plant height (cm.)	0.1659	-0.2447*	0.2916**	1	0.3078**	0.2221*	-0.2624*	-0.1092	-0.2948**	-0.0718	0.1784
Branches per plant (No.)	-0.1712	-0.2287*	-0.2131*	0.2941**	1	0.1748	0.0478	0.0008	-0.0468	-0.1771	0.2836**
Pods per plant (No.)	0.2380*	0.0490	-0.1858	0.2147*	0.1653	1	0.1645	0.1080	-0.3281**	0.0803	0.8471**
100 seed weight (g)	0.1287	0.1714	-0.1302	-0.2542*	0.0424	0.1434	1	-0.0936	-0.1820	0.2956**	0.4087**
Pod Blight Incidence (%)	-0.1376	0.2211*	0.1505	-0.1121	-0.0033	0.1052	-0.0900	1	0.0502	0.0274	0.0520
Protein content (%)	0.1497	-0.0588	0.0877	-0.2747**	-0.0114	-0.3038**	-0.1674	0.0540	1	-0.7262**	-0.1600
Oil Content (%)	-0.0081	0.2134*	-0.1537	-0.0790	-0.1751	0.0799	0.2767**	0.0277	-0.6791**	1	0.0194

*, ** significant at 5 % and 1% level respectively

Pod blight incidence had positive and non-significant correlation with seed yield per plant (0.0520), protein content (0.0502) and oil content (0.0274). It showed negative and non-significant correlation with 100 seed weight (-0.0936).

Protein content showed highly negative and significant correlation with oil content (-0.7262) and negative non-significant correlation with seed yield per plant (-0.1600).

Oil content showed positive and non-significant correlation with seed yield per plant (0.0194) at both genotypic and phenotypic level.

The characters days to 50 percent flowering, days to maturity, plant height and branches per plant showed highly significant and positive correlation among themselves indicating that simultaneous selection for these characters would result in improvement of high yielding soybean genotypes.

4.5 Path coefficient analysis

Path analysis is a partial coefficient which splits correlation coefficient into direct and indirect effects. In the present investigation, path analysis was done as per the procedure given by Dewey and Lu (1959) to know the direct and indirect effects of various characters. Correlation along with path analysis proves more reliable for application in breeding programme.

Yield is a complex character and the result of several component traits. Some characters contribute directly towards yield, whereas, others indirectly affect the yield. Hence, there is a need to study direct and indirect effects of various characters on seed yield.

The inter-relationship of the characters as revealed by the path coefficient analysis using genotypic and phenotypic correlation is presented in Table No. 4.5 and Table No. 4.6 respectively.

The residual effect determines how best the causal factors account for the variability of the dependent factor, seed yield per plant, in this case. In this study, residual effect was low (0.3435) indicating that characters studied account for sufficient variability in seed yield per plant of soybean. Therefore, seed yield was the result of mainly days to 50 percent flowering, nodulation count per plant at 50 percent flowering, days to maturity, plant height, branches per plant, pods per plant, 100 seed weight, pod blight incidence, protein content and oil content as they were significantly correlated with it. These characters affected the seed yield directly and indirectly through other characters.

It is evident from Table No. 4.5 and Table No. 4.6 that the characters pods per plant had high direct positive effect on seed yield per plant, while 100 seed weight and days to 50 percent flowering had moderate direct effect on seed yield per plant. Thus, direct selection of these traits will be beneficial in crop improvement programme.

Table No. 4.5 Direct (diagonal) and Indirect (above and below diagonal) path effects of different characters towards seed yield at genotypic level in soybean

Sr. No.	Character	Days to 50% flowering (No.)	Nodulation count per plant at 50 % flowering (No.)	Days to maturity (No.)	Plant height (cm.)	Branches per plant (No.)	Pods per plant (No.)	100 seed weight (g)	Pod Blight Incidence (%)	Protein content (%)	Oil content (%)	Seed yield per plant (g)
1	**Days to 50% flowering (No.)**	**0.2333**	0.0013	0.1088	0.0425	-0.0388	-0.0587	0.0338	-0.0365	0.0394	-0.0039	0.0276
2	**Nodulation count per plant at 50 % flowering (No.)**	0.0004	**0.0698**	0.0109	-0.0175	-0.0171	0.0034	0.0124	0.0156	-0.0043	0.0151	0.0882
3	**Days to maturity (No.)**	-0.0354	-0.0119	**-0.0758**	-0.0228	0.0179	0.0144	0.0099	-0.0112	-0.0067	0.0120	-0.1566
4	**Plant height (cm.)**	0.0097	-0.0133	0.0160	**0.0532**	0.0164	0.0118	-0.0140	-0.0058	-0.0157	-0.0038	0.1784
5	**Branches per plant (No.)**	-0.0251	-0.0369	-0.0357	0.0464	**0.1509**	0.0264	0.0072	0.0001	-0.0071	-0.0267	0.2836**
6	**Pods per plant (No.)**	-0.2169	0.0420	-0.1642	0.1913	0.1505	**0.8612**	0.1417	0.0930	-0.2826	0.0692	0.8471**
7	**100 seed weight (g)**	0.0359	0.0441	-0.0325	-0.0650	0.0118	0.0407	**0.2476**	-0.0232	-0.0451	0.0732	0.4087**
8	**Pod Blight Incidence (%)**	-0.0018	0.0026	0.0017	-0.0013	0.0000	0.0013	-0.0011	**0.0117**	0.0006	0.0003	0.0520
9	**Protein content (%)**	0.0276	-0.0101	0.0145	-0.0482	-0.0076	-0.0537	-0.0298	0.0082	**0.1635**	-0.1188	-0.1600
10	**Oil Content (%)**	0.0000	0.0006	-0.0005	-0.0002	-0.0005	0.0002	0.0008	0.0001	-0.0021	**0.0028**	0.0194

