

Genetic Assessment and Morphological Characterization of Soybean Germplasm

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By

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2020

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All the assistance and help received during the course of the investigation has been acknowledged by her.

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(Surbhi Pachori)

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LIST OF ABBREVIATIONS AND SYMBOLS

Symbol/abbreviation		Stand for
%	-	Percentage
$\sqrt{\square}$	-	square root
Σ	-	Summation
Σ	-	Sigma
't' test	-	student 't' test
Cm	-	Centimeter
d.f.	-	degree of freedom
et al.	-	and others
G	-	Gram
SE	-	standard error
S.V.	-	sources of variations
S.S.	-	sums of squares
M.S.S.	-	mean sums of squares
viz.	-	Namely
HI	-	harvest index
Min	-	Minimum
Max	-	Maximum
No.	-	Number
PCV	-	Phenotypic coefficient of variation
GCV	-	Genotypic coefficient of variation
PC	-	Principal Component
PCs	-	Principal Components
PCA	-	Principal Component Analysis

Chapter-1



INTRODUCTION

INTRODUCTION

Soybean (*Glycine max* (L.) Merrill), a yellow jewel is also known as "miracle crop" of the twenty-first century that contains approximately 20 percent of good quality oil, a very high amount of protein (around 40 percent) and, 25% percent carbohydrates. Soybean serves as an excellent source of vegetable oil and protein for human use as well as animal feed (USDA,2009). Unlike most of the vegetable proteins which are deficient in supplying most of the essential amino acids (EAAs), the quality protein of soybean stands exclusive in comparison to other protein-rich crops by way of supplying all the ten EAAs including lysine. Soybean having cardio friendly oil that satisfies around 30% of world vegetable oil necessity. Apart from quality protein and oil, soybean also has many therapeutic constituents viz., lactose-free fatty acids, antioxidants like vitamins C, D, and K and folic acid, vitamins of B complex group viz., nicotinic acid- B₃ (23pg./g), pantothenic acid- B₅ (15g), thiamine- B₁ (12pg./g), pyridoxine- B₆ (8pg./g), riboflavin- B₂ (3.5 pg./g) and biotin- B₇ (0.7g), and isoflavones like genistein and daidzein (Mathur,2004).

The cultivated and wild soybeans have small reproductive differences and have very comparable genomes in both its contents and size (Singh and Hymowitz,1999). Soybean is grown under diverse climatic and geographical locations in India. However, the origin of crop and its early history is not accurately known yet. The middle and lower Yellow River valley in China has been assumed to be the probable place of origin (Chang,1980). Since the first century AD, this ancient domesticate become more widely introduced, and landraces were developed in China, Korea, India, and other parts of Asia (Zeven and de Wet,1982). Soybean was early introduced to the USA in 1804 (Mores and Markley,1950) and become an important crop of South and Midwest by the twentieth century. Major soybean-producing countries are the USA, Brazil, Argentina, China, and India. India stands fifth in the world which occupies an area 11.25 Mha and accounting to the production of 9.30 Mt, with the productivity of 830 kg per ha. (Director's Report, IISR, 2019-20).

Taxonomically, soybean belongs to the order Fabales, family Fabaceae, subfamily Faboideae and the genus *Glycine*. The genus *Glycine* is divided into two subgenera, *Glycine* including 16 perennial species and *Soja* (Moench) F.J.

Herm having two annual species, *Glycine soja* Siebold and Zucc ($2n=40$) and *Glycine max* (L.) Merrill ($2n=40$). The cultivated species, *G. max*, hybridizes easily with its wild annual relative and most probable progenitor, *G. soja* while with the perennial relatives, it has a low crossability rate (Singh and Hymowitz, 1999).

Genetic diversity in genus *Glycine* has been covered in detail by Ratnaparkhe et al. (2011). Based upon the views on recent taxonomic, cytological and molecular systematic research on the genus *Glycine* and allied genera, it has been hypothesized that soybean genome is the product of a diploid ancestor ($n=11$), which underwent aneuploid loss to $n=10$ followed by polyploidization. (Singh and Hymowitz 1988; Blanc and Wolfe 2004). Soybean (*Glycine max* L. Merr.) has a genome size of 1.1 - 1.115 Gb (Arumuganathan and Earle 1991; Schmutz et al. 2010).

Soybean is known to be introduced in India during 1870 and 1880. However, the cultivation of soybean at a large-scale started in some states during the year 1971-72 with an area of 32,331 hectares with the production of 13,782 tonnes (Wasnik, 1986). During 2018-19, in India, soybean area has increased to 11.30 mha with the production of 10.93 mt and productivity of 960 kg/ha (Directors Report, IISR, 2019-2020). During the same period, the state of Madhya Pradesh cultivated soybean in 5.24 m ha area and produced 6.73 mt with the productivity of 1285 kg/ha (Directors Report, IISR, 2019). Madhya Pradesh has played a major role ever in the development and expansion of soybean cultivation and contributes substantially in all respect by producing more than 50% soybean of India and is known as "Soya State".

Genetic resources play a key role in developing new cultivars. For the genetic improvement of soybeans, a vast collection of soybean germplasm (1,70,000 accessions) is present in the world, with some duplicated accessions (Nelson, 2009). China has the largest collection of germplasm (>23000 cultivated and 7000 wild accessions), and this germplasm has been preserved and maintained at the Chinese National Soybean Gene Bank (Dong et al., 2004; Wang et al., 2006; Limei et al., 2005). The USDA-Agricultural Research Service has the second-largest soybean germplasm collection, which is comprised of >20000 accessions of the genus *Glycine* with a wide range of natural variations (Carter et al., 2004).

In India, work on soybean was undertaken at the Indian Agricultural Research Institute (IARI), New Delhi, on a small scale, with material built-up by the Plant Introduction Division during the 1950s. The Indian Council of Agricultural Research sanctioned the All India Coordinated Research Project on Soybean on April 1st, 1967, with the main centers located in Pantnagar, Jabalpur, and Delhi. The National Bureau of Plant Genetic Resources (NBPGR) (formerly a plant introduction division of IARI, New Delhi) made efforts to collect germplasm from exotic and indigenous sources through direct introductions and explorations. Indian soybean germplasm collections are meagre with nearly 3000 germplasm accessions at ICAR NBPGR and nearly 2500 accessions at ICAR-IISR Indore.

Realizing the production potential of the crop, the present study was carried out to evaluate the available germplasm for the character association, direct and indirect effects of different attributes concerning yield and emphasis was also given variability estimation which is of great significance to the plant breeders and gene-bank curators as it plays a crucial role in designing a triumphant breeding programme. The assessment of genetic diversity at phenotypic, genotypic, and biochemical levels are not only important for crop improvement but also helps in the efficient management for the protection of available plant genetic resources. Therefore, apart from the collection, evaluation and, conservation of germplasm, assessment of its genetic variability is a basic step for any crop improvement program.

Morphological characterization is an important step in the description and classification of accessions or genotypes, because a breeding program mainly depends upon the magnitude of genetic variability (Zubair et al.,2007). Presence of sufficient amount of variability for the different agro- morphological trait, improvement of these traits through selection and introduction of new alleles, lines and accessions into breeding activity both from exotic and indigenous collection helps in the identification of potential donors and in varietal development and release for the seed production chain.

The possibility of improvement in any crop is dependent on variability available in the crop, wider the genetic variability in a trait, better the chances of improvement through selection. An evaluation to detect the extent of variability available for the yield attributes and their heritability values is of immense help

to the breeders to select the breeding methods for improvement of yield attributing traits. But heritability alone does not give a true picture of genetic improvement through selection, therefore, the study of genetic advance coupled with heritability is more useful. Correlation and path analysis are important tools useful for getting information regarding the association of characters. Path coefficient analysis furnishes information on the influence of each contributing trait to yield directly as well as indirectly and also enables breeders to rank the genetic attributes according to their contribution.

Genetic divergence analysis is an important tool to determine the percentage contribution of the characters in a hybridization program and the genetic variability present among the genotypes. Characters like yield and its components being polygenic, the breeder has to isolate desired genotypes from the knowledge of components of variations, association analysis, and genetic divergence analysis, thus, it helps in deciding a breeding procedure for the genetic improvement of yield traits.

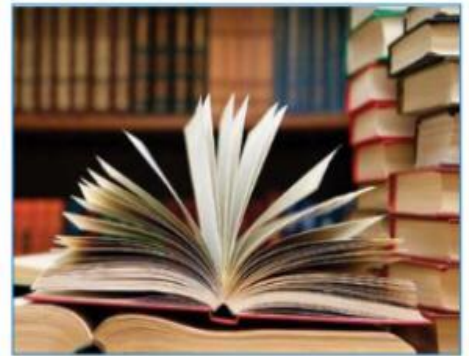
However, not enough attempts have been made to evaluate the available soybean germplasm for efficient utilization in breeding programs. Therefore, the present study will help in characterizing more qualitative and quantitative traits in specific germplasm for planning the soybean improvement program. Keeping in view the importance of genetic diversity, a study for the assessment of soybean genotypes was undertaken during Kharif, 2019.

Considering the above-mentioned important aspects, it became imperative to conduct the present investigation with the following broad objectives:

Objectives of Investigation

1. To classify the germplasm based on their morphological characterization
2. To assess the extent of genetic variability, the correlation among the traits and the direct and indirect effects on the seed yield
3. To estimate the genetic divergence (D^2 statistics) among soybean accessions
4. Identification of promising genotypes using principal component analysis coupled with multiple disease resistance

Chapter-2



REVIEW OF LITERATURE

REVIEW OF LITERATURE

Soybean is considered as one of the most important grain legumes, because of its high nutri-rich value. In India, it is extensively cultivated during *Kharif* season. Soybean has witnessed linear increasing trends in the production and productivity over the years. An attempt has been made in the present investigation to understand the variability, heritability, genetic advance, association, divergence (Genetic and Molecular) and principal component analyses. Reviews of literature pertaining to these aspects are presented in this chapter under the following headings:

1. **Morphological characterization**
2. **Analysis of Variance (Federer, 1961)**
3. **Heritability (Hanson *et al.*, 1956)**
4. **Genetic advance (Johnson *et al.*, 1955)**
5. **Correlation Coefficient (Miller *et al.*, 1958)**
6. **Path coefficient analysis (Wright, 1921 and Dewey and Lu 1959).**
7. **Principal Component Analysis (Massay 1965 and Jolliffe, 1986)**
8. **D² analysis (Mahalanobis, 1928).**
9. **Physiological growth parameters**
10. **Biochemical estimations**
11. **Screening against multiple disease resistance**

Morphological Characterization

Germplasm provides the base material for crop improvement. A need for germplasm collection, evaluation and cataloguing is of utmost importance to have a dynamic crop improvement programme. Characterization of cultivars is based on different morpho-physiological traits which is the most important step in the genetic improvement programme.

Sawarkar (2010) reported wide range of variation for hilum colour, seed size and shape, leaf shape, flower colour and intensity of brown colour on pod. Seed size, days to flowering and days to maturity are the uniform characters but their expression is altered by the fluctuations of environment. Plant growth type

and growth habit were the most stable and distinguishing traits and could be used for development of a varietal identification key.

Badkul *et al.* (2014) characterized twenty-six advanced generation soybean genotypes based on NDUS guidelines for twelve morphological characters viz., hypocotyl colour, growth type, growth habit, pubescence, pubescence colour, leaf shape, flower colour, pod colour, seed coat colouration, seed size, seed shape and hilum colour.