(R= 0.3435). *, Significant at 5 and 1 percent respectively**

Table No. 4.6 Direct (diagonal) and Indirect (above and below diagonal) path effects of different characters towards seed yield at phenotypic level in soybean

Sr. No.	Character	Days to 50% flowering (No.)	Nodulation count per plant at 50 % flowering (No.)	Days to maturity (No.)	Plant height (cm.)	Branches per plant (No.)	Pods per plant (No.)	100 seed weight (g)	Pod Blight Incidence (%)	Protein content (%)	Oil content (%)	Seed yield per plant (g)
1	**Days to 50% flowering (No.)**	**0.2226**	0.0015	0.1010	0.0369	-0.0381	-0.0530	0.0286	-0.0306	0.0333	-0.0018	0.0265
2	**Nodulation count per plant at 50 % flowering (No.)**	0.0005	**0.0682**	0.0106	-0.0167	-0.0156	0.0033	0.0117	0.0151	-0.0040	0.0146	0.0874
3	**Days to maturity (No.)**	-0.0403	-0.0138	**-0.0887**	-0.0259	0.0189	0.0165	0.0116	-0.0134	-0.0078	0.0136	-0.1544
4	**Plant height (cm.)**	0.0118	-0.0174	0.0207	**0.0710**	0.0209	0.0152	-0.0180	-0.0080	-0.0195	-0.0056	0.1773
5	**Branches per plant (No.)**	-0.0205	-0.0274	-0.0256	0.0353	**0.1200**	0.0198	0.0051	0.0004	-0.0014	-0.0210	0.2602**
6	**Pods per plant (No.)**	-0.1998	0.0411	-0.1559	0.1802	0.1387	**0.8393**	0.1204	0.0883	-0.2550	0.0671	0.8394**
7	**100 seed weight (g)**	0.0347	0.0462	-0.0351	-0.0684	0.0114	0.0386	**0.2693**	-0.0242	-0.0451	0.0745	0.3968**
8	**Pod Blight Incidence (%)**	-0.0021	0.0034	0.0023	-0.0017	0.0001	0.0016	-0.0014	**0.0155**	0.0008	0.0004	0.0484
9	**Protein content (%)**	0.0195	-0.0077	0.0114	-0.0358	-0.0015	-0.0396	-0.0218	0.0070	**0.1302**	-0.1188	-0.1471
10	**Oil Content (%)**	0.0003	0.0067	-0.0048	-0.0025	-0.0055	-0.0025	-0.0087	-0.0009	0.0213	**-0.0314**	0.0220