Dubey (2015) characterized fifty advanced generation soybean genotypes based on NDUS guidelines for twelve morphological characters viz., hypocotyl colour, growth type, growth habit, pubescent, pubescent colour, leaf shape, flower colour, pod colour, seed coat colour, seed size, seed shape and hilum colour.

Mishra (2016) characterized fifty soybean genotypes based on NDUS guidelines for eleven morphological traits viz., hypocotyl colour, growth type, pubescent, pubescent colour, leaf shape, flower colour, pod colour, seed coat colour, seed size, seed shape, hilum colour.

Lal *et al.* (2018) categorized 26 soybean genotypes on the basis of pod characters and indicated that JS 21-68, JS 21-69, JS 20-69 and JS 21-49 are having higher number of pods as well as higher percentage of three seeded pods. Whereas, JS 21-58, JS 21-53, JS 21-55 and JS 21-54 exhibited higher expression of four seeded and three seeded pods. Hence, hybridization between these two groups may contribute profuse podding with higher frequencies of four seeded and three seeded pods which ultimately enhance the number of seeds per plant.

Panikar (2019) evaluated two hundred seventy-three germplasm lines of soybean including three checks (JS-97-52, Bragg and JS-335) for agro-morphological characters in an augmented block design and observed that these traits belonged to two categories viz., qualitative-measured through visual observation like anthocyanin pigmentation (present or absent), flower colour, pod colour, leaf colour, etc and quantitative- measurable traits like plant height, size of seed (100-seeds weight g), etc. The entire (273 genotypes) soybeans under study showed a wide range of genetic variation in respect to these traits.

Mehra (2019) characterized forty-six soybean genotypes based on NDUS guidelines for seventeen morphological traits viz., hypocotyl colour, growth habit, growth type, leaf shape, flower colour, leaf size, leaf intensity of green, pubescent, pubescent colour, pod colour, seed coat colour, seed size, seed shape, seed coat lusture, hilum colour, hilum funicle colour, peroxidase activity.

Saraswat (2019) 30 soybean genotypes were characterized using DUS guidelines on the basis of twelve morphological traits viz., hypocotyl anthocyanin coloration, plant growth habit, plant growth type, leaf shape of lateral leaflet, leaf size of lateral leaflet, flower colour, pod intensity of brown colour, pod hairiness, pod colour of hairs, seed size, seed shape and seed coat lusture.

Genetic Variability

The phenotypic variance measures the magnitude of variation arising out of differences in phenotypic values, while the genotypic variance measures the magnitude of variation due to differences in genotypic values. The absolute values of phenotypic and genotypic variances can not be used for comparing the magnitude of variability for different characters, since the mean and units of measurements of the characters may be different. Hence, the coefficient of variation expressed at phenotypic and genotypic levels have been used to compare the variability observed among different characters. While, genotypic coefficient of variation indicates the amount of genetic variability present in the character.

Abady *et al.* (2013) studied forty-eight soybean genotypes for genetic variability, heritability and genetic advance for nine important traits during 2012. High GCV were recorded for plant height, number of pods, number of primary branches and yield/hectare while, low GCV was recorded for days to maturity. High PCV was observed for plant height and stand count at harvest.

Chandel *et al.* (2013) conducted experiment to estimate the genetic variability in seventy diverse soybean genotypes. Results revealed that number of primary branches/plants, number of clusters/plant and number of pods/plants registered high magnitudes of GCV. Moderate magnitudes GCV was observed for plant height, number of seeds/pods, seed yield/plant, biological yield/plant and harvest index.

Ghodrati (2013) conducted experiment with twelve soybean genotypes during three growing seasons. Results showed significant differences for seed yield and quality characters. The highest GCV and PCV were observed for branches/plant, pods/plant and plant height.

Osekita and Ajayi (2013) grew five accessions of soybean to study the inter-relationship among quantitative characters during *Kharif* 2012. The findings indicated that seed yield/plant had the highest estimate of PCV and GCV followed by seed dry weight and number of seeds/plants.

Reni & Rao (2013) studied genetic variability on forty-five genotypes of soybean. Results showed that considerable amount of variability existed among the characters under study. High PCV coupled with high GCV was observed for number of branches/plants, number of pods/plants, biological yield/plant, harvest index and seed yield/plant.

Hakim *et al.* (2014) conducted experiment during the dry season of 2011 among the F₂ progenies of crosses among three soybean varieties for genetic variability. Results revealed that seed weight/plant, number of pods/plant and days to maturity had the highest coefficient of variability.

Malek *et al.* (2014) studied genetic parameters of yield components for twenty-seven soybean genotypes including mutants during 2011. Results exhibited narrow difference between phenotypic and genotypic coefficients of variation (PCV and GCV) for most of the characters. The highest PCV and GCV was observed for number of branches/plant and the lowest PCV and GCV was recorded for days to maturity.

Pawar *et al.* (2014) studied forty-two genotypes of soybean procured from Directorate of Soybean Research, Indore, MP to estimate variance and genetic divergence among yield traits. They concluded that pods/plant, number of branches/plants, grain yield/ plant and harvest index showed high PCV and GCV, while plant height and 100-grain weight showed moderate PCV and GCV values, whereas days to 50 per cent flowering, pod length and days to maturity showed low PCV and GCV.

Mahbub *et al.* (2015) evaluated twenty-eight soybean genotypes for eleven morphological characters during Rabi, 2011. The highest GCV was

observed for seed yield/plant followed by number of branches/plant and plant height.