(R= 0.3435). *, Significant at 5 and 1 percent respectively**

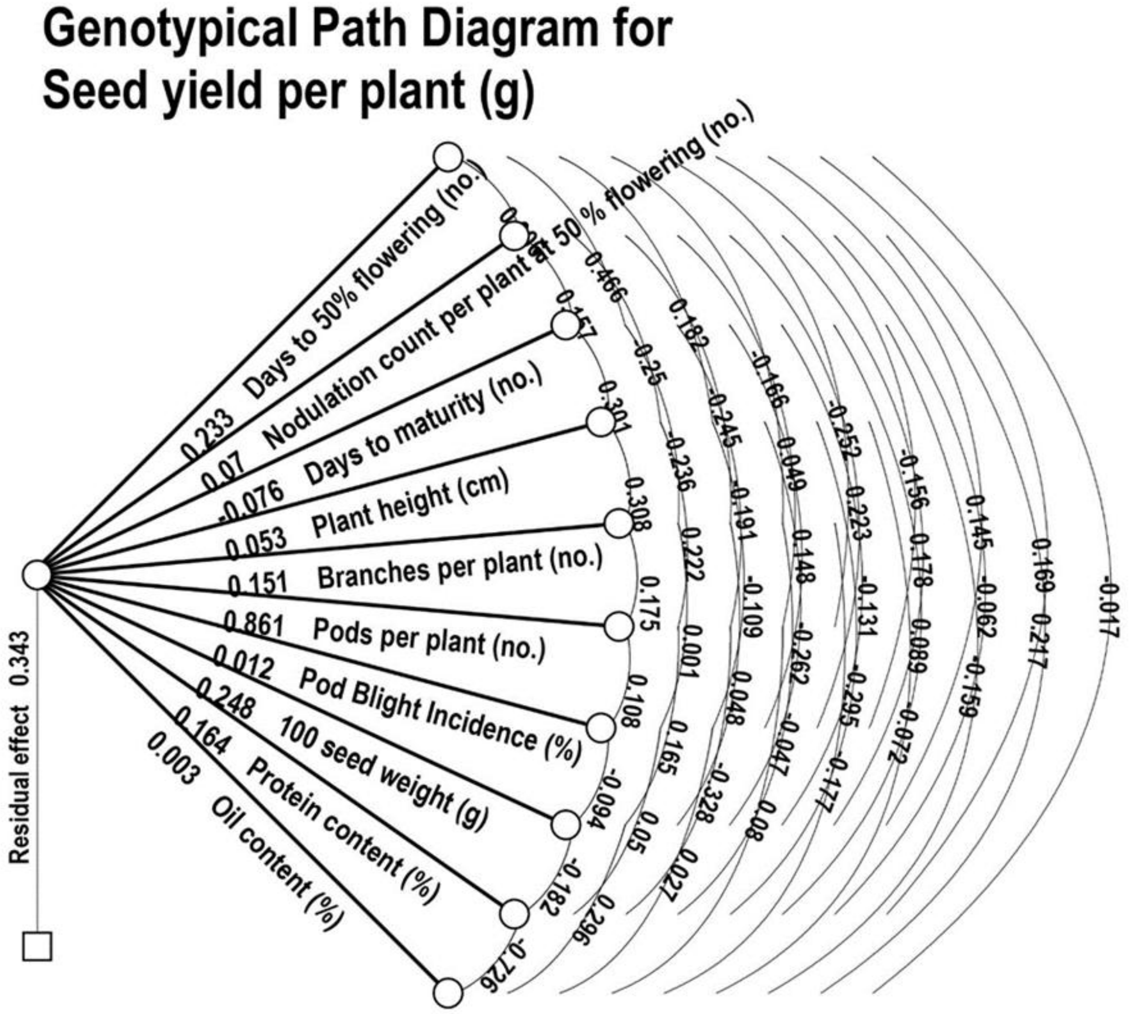


Fig 1. Genotypical path diagram for seed yield per plant in soybean

4.5.1 Days to 50% flowering (No.)

Its direct effect on seed yield per plant was positive and moderate (0.2333). The indirect effect of this trait *via* days to maturity (0.1088) was positive and low. While remaining characters showed negligible indirect effect, with pods per plant, branches per plant, pod blight incidence and oil content negative and the rest positive.

4.5.2 Nodulation count per plant at 50% flowering (No.)

The direct effect was positive and negligible (0.0698). The indirect effect *via* pod blight incidence, oil content, 100 seed weight, days to maturity was positive and negligible, while *via* plant height and branches per plant was negative and negligible.

4.5.3 Days to maturity (No.)

The direct effect was negative and negligible (-0.0758). The indirect effect *via* branches per plant, pods per plant, oil content and 100 seed weight was positive and negligible while *via* days to 50% flowering, plant height, nodulation count per plant at 50 percent flowering, pod blight incidence and protein content was negative and negligible.

4.5.4 Plant height (cm.)

Its direct effect on seed yield per plant was positive and negligible (0.0532). The indirect effect *via* branches per plant, days to maturity, pods per plant and days to 50 percent flowering was positive and negligible. The indirect effect *via* protein content, 100 seed weight, nodulation count per plant at 50 percent flowering, pod blight incidence and oil content was negative and negligible.

4.5.5 Branches per plant (No.)

The direct effect of this trait on seed yield per plant was positive and low (0.1509). The indirect effect *via* plant height, pods per plant, 100 seed weight and pod blight incidence was positive and negligible. The indirect effect *via* nodulation count per plant at 50 percent flowering, days to maturity, oil content, days to 50 percent flowering and protein content was negative and negligible.

4.5.6 Pods per plant (No.)

The direct effect of this trait in seed yield per plant was positive and high (0.8612). The indirect effect of pods per plant through plant height (0.1913), branches per plant (0.1505) and 100 seed weight (0.1417) was positive and low. Protein content (-0.2826) and days to 50% flowering (-0.2169) had negative and moderate whereas, days to maturity (-0.1642) had negative and low indirect effect. Pod blight incidence, oil content and nodulation count per plant at 50 percent flowering had positive negligible indirect effect.

4.5.7 100 seed weight (g)

100 seed weight had positive and moderate direct effect (0.2476) on seed yield. Its indirect effect *via* oil content, nodulation count per plant at 50 percent flowering, pods per plant, days to 50 percent flowering and branches per plant was positive and negligible, while for plant height, protein content, days to maturity and pod blight incidence was negative and negligible.

4.5.8 Pod blight incidence (%)

The direct effect was positive and negligible (0.0117). The indirect effect *via* nodulation count per plant at 50 percent flowering, days to maturity, pods per plant, protein content, oil content and branches per plant was positive and negligible. Days to 50 percent flowering, plant height and 100 seed weight showed negative and negligible indirect effect.

4.5.9 Protein content (%)

This trait had positive and low direct effect (0.1635) on seed yield per plant. Oil content (-0.1188) had negative and low indirect effect. Days to 50 percent flowering, days to maturity and pod blight incidence had positive and negligible indirect effect while the rest of the traits showed negative and negligible indirect effect.

4.5.10 Oil content (%)

This trait had positive and negligible direct effect (0.0028). 100 seed weight, nodulation count per plant at 50 percent flowering, pods per plant, pod blight incidence and days to 50 percent flowering showed positive negligible indirect effect and the rest of the traits showed negative negligible indirect effect.

The characters pods per plant, 100 seed weight and days to 50 percent flowering had high to moderate positive direct effect on seed yield per plant. Correlation of these characters with seed yield per plant was positively significant except for days to 50 percent flowering, indicating true and perfect relationship between yield and these characters and suggesting that direct selection based on these characters would help in selecting for high yielding genotypes of soybean. Similar findings were reported by Gohil *et al.* (2003), Mukhekar *et al.* (2004), Kamwal *et al.* (2009), Ghodrati *et al.* (2013), Jain *et al.* (2015), Akram *et al.* (2016), Shekar *et al.* (2018) and Parihar *et al.* (2020).