Akram *et al.* (2016) studied 11 different soybean genotypes and revealed that genetic analysis showed a higher phenotypic coefficient of variation compared to other corresponding genotypic coefficient of variation indicating that the traits were influenced by environment to some extent. Yield/plant showed a significant positive correlation with number of branches/plant, number of pods/plant, number of seeds /plant and 100 seed weight, whereas it showed non-significant positive correlation with pod length.

Jha (2016) found that the phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the characters. High magnitude of PCV and GCV was observed for the number of seeds per plant, number of pod clusters per plant, biological yield per plant, 100 seed weight and number of pods per plant.

Jain *et al.* (2017) studied 24 genotypes of soybean and identified that the highest genotypic (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.

Neelima *et al.* (2018) conducted an experiment to estimate the genetic variability in 124 diverse soybean germplasm accessions. Results showed that the values of phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all the characters indicating the influence of environmental factors.

Shruti *et al.* (2019) carried out experiment on 13 genotypes of soybean for yield and yield component traits and found out that the genotypic coefficient of variation and phenotypic coefficient of variation were high for pod weight per plant (g) followed by seed yield per plant (g) indicate the presence of wider adaptability for these traits in the genotypes studied, suggested the less influence of environment in the expression of characters.

Ghimire *and Sah* (2019) studied sixteen genotypes. Statistical analysis revealed all characters: days to fifty percent flowering, days to maturity, plant

height, number of pods per plant, hundred seed weight, and grain yield were highly significant differences (<0.01) indicating sufficient genetic variability among the tested genotypes for concerned traits.

Bhairwa *et al.* (2020) studied 276 genotypes and four checks and found that characters days to 50% flowering, days to maturity, plant height, number of nodes per plant, number of pods per plant, 100 seed weight, dry matter weight per plant, plant population per plot and harvest index (%) showed highly significant difference among check and significant difference showed for seed yield per plant. The PCV and GCV values ranged between 17.87% and 17.83% for plant population per plot and 4.75% and 2.62 for, days to 50% flowering and days to maturity, respectively.

Heritability and genetic advance

Heritability in broad sense refers to the ratio of genotypic variance to the total phenotypic variance. The estimates of heritability help the plant breeders in selection of elite genotypes from diverse genetic population and also a good index of the transmission of characters from parents to their off springs. Genetic advance refers to the realized gain in the genetic value of the selected single plant over the base population. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection from heritability estimate alone.

Ghodrati (2013) evaluated twelve soybean genotypes and obtained high broad sense heritability combined with high genetic advance for number of nodes/plant and plant height.

Badkul *et al.* (2014) evaluated twenty-six advanced generation fixed genotypes of soybean. Results indicated that number of branches/plant, number of pods/plant, number of seeds/plant, biological yield/plant and seed yield/plant showed high heritability coupled with high genetic advance whereas, high heritability with moderate genetic advance was found for plant height and 100 seed weight.

Hakim *et al.* (2014) studied three soybean varieties and observed that number of pods/plant, days to maturity, plant height and seed size had high heritability coupled with high genetic advance.

Sureshrao *et al.* (2014) have evaluated twelve soybean genotypes and recorded high estimates of heritability for days to maturity, number of pods/plant, seed yield/plant and plant height. High genetic advance as percentage of mean was observed for number of pods/plant, seed yield/hectare and seed yield/plant.

Tantway (2015) evaluated thirty genotypes of soybean and obtained high heritability coupled with high genetic advance as percentage of mean for dry matter accumulation at flowering, number of nodules/plant, dry weight of nodules/plant, number of pods/plant, biological yield/plant, number of seeds/plant and seed yield/plant.

Mahbub *et al.* (2015) have studied twenty-eight genotypes of soybean and found high heritability for number of pods /plant, number of seeds/plant and number of branches/plant. High genetic advance in this study was recorded for plant height and number of seeds/plant.

Adsul *et al.* (2016) reported that additive gene action was found predominant in inheritance of yield and yield contributing characters viz., number of primary branches per plant, number of clusters per plant, number of pods per cluster, 100 seed weight and yield per plant. Both additive and non-additive gene effects were significantly involved in the expression of quantitative traits with duplicate epistasis. Duplicate epistasis was significantly importance in inheritance of the most traits studied.

Mahbub and Shirazy (2016) reported high heritability coupled with high genetic advance for number of branches per plant, plant height, number of seeds per plant, number of pods per plant and 100-seed weight in soybean.

Akram *et al.* (2016) reported that high heritability values along with high genetic advance and genetic advance as percentage of mean were found for plant height, yield/plant, number of pods/plant and number of seeds per plan.

Chandel *et al.* (2017) studied 70 diverse soybean genotypes and observed high heritability for pods per plant (97.60) followed by harvest index (94.60), biological yield plant per plant (90.60), plant height (82.20) and seed yield per plant. Whereas, high genetic advance coupled with high heritability was observed for biological yield plant per plant (22.10) and pods per plant (21.02).

Jain *et al.* (2017) studied 24 genotypes of soybean and observed high heritability and high genetic advance in the test weight, number of pods per plant, harvest index and plant height.

Neelima *et al.* (2018) observed high estimates of heritability coupled with high genetic advance expressed as percentage of mean for plant height, number of branches per plant, number of pods per plant and seed yield per row which may be attributed to the preponderance of additive gene action and possess high selective value and thus, selection pressure could profitably be applied on this character for their improvement.

Getnet *et al.* (2019) conducted an experiment on 49 soybean genotypes and identified that the highest heritability value was recorded for days to 50% flowering followed by days to maturity and days to pod setting with wide range of mean values in all the characters evaluated.

Bhairwa (2020) observed 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 (%).

Correlation Coefficient

Badkul *et al.* (2014) found that seed yield per plant exhibited positive and highly significant correlation with biological yield, number pods per plant, number of seeds per plant, plant height, harvest index and number of seeds per pod.

Koraddi *et al.* (2015) reported that seed yield per plant (g) was found to have significant and positive correlation with days to 50% flowering, plant height, number of branches per plant, number of pods per plant, 100 seed weight, biomass and harvest index.

Alpna *et al.* (2015) reported that number of pods per plant, 100 seed weight, harvest index and dry matter weight per plant had major contribution in determining seed yield per plant in soybean.

Mahbub and Shirazy (2016) studied that plant height, pod length, number of seeds per pod, number of pods per plant, hundred seed weight, branches per

plant and number of seeds per pod showed significant positive correlation with seed yield.

Chavan *et al.* (2016) revealed that seed yield per plant showed highly significant positive association with 100 seed weight, followed by number of pods per plant, while branches per plant and seeds per pod showed negative and non-significant association with seed yield per plant.

Balla M. Y. and Ibrahim S. E. (2017) identified that highly significant positive genotypic correlations were detected for grain yield with days to 50% flowering, days to maturity, plant height, number of pods/plant and fodder yield.

Dessia and Gemechu (2018) in correlation studies among 16 soybean genotypes planted in RCBD with three replications found that genotypic and phenotypic correlation of seed yield was positive and significantly related with number of pod per plant, number of seed per pod, biological yield, hundred seed weight, and number of branch per plant and leaf area index. Whereas, plant height, days to 50% flowering and days to maturity were negative and not significantly associated with grain yield.

Mishra (2019) carried out association analysis to know the behaviour of yield and its components in parent, F₁ and F₂ populations. None of the character showed positive association with yield among themselves.

Li M *et al.* (2020) did correlation studies and found that the yield showed very significant ($P \leq 0.001$, $P \leq 0.01$) or significant ($P \leq 0.05$) positive correlations with plant height, nodes on main stem, branches, pods, grains, 100-grain weight, and growth periods (R1–R7) ($0.17 < r < 0.80$).

Path coefficient analysis

The concept of path coefficient analysis was originally developed by Wright (1921), but the technique was first used in plant breeding by Dewey and Lu (1959). This method was illustrated as a means of analyzing correlation coefficient. A path coefficient is simply standardized partial-regression coefficient and as such measures the direct influence of one variable upon another and permits the separation of the correlation coefficients into components of direct and indirect effects.

Abady *et al.* (2013) reported that number of pods per plant, days to maturity and harvest index had positive direct effect on seed yield per plot. Number of branches per plant and plant height exerted positive and indirect effect on seed yield per plot through number of pods per plant and plant height also exert positive indirect effect on seed yield per plot through days to flowering and days to maturity.

Badkul *et al.* (2014) found that number of pods per plant, biological yield per plant, number of seeds per plant and harvest index depicted substantial phenotypic and genotypic direct effects on seed yield.

Malek *et al.* (2014) reported that chlorophyll content, number of branches per plant, number of pods per plant and 100-seed weight exerted positive direct effects.

Mishra *et al.* (2015) recorded highest positive direct effect on seed yield per plant was shown by number of seeds per plant followed by 100 seed weight and number of pods per plant while negative direct effect on seed yield per plant was caused by plant height.

Mahbub *et al.* (2015) found that seeds per pod, 100 seed weight, days to maturity and plant height showed positive direct effect on yield.

Chavan *et al.* (2016) showed that 100 seed weight, number of pods per plant, days to 50% flowering and days to maturity had high positive direct effect on seed yield per plant.

Akram *et al.* (2016) reported 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.

Deshmukh (2016) concluded that results of Path coefficient analysis showed 100 seed weight (0.4996), number of pods per plant (0.2919), days to 50% flowering (0.2068), and days to maturity (0.0531) had high positive direct effect on seed yield per plant.

Balla M Y and Ibrahim S E (2017) on path analysis revealed that fodder yield, plant height and days to maturity had the highest positive direct effect on

grain yield. Number of pods/plant via plant height gave the highest positive indirect effect on grain yield.

Chandel *et al.* (2017) revealed that the highest and positive direct effect on seed yield per plant was exhibited by biological yield per plant followed by harvest index, days to 50 percent flowering. On the other hand, the characters: pods per plant, pods per cluster and primary branches per plant had low negative direct effect, but these traits supplemented positive and direct effect on seed yield per plant via other yield contributing traits.

Dessia and Gemechu (2018) with studies on path coefficient analysis among 16 genotypes of soybean identified that genotypic direct path and phenotypic direct path correlation of seed yield was positive and maximum for number of pod per plant, number of seed per pod, biological yield and hundred seed weight, whereas number of pod per plant, number of seed per pod, hundred seed weight and biological yield showed high genotypic and phenotypic indirect path effects on seed yield.

Hang Vu *et al.* (2019) concluded highly positive direct effects on grain yield for total number of pods, total number of seeds and 100 seed weight.

Mishra (2019) with studies on path coefficient analysis study in parents, F_1 and F_2 populations revealed the existence of positive direct effect of 100-seed weight, number seeds per plant and number of pods per plant on seed yield. Though, 100-seed weight had substantial positive direct effect, but indirect effect for all the characters were found to be negative.

Principal component analysis

Principal component analysis is intended to derive a small number of linear combinations (principal components) of a set of variables that retain many of the existing information in the original variables. Thus, this analysis may also be seen as an attempt of evidencing the approximate linear dependences existing between variables. Often a small number of principal components may be used to replace the original variables to draw graphical representations, regression analysis, cluster analysis, factor analysis among other traits.

Iqbal *et al.* (2008) conducted experiment on one hundred thirty-nine soybean genotypes evaluated for yield and yield associated traits for PCA. The

results revealed significant differences among genotypes for all studied traits. Principal component analysis (PCA) showed that first three components accounted 69.77% of the total variance. PC1 indicated that seed yield and biological yield/plant were important traits for classification. While, 100-seed weight, oil content and harvest index were important in PC2. In the PC3, days to maturity and number of branches/plant are important.