Days to maturity had negative direct effect on seed yield per plant. Days to maturity is also non-significantly and negatively correlated with seed yield per plant. Similar result was obtained by Mukhekar *et al.* (2004) and Malik *et al.* (2006).

The characters number of pods per plant and days to 50 percent flowering had indirect effect on seed yield per plant. Similar findings were reported by Gohil *et al.* (2003), Machikowa and Laosuwan (2011) and Jain *et al.* (2015) for pods per plant.

4.6 Genetic divergence

Genetic diversity between genotypes was calculated by distance statistic (D^2) given by Mahalanobis (1936). This is used in plant breeding for classifying the genetic stocks, on the basis of genetic divergence between populations.

4.6.1 Genetic distance (D^2)

Genetic divergence in 30 genotypes of soybean was measured by Mahalanobis's (1936) D^2 statistics. The calculated D^2 values ranged from 15.27 to 81.08 (Table No. 4.8).

4.6.2 Cluster formation

Cluster formation and cluster divergence are used as the basis for selection of better parents for hybridization programme. Cluster formation was done by following Tocher's method as described by Rao (1952). The 30 genotypes were grouped into 6 clusters. Cluster IV was the largest with 10 genotypes followed by clusters II, III, and I with 8, 6 and 4 genotypes respectively. While remaining two clusters *viz.*, V and IV were solitary.

Grouping of genotypes into six clusters suggested the presence of relatively high amount of genetic diversity in the material under investigation.

The genotypes *viz.,* AMS-353 and JS 93 05 were monogenotypic which indicated wide diversity from the genotypes in other clusters as well as from each other. Thus, these genotypes have entirely different genetic makeup from the others.

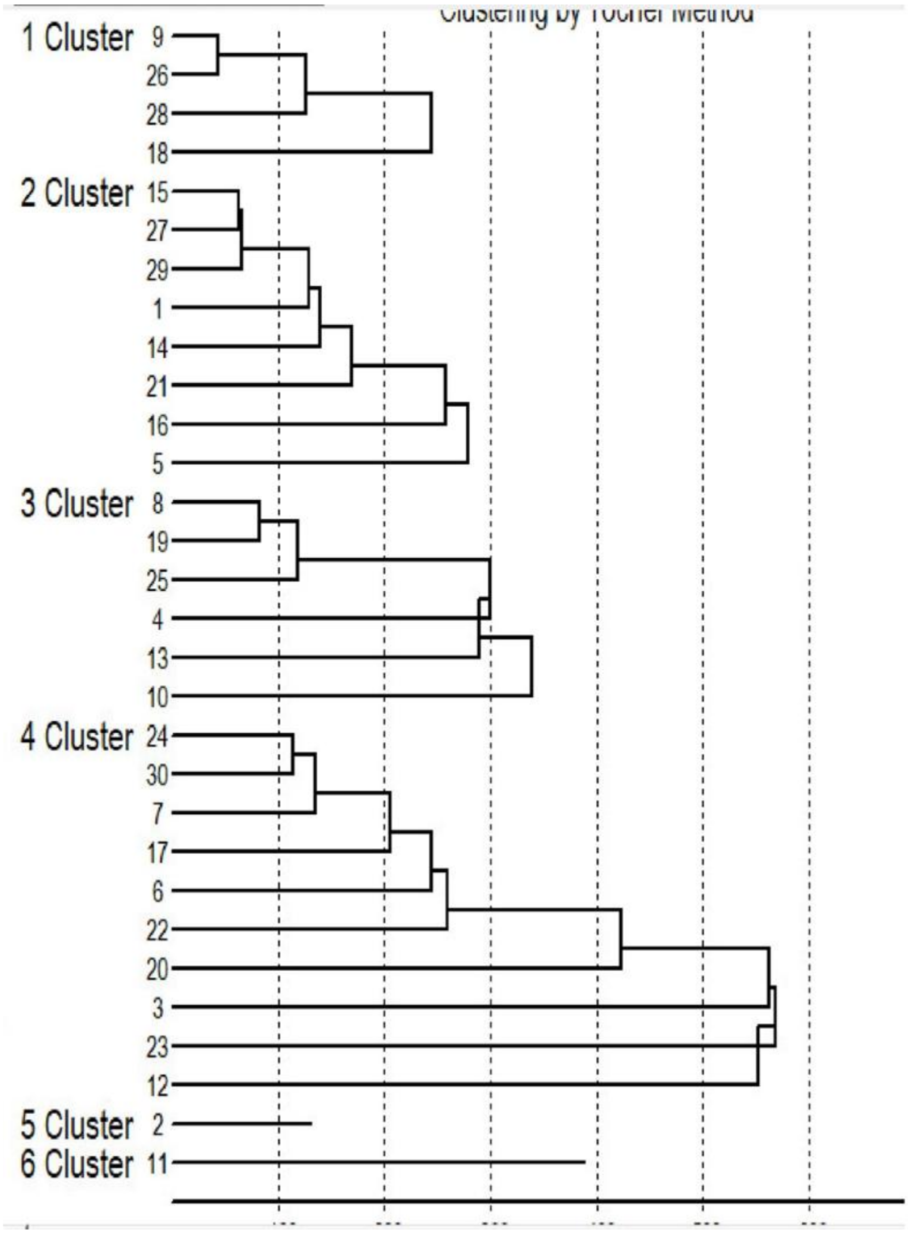


Fig. 2. Dendrogram: Cluster formation of genotypes

Table No. 4.7 Distribution of 30 genotypes of soybean into different clusters

Cluster	No. of genotypes included	Name of genotypes
I	4	HIMSO-1690, NRC-142, RSC-11-22, KDS-1095
II	8	KDS-980, NRC-168, RVS-2011-76, AMS-20-19, KDS-753, KDS-1144, KDS-992, DS-228
III	6	GBIC-18758, KDS-1096, MAUS-8060, AMS-100-39, KDS-726, JS-335
IV	10	MAUS-732, TS-46, DSb-36, KDS-1045, DSb-33, KDS-1149, KDS-1097, AMS-MB-5-19, KDS-1150, KDS-344
V	1	AMS-353
VI	1	JS 93 05