Ojo *et al.* (2012) conducted an investigation utilizing forty accessions of soybean and found three principal components. The PC1 had 52%, PC2 showed 26% and PC3 exhibited 10% variability among the genotypes for traits under his study. The first principal component was mostly correlated with the number of pods/plant, pod length, pod yield/plant, 100-seed weight, and seed yield/plot. The characters that were mostly correlated with the second principal component were days to 50 % flowering and days to maturity.

Shaahu *et al.* (2013) findings revealed that PCA implicated pods/plant, seed yield, plant height and first pod height for accounting for the most variability in the soybean genotypes.

Badkul *et al.* (2014) conducted experiment on twenty-six fixed advanced generation genotypes of soybean with two replications. Results showed that out of eleven, only five principal components (PCs) showed about 94.62% variability. PC1 showed a maximum of 56.29% variability and was more related to the phenological and yield attributing traits viz., vegetative phase, plant height, number of branches/plant, number of pods/plant, number of seeds/plant, biological yield/plant, harvest index and yield/plant.

Birla and Ramgiri (2015) evaluated twenty-five genotypes of soybean and concluded that Principal Component Analysis 1 and 2 were statistically significant for all the traits, except for days to 50% flowering and days to maturity. The contribution of PCA 1 for G x E sums of squares was greater for days to maturity followed by days to 50% flowering. The highest contribution for PCA 2 was for seed yield/plant.

Mishra (2015) reported that the first three principal components (PCs) exhibited 72.115%, 70.097% and 69.758% variation in *Kharif* 2013, *Kharif* 2014 and pooled analysis respectively. In *Kharif*, 2013 rotated component matrix

indicated that first PC reported for the highest variation (46.286%) related with five traits viz., number of pods/plant, plant height, number of pod clusters/plant, seed yield/plant, and harvest index (%). In *Kharif* 2014 first principal components showed about 38.657%, variability among the traits namely seed yield/plant, plant height, harvest index, biological yield/plant, vegetative phase and number of seeds/plant. Whereas, under pooled analysis first PC accounted for the highest variation i.e. 38.36%, was related with the traits number of pod clusters/plant, reproductive phase, plant height, number of pods/plant, seed yield/plant, number of seeds/plant and biological yield/plant.

Tantway (2015) findings revealed that PC1 accounting for the most variability in the soybean genotypes showed positive effect for the specific traits viz., number of seeds/plant, biological yield/plant, number of pods/plant and seed yield/plant.

Jha (2016) reported that out of total principal components, five principal components were considered to be more important because they have more than one Eigen value that showed total variation among 50 soybean genotypes under study. The PC1 had the highest variability (31.95%) followed with PC2 (14.46%), PC3 (10.15%), PC4 (8.27%) and PC5 (7.34%) for traits under study. Five principal components exhibited about 72.17% variability among the traits studied.

Manav (2017) revealed that the first 3 principal components accounted for 79.37% of the total variation. PC₁ contributed 52.85% of the total variation and dominated by 100-seed weight, number of days to maturity, number of branches per plant, pods per plant, seed yield per plant and plant height. The second principal component explained an additional 14.94% of the total variation dominated by highly positive pod length and number of seeds per pod while the PC₃ explained an additional 11.58% of the total variation and only number of days to 50% flowering showed positive relation with the third component (PC₃) signifying its importance in divergence.

Avinashe *et al.* (2018) found that out of eighteen, only five principal components considered to be more important. The PC1 recorded the highest variation 37.13% followed by 13.02% (second PC), 10.17% (third PC), 6.88%

(fourth PC) and 6.24% (fifth PC). Rotated component matrix revealed that the PC1, which accounted for the highest variability (37.13%) was mostly related with traits such as days to 50% flowering, days to maturity, plant height, number of branches per plant, number of nodes per plant, number of pods per plant, number of pods per node, number of seeds per plant, biological yield per plant and seed yield per plant.

Getnet *et al.* (2019) with studies on Principal Component Analysis of 49 soybean genotypes revealed that five principal components of PC1 to PC5 with Eigen values 4.27, 2.53, 1.91, 1.28 and 1.08 respectively, have accounted for 73.81% of the total variation.

Singh *et al.* (2020) evaluate sixteen soybean genotypes. The principle components analysis showed that PC1 and PC2 having eigen values the highest than unity explained 76.6% of total variability among soybean genotypes attributable to plant height, days to maturity, number of pods/plant, 100 seed weight and grain yield.

Genetic Divergence by Mahalanobis D² Analysis

D² statistics developed by Mahalanobis (1928), provides a measure of magnitude of divergence between biological populations and relative contribution of each component character to the total divergence. Mahalanobis D² statistics is more reliable in selection of potential parents for hybridization programme.

Satyavathi *et al.* (2004) characterized seventy-five soybean cultivars based on the National Test Guidelines and the International Union for Protection of New varieties of plants table characteristics for soybean and identification key based on 19 morphological characters, i.e. hypocotyls anthocyanin colour, growth type, growth habit, shape of lateral leaflet, size of lateral leaflet, intensity of green colour, flower colour, presence of hair in pods, colour of hairs, plant height, intensity of brown colour of pods, seed size, seed shape, colour of ground testa, seed coat colour, seed hilum, colour of hilum funicle, and timing of flowering and maturity.

Dubey (2015) obtained six clusters during *Kharif*, 2014 using Mahalanobis' D^2 statistics and found substantial genetic diversity between the genotypes.

Alpna *et al.* (2015) reported that number of pods per plant contributed maximum towards the genetic divergence followed by plant height, 100 seed weight, dry matter weight per plant and days to 50% flowering.