4.6.3 Intra and inter-cluster distance

The average inter and intra cluster 'D' values are presented in Table No. 4.8. The maximum inter cluster distance was found between cluster III and IV (9.00), followed by cluster III and V (7.94) and cluster I and IV (7.91) suggesting that genotypes included in the clusters might have originated from different genetic pools. Whereas the minimum inter cluster distance was found between cluster II and V (4.73). Considering the intra cluster distance, cluster IV had had maximum intra cluster distance (4.71) suggesting that the genotypes included in this cluster might have different genetic makeup making this cluster heterogenous, whereas, intra cluster distance was not found in the cluster V and VI as they were solitary clusters.

Similar results were also seen by Dev Vart *et al.* (2002), Sharma *et al.* (2005), Dhapke *et al*. (2011) and Dubey *et al.* (2018).

Table No. 4.8 Average intra and inter cluster D^2 and D (in parenthesis) values of 6 clusters formed from 30 genotypes of soybean

Cluster	I	II	III	IV	V	VI
I	**15.29 (3.91)**	32.56 (5.71)	27.27 (5.22)	62.49 (7.91)	47.87 (6.92)	23.48 (4.84)
II		**15.27 (3.91)**	48.20 (6.94)	38.84 (6.23)	22.37 (4.73)	26.94 (5.19)
III			**18.48 (4.30)**	81.08 (9.00)	62.99 (7.94)	33.40 (5.78)
IV				**22.22 (4.71)**	29.81 (5.46)	55.45 (7.45)
V					**0**	41.03 (6.41)
VI						**0**

4.6.4 Cluster means for different characters

The mean performances of cluster values of eleven characters are presented in Table No. 4.9. A considerable inter cluster variation in respect of cluster was observed among the various clusters for the eleven characters studied. Based on mean performances of clusters for 11 characters, it is revealed that a wide range of variability among the clusters is present for all the characters.

4.6.4.1 Days to 50% flowering

The cluster mean for days to 50 percent flowering varied from 37.00 (cluster VI) to 40.33 (cluster V). Cluster III (40.22) and cluster IV (40.20) showed higher cluster means.

4.6.4.2 Nodulation count per plant at 50% flowering

The cluster mean for nodulation count per plant at 50 percent flowering varied from 30.03 (cluster IV) to 86.06 (cluster III). Cluster I (71.67) and cluster VI (65.00) showed higher cluster means.

4.6.4.3 Days to maturity

The cluster mean for days to maturity varied from 92.00 (cluster VI) to 110.17 (cluster I). Cluster II (107.04) and cluster V (106.00) showed higher cluster means.

4.6.4.4 Plant height

The cluster mean for plant height varied from 31.33 (cluster VI) to 53.51 (cluster V). Cluster IV (49.06) and cluster II (46.05) showed higher cluster means.

4.6.4.5 Branches per plant

The cluster mean for branches per plant varied from 3.44 (cluster V) to 4.97 (cluster IV). Cluster III (4.84) and cluster II (4.73) showed higher cluster means.

4.6.4.6 Pods per plant

The cluster mean for pods per plant varied from 107.33 (cluster V) to 49.08 (cluster I). The cluster II (84.13) and cluster III (75.28) showed higher cluster means.

4.6.4.7 100 seed weight

The cluster mean for 100 seed weight varied from 13.06 (cluster IV) to 15.10 (cluster II). The cluster III (14.46) and cluster V (14.43) showed higher cluster means.

4.6.4.8 Pod blight incidence

The cluster mean for pod blight incidence varied from 9.39 (cluster VI) to 29.03 (cluster I). Cluster III (17.55) showed higher cluster mean.

4.6.4.9 Seed yield per plant

The cluster mean for seed yield per plant varied from 17.80 (cluster I) to 31.34 (cluster II). The cluster V (28.94) and cluster III (27.99) showed higher cluster means.

4.6.4.10 Protein content

The cluster mean for protein content varied from 37.68 (cluster V) to 40.72 (cluster VI). The cluster I (40.21) and cluster II (39.59) showed higher cluster means.

4.6.4.11 Oil content

The cluster mean for oil content varied from 17.88 (cluster IV) to 19.61 (cluster V). The cluster III (18.56) showed higher cluster mean.

Table No. 4.9 Mean performance of 6 clusters for 11 characters in soybean

Cluster no.	**Days to 50% flowering (No.)**	**Nodulation count per plant at 50 % flowering (No.)**	**Days to maturity (No.)**	**Plant height (cm.)**	**Branches per plant (No.)**	**Pods per plant (No.)**	**100 seed weight (g)**	**Pod Blight Incidence (%)**	**Seed yield per plant (g)**	**Protein content (%)**	**Oil content (%)**
I	40.00	71.67	110.17	41.66	3.84	49.08	14.05	29.03	17.80	40.21	17.94
II	39.00	54.21	107.04	46.05	4.73	84.13	15.10	15.86	31.34	39.59	18.04
III	40.22	86.06	105.61	45.94	4.84	75.28	14.46	17.55	27.99	39.08	18.56
IV	40.20	30.03	105.07	49.06	4.97	63.70	13.06	15.41	23.01	39.52	18.08
V	40.33	47.33	106.00	53.51	3.44	107.33	14.07	15.39	28.94	37.68	19.61
VI	37.00	65.00	92.00	31.33	4.66	66.33	14.43	9.39	23.66	40.72	17.88

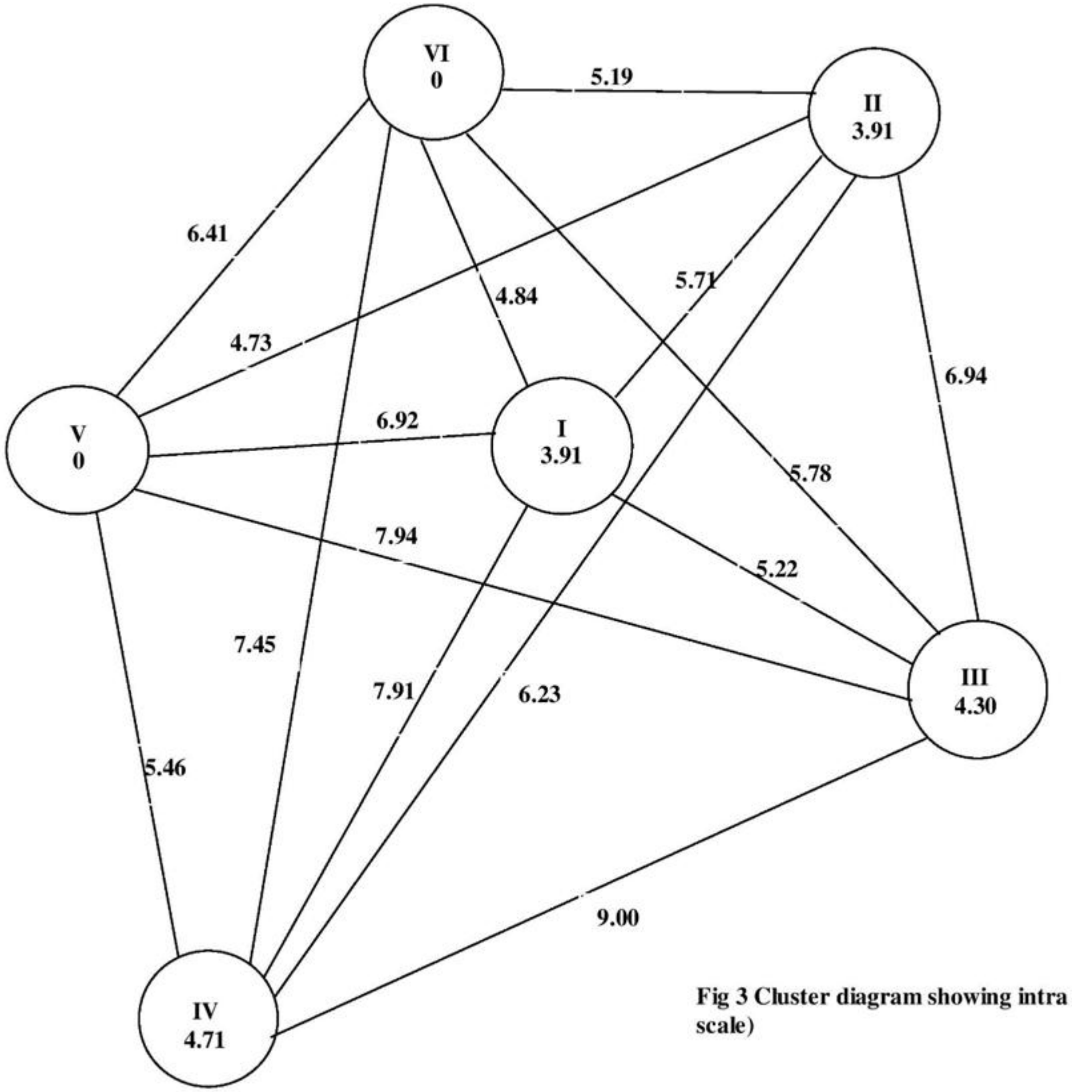


Fig 3 Cluster diagram showing intra and inter cluster distance (Not to scale)

4.7 Percent contribution of 11 characters for divergence

All the 30 genotypes of soybean were studied for 11 characters and the data collected was used to determine divergence (Table No. 4.10). Out of the 11 characters studied, the character nodulation count per plant at 50 percent flowering (81.15%) showed maximum contribution to divergence. It was followed by pods per plant (5.75%), days to maturity (4.14%), pod blight incidence (3.91%), oil content (2.06%) and seed yield per plant (1.61%). The positive contriution of these yield components in genetic divergence may considerably help in selecting genotypes for yield. Plant height (0.69%), 100 seed weight (0.46%) and days to 50% flowering (0.23%) contributed less to divergence. The remaining characters did not contribute to divergence.

Similar results were also reported by Chandankar *et al.* (2002), Sharma *et al.* (2005), Kayande *et al.* (2008) and Mishra *et al.* (2018).