Mishra *et al.* (2016) based on studies on genetic divergence grouped fifty genotypes into eleven clusters. Cluster I and cluster II were polygenotypic found to be the largest cluster each comprising of 13 genotypes. Cluster X showed maximum intra cluster D^2 value followed with cluster V and cluster IV. The trait, number of pods per plant (30.86%) contributed most towards genetic divergence followed by biological yield (30.04%).

Mahesh *et al.* (2017) grouped forty soybean genotypes into six clusters. The cluster III was the largest cluster with thirteen genotypes. Highest inter cluster distance was observed between cluster I & cluster VI followed by between V & VI and V and VI, respectively.

Yadav *et al.* (2017) grouped twenty-nine advance generations of soybean into seven clusters. Cluster I, II, III, and cluster VI were polygenotypic, remaining three were monogenotypic. Genetic Divergence results revealed that the newly developed recombinants have sufficient genetic diversity as indicated by sufficient inter and intra cluster distance and distribution of genotypes among more clusters. Generation of crosses from cluster I, III, V and VI can be used for further hybridization programme in the development of promising lines.

Mishra (2018) based on the studies on degree of divergence, grouped thirty three genotypes of soybean into six cluster of which cluster II had maximum eleven genotypes in each group followed by cluster I, IV, III, V and VI which had eight, six, five, two and one genotypes, respectively.

Getnet *et al.* (2019) in his studies on Genetic divergence on 49 soybean genotypes grouped them into three distinct clusters indicating that the soybean genotypes were moderately divergent.

Singh *et al.* (2020) evaluated sixteen soybean genotypes. Sixteen soybean genotypes were divided into four clusters. The genotypes grouped into

cluster I which showed the highest value for days to maturity. The genotypes belonging to cluster II had the highest values for grain yield and plant height.

Physiological Growth Parameters

Watson (1952) observed that the increase in dry matter is associated with increase in Leaf Area Index (LAI) to a stage where the mutual shading of leaves does not take place. After that with increasing LAI the dry matter accumulation decreases.

Hanson (1972) observed, while working with the soybean that the principle factors influencing canopy net photosynthesis were light, genotype and LAI. Maximum CO₂ assimilation occurs at a LAI of 5-6 under high irradiance, whereas under low irradiance it occurs at a LAI of 3-4.

Gupta and Olugbemi (1978) postulated that the maximum yield was achieved due to rapid attainment of optimum LAI.

Welbank *et al.* (1988) reported that the ratio of grain yield to Leaf Area Duration (LAD) increased with increase in daily radiation during grain filling.

Egli and Zhenwen (1991) suggested that seeds per unit area were related to canopy photosynthesis during flowering and pod set and canopy photosynthesis rate is determined through LAI and CGR.

Sharma and Sharma (1993) reported that variety JS 81-335 registered greater LAI (5.9) than other varieties.

Sahoo and Guru (1998) observed the positive association of SLA, CGR, and LAD with grain yield.

Chauhan *et al.* (1999) reported that the LAD and LAI measured at 30-45 days after sowing (DAS) had positive and significant association with dry accumulation at 50% flowering.

Rajput *et al.* (2004) found that the differences in the leaf area index of the genotypes examined were not significant. Leaf area index ranged from 0.54 to 3.17.

Betzelberger *et al.* (2010) reported that the Chlorophyll content and photosynthetic parameters were positively correlated with seed yield, while

antioxidant capacity was negatively correlated with photosynthesis and seed yield.

Bang *et al.* (2011) observed that the content of total chlorophyll and apparent quantum yield (Phi) of both crops increased and light compensation point (LCP) and light saturation point (LSP) decreased with increasing degree of shade.

Nguy-Robertson *et al.* (2012) reported that the LAI ranged from 0 to 5.5 m²/m² in soybean.

Hu *et al.* (2013) showed that supplemental UV- beta radiation decreased chlorophyll contents by 5.5% (P=0.048), 8.7% (P=0.046), and 10.5% (P=0.005) in seedling, in branching, flowering, and in pod-setting stages. The supplemental-Beta radiation adversely affected Chl content and electron transport activity in PSII and consequently decreased the photosynthetic efficiency of soybean plants.

Vyas and Khandwe (2014) reported that the two cultivars JS 95-60 and JS 97-52 showed more chlorophyll content.

Biochemical Estimations

Hartwing and Hinson (1972) reported that seed yields are positively correlated with oil percentage and negatively correlated with protein percentage in soybean.

Singh and Gupta (1976) reported that value of protein content in soybean seed varied from 34 per cent to 46 per cent.

Satwe (1992) worked studied quality traits and their correlation with oil and protein in seventy-four soybean genotypes. He reported oil correlates negatively with protein, cooking time and volume expansion after soaking. Water absorption after soaking correlates positively with volume expansion, while protein content correlates negatively with yield.

Jadhav *et al.* (1994) indicated that seed protein and oil contents significantly decreased with increasing plant density from 17 to 44 plant m².

Joshi (1997) worked on soybean at Indore, (Madhya Pradesh) and observed that early maturity genotypes contained more oil than normal maturing ones.

Sridhara *et al.* (1997) observed that there were significant differences among Soybean varieties in respect of oil content.

Sridhara *et al.* (1997) observed that soybean genotypes differed significantly in respect of protein content composition.

Bhardwaj (1998) observed negative and significant correlation between seed yield and protein content in soybean.

Rahman and Hanif (2006) and Rahman *et al.* (2011) revealed that soybean seed yield was increased with increasing plant density and the highest seed yield and lowest seed 100 plants depending on cultivar and season.

Sharma *et al.* (2008) studied quality traits and their correlation with oil and protein in seventy-four soybean genotypes.