Table No. 4.10 Percent contribution of 11 characters for divergence in soybean

Sr. No.	Source	Times ranked first	Contribution %
1	Days to 50% flowering (No.)	1	0.23%
2	Nodulation count per plant at 50 % flowering (No.)	353	81.15%
3	Days to maturity (No.)	18	4.14%
4	Plant height (cm.)	3	0.69%
5	Branches per plant (No.)	0	0.00%
6	Pods per plant (No.)	25	5.75%
7	100 seed weight (g)	2	0.46%
8	Pod Blight Incidence (%)	17	3.91%
9	Seed yield per plant (g)	7	1.61%
10	Protein content (%)	0	0.00%
11	Oil content (%)	9	2.06%
		Total	100%

4.8 Genetic divergence and selection of potential parents

Crop improvement programme requires parents with high diversity as the success of any crop improvement programme depends on the selection of the best parents. Therefore, diversity among genotypes was studied to obtain best potential parents.

The possible limits of parental divergence within which there are high chances of occurrence of heterosis were calculated by the following procedure given by Arunachalam and Bandyopadhyay (1984). According to them, divergence among parents was classified into four divergence classes. To study the magnitude of variation in parental divergence, the mean (m) and standard deviation (s) of the values of divergence were calculated. The divergence classes were defined as given below:

DC1 = D > or = m+s

DC2 = D < (m+s) and > or = m

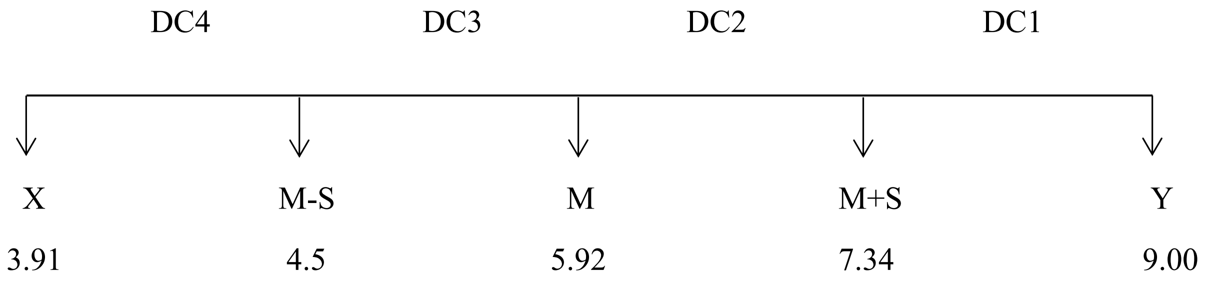
DC3 = D > or = (m-s) and < m

DC4 = D < (m-s)

They proposed that two parents whose genetic divergence falls between (m-s) and (m+s) *viz.*, in the classes DC2 and DC3 when crossed with each other have higher chances of producing high heterosis when compared to a cross whose parental divergence falls outside the limits [(m-s), (m+s)]. The cluster combinations were classified into four divergence classes, following the method suggested by Arunachalam and Bandyopadhyay (1984).

On the basis of the results of Table 4.11, the selection of parents should be done from the cluster combinations in the divergence classes DC1, DC2 and DC3 whereas for selection among the genotypes of a cluster, the *per se* performance of nodulation count per plant at 50 percent flowering, pods per plant, days to maturity, pod blight incidence, oil content, seed yield per plant etc. should be considered to obtain segregants after hybridisation.

Table 4.11 Distribution of different cluster combinations into 4 divergent classes based on D values between them.



	9.00
DC1	(III, IV), (III, V), (II, IV), (IV, VI)
	7.34
DC2	(II, III), (II, V), (V, VI), (II, IV)
	5.92
DC3	(III, VI), (I, II), (IV, V), (I, III), (II, VI), (I, VI), (II, V), (IV, IV)
	4.5
DC4	(III, III), (I, I), (II, II)
	3.91

On the basis of divergence classes studied the genotypes *viz.*, JS 93 05, JS-335, GBIC-18758, AMS-353, DSb-33, NRC-168 and KDS-992 can be used for further breeding programme.

4.9 Screening for pod blight resistance under natural inoculum pressure

All the genotypes studied were screened for pod blight and the classification of the genotypes is depicted in Table No. 4.12.

Most of the genotypes were found to be moderately resistant (6-25% PPI). AMS-MB-5-19, HIMSO-1690, JS-335, KDS-992, KDS-1095, KDS-1149, NRC-142, RSC-11-22, RVS-2011-76 were found to be susceptible to pod blight (25-50% PPI). The rest of the genotypes were moderately resistant. None of the genotypes were found to be immune or resistant to pod blight.

Similar results were obtained by Singh (1993), Sajeesh *et al.* (2014) and Chavan *et al.* (2018).

The genotype showing least pod blight incidence was DSb-33.

Table 4.12 Reactions of soybean genotypes against pod blight under natural inoculum pressure

S. No	Reaction	PPI (%)	Name of genotypes
1	Immune	0	**NIL**
2	Highly Resistant	< 1	**NIL**
3	Resistant	2-5	**NIL**
4	Moderately Resistant	6-25	AMS-20-19, AMS-353, AMS-100-39, DS-228, DSb-33, DSb-36, GBIC-18758, JS 93 05, KDS-344, KDS-726, KDS-753, KDS-980, KDS-1045, KDS-1096, KDS-1097, KDS-1144, KDS-1150, MAUS-732, MAUS-8060, NRC-168, TS-46
5	Susceptible	25-50	AMS-MB-5-19, HIMSO-1690, JS-335, KDS-992, KDS-1095, KDS-1149, NRC-142, RSC-11-22, RVS-2011-76
6	Highly Susceptible	>75	**NIL**

5 SUMMARY AND CONCLUSION

The present investigation entitled, "Genetic evaluation of elite lines of soybean [*Glycine max* (L.) Merrill] was conducted at Botany Farm, Division of Botany, College of Agriculture, Pune during *Kharif,* 2020 with the following objectives:-

1. To study yield and yield contributing characters of soybean.
2. To screen genotypes for pod blight resistance under natural inoculum pressure.

The 30 genotypes of soybean were sown in a randomized block design with three replications and observations were recorded from randomly selected five plants for eleven characters *viz.,* days to 50% flowering, nodulation count per plant at 50 percent flowering, days to maturity, plant height, branches per plant, pods per plant, 100 seed weight, pod blight incidence, seed yield per plant, protein and oil content.

Highly significant differences among the 30 genotypes were obtained. The genotype NRC-168 recorded highest *per se* performance for seed yield per plant and protein content. AMS-353 recorded higher number of pods per plant and oil content. KDS-726 exhibited highest performance for 100 seed weight and desirable *per se* performance for nodulation count per plant at 50% flowering. KDS-992 performed better in terms of branches per plant and pods per plant. JS 93 05 was desirably early to flower and earliest to mature. KDS-1097 was earliest to flower. DSb-33 showed lowest pod blight incidence.

All characters studied revealed the presence of highly significant treatment mean sum of squares and showed considerable amount of genetic variability among the genotypes evaluated.

The GCV and PCV both were observed to be high for pod blight incidence followed by nodulation count per plant at 50 percent flowering, seed yield per plant, pods per plant, branches per plant, plant height, 100 seed weight, days to 50 percent flowering, days to maturity and oil content. Thus, these characters provide good source of variation that can be useful in crop improvement programme in soybean.

High heritability estimates were obtained for almost all characters. Therefore it can be concluded that environmental effects are least on the characters studied. So, there is scope for improvement of these characters by breeding programme.

Nodulation count per plant at 50 percent flowering showed highest genetic advance, followed by pods per plant and pod blight incidence. This suggests that the characters are governed by additive gene action and selection will be effective. The lowest genetic advance was observed for oil content followed by branches per plant, protein content and 100 seed weight which indicates the presence of non-additive gene action, which means heterosis breeding will be effective for improving these characters.

Almost all traits were positively correlated with seed yield per plant except days to maturity and protein content. Days to 50 percent flowering, days to maturity, plant height and branches per plant showed highly positive correlation among themselves.

The path coefficient analysis indicated that pods per plant had the highest positive direct effect on seed yield per plant followed by 100 seed weight and days to 50 percent flowering. So, the improvement in seed yield can be achieved by selecting these characters directly.

The characters days to 50 percent flowering and number of pods per plant had indirect effect on seed yield per plant.

On the basis of D^2 analysis, 30 genotypes were grouped into six clusters with a wide range of divergence between them. D^2 values ranged from 15.27 to 81.08. The highest D^2 value was observed between the cluster III and IV. This suggests that these genotypes have a large variation and are useful for future breeding programme.

The maximum cluster mean for days to maturity was observed in genotypes of cluster I, followed by pods per plant in genotypes of cluster V and nodulation count per plant at 50% flowering of cluster III.

Nodulation count per plant at 50 percent flowering contributed maximum to total divergence.

On the basis of divergence classes studied the genotypes *viz.*, JS 93 05, JS-335, GBIC-18758, AMS-353, DSb-33, NRC-168 and KDS-992 can be used for further breeding programme.

Most genotypes were found to be moderately resistant to pod blight and none were found to be resistant or immune. The genotype showing least pod blight incidence was DSb-33.

Therefore, from the present investigation it can be concluded that:

1. The genotypes *viz.*, NRC-168, AMS-353, GBIC-18758, JS-93 05, KDS-726, KDS-344, KDS-992, KDS-1097, JS-335 and DSb-33 were found to be superior on the basis of mean performance. Therefore, these genotypes can be considered for future breeding programme.
2. Considering the estimates of genetic parameters like genotypic coefficient of variation, heritability and genetic advance nodulation count per plant at 50 percent

flowering pods per plant and seed yield per plant are the most important characters in soybean for further improvement through selection.

3. Seed yield per plant recorded highly significant positive correlation with pods per plant followed by 100 seed weight and branches per plant at the genotypic level.
4. In path coefficient analysis, pods per plant had the highest positive direct effect on seed yield per plant followed by 100 seed weight and days to 50 percent flowering and correlation of these characters with seed yield per plant was positively significant except days to 50 percent flowering indicating true and perfect relationship between seed yield per plant and these characters. Thus, direct selection based on these characters would help in selecting high yielding genotypes.
5. On the basis of D^2 analysis, 30 genotypes were grouped into six clusters with a wide range of divergence between them. The highest D^2 value was observed between the cluster III and IV. This suggests that the genotypes included in these clusters have a large variation and might have genetically different architecture. These genotypes would be useful for future breeding programme. Nodulation count per plant at 50 percent flowering contributed maximum to total divergence indicating that it was considerably responsible for total divergence in the material under study.
6. On the basis of divergence classes studied the genotypes *viz.*, JS 93 05, JS-335, GBIC-18758, AMS-353, DSb-33, NRC-168 and KDS-992 can be used for further breeding programme.
7. According to mean values, DSb-33, KDS-344, AMS-20-19 showed the lowest pod blight incidence among the genotypes studied.

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IN

AGRICULTURAL BOTANY (GENETICS AND PLANT BREEDING)

2021

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