Pal *et al.* (2012) reported that dry matter and yield components had strong negative association with protein content. Variety Awassa 95 (45%) recorded significantly higher protein content than variety Belessa 95 (40%).

Daniel *et al.* (2012) reported that the variety Awassa 95 recorded the significantly higher protein content (45%) than variety Belessa 95 (40%).

Min *et al.* (2015) studied and developed differential protein profiles of soybean (*Glycine max*) seeds (cv. Saedanbaek and Daewon) varying in protein (47.9 and 39.2%) and oil (16.3 and 19.7%) content.

Screening for multiple disease resistance

Diseases like charcoal rot (CR) and *Rhizoctonia* aerial blight (RAB) have become major constraints in the production of major soybean growing areas of India. Due to Charcoal rot, complete plant mortality occurs during reproductive stages of crop and it is characterized by Charcoal like appearance of black microsclerotia in the vascular tissues and on lower part of plant (Bradley and Rio, 2003). *Rhizoctonia aerial blight* causes light to dark brown spots, vein reddening, superficial cobweb like mycelium and the development of sclerotia above ground parts (Verma and Thapliyal, 1976).

Panceshwar *et al* (2016) screened twenty-two isolates against soybean cultivar Monnetta. The mortality percent of different isolates ranged between 32-96%. Only two entries *viz*, JS 97-52 and JS 93-05 reacted as moderately susceptible under disease grade 5, ten entries *viz*, NSO 383, RKS 52, Himso 1676, JS 20-18, MACS 1188, JS 20-09, NRC 76, RKS 39, JS 335 and JS 95-60

as susceptible (Grade 7) remaining 65 entries were found highly susceptible under disease grade 9 against isolates L2.

Amrate *et al.* (2018) studied one hundred and nineteen soybean genotypes and results revealed that among all, forty four, fifty one and sixty three genotypes were found to be absolute/highly resistant against charcoal rot, aerial blight, and yellow mosaic diseases of soybean, respectively. While considering multiple resistance, only seventeen germplasm i.e. CAT 1483, CAT 1847, CAT 1927, CAT 411B, CAT 418, CAT 87, CAT 783, Himso 1681, JS 20-19, JS 20-21, JS 20-27, JS 21-05, JS 21-17, SL 710, SL 738, SL 900, SL 955 showed absolute/highly resistant reaction against all of three diseases *i.e* charcoal rot, aerial blight and YMV.

Joshi *et al.* (2018) evaluated soybean genotypes for resistance to *Rhizoctonia* aerial blight, Bacterial pustule, and mosaic and results revealed that only accession AMS 115 showed resistant with disease rating of 1 for all the three diseases *i.e.* YMV, BP and RAB, indicate no damage by all three important diseases. Whereas, 12 accessions (GP 499, JS 20-72, G5P22(IR), PKS 54, JS 20-80, PS 1241, Cat 586, Cat 751, PS 1347 (c), PS 1092 (c), Bragg (c) and PS 1042 (c) showed resistant with disease rating of 1 for YMV and BP, showing no damage by YMV and BP.

Mehra (2019) studied 46 genotypes of soybean, out of which 14 genotypes viz., AMS 59, EC 383165, YOUNG, HARDEE , JS 21-71, JS 21-72, JS -12, JS 12-01, JS 10-01,JS -06,JS 12-03, JS 10-02,JS 10-03 were identified as absolutely resistant to both *Rhizoctonia aerial blight* and charcoal rot incidence.

Nataraj *et al.* (2020) aimed to screen 125 Recombinant Inbred Lines (RILs) derived from the cross JS 97-52 × JS 90-41 for charcoal rot resistance using cut-stem inoculation technique. Out of 125, 21 lines were found to be resistant compared to the better parent JS 97-52

Chapter-3



MATERIALS AND METHODS

MATERIAL AND METHODS

The present research entitled “**Genetic Assessment and Morphological Characterization of Soybean Germplasm**” was carried out in *Kharif*, 2019. The materials used and methodologies employed to conduct the field experiment during the course of investigation are concisely described in this chapter.

3.1. Experimental material and other details

3.1.1. Experimental site

The experiment was conducted at Seed Breeding Farm, Department of Plant Breeding and Genetics, College of Agriculture, JNKVV, Jabalpur (M.P.) during *Kharif*, 2019. The soil of the experimental site is medium black with uniform topography and free from water logged conditions.

3.1.2. Climate and Weather

Jabalpur is located in “Kymore Plateau and Satpura Hills” agro-climatic area of Madhya Pradesh at 23.91° North latitude, 79.5° East longitudes and an altitude of 411.78 m above the mean sea level. The region has sub-tropical, semi-arid climate, hot and dry summer, and cold winter with occasional rains. The average rainfall is about 1200 mm. Nearly 90% of the total annual rainfall is mainly received between June last week to September last week. The minimum temperature goes to 22°C and maximum temperatures reach up to 35°C, respectively. The relative humidity varies from season to season and it ranges between 80% to 90% during rainy season, which reduces to 60% to 70% and 30% to 40% during winter and summer seasons, respectively.

As per National Bureau of Soil Science and Land Use Planning of ICAR, Jabalpur comes under agro-ecological sub region number 10.1 named as sub-humid dry eco-region. The climatic condition during the crop period were optimum for a normal plant growth (Appendix I)

Appendix I: Weekly meteorological parameters during Kharif season (June to October2019)

Month	SW	T max.	Tmin.	Sun Shine hrs.	Rainfall (mm)	RH Mor	RH Eve	Wind Speed	Vapur Presure (MM)		Evapo (mm)	Rainy days
									Morning	Evening		
July	27	29.9	23.1	1.3	178.8	94	87	5.9	22.5	24.5	2.9	3
	28	31.4	25.0	2.6	59.8	82	64	6.9	22.3	22.8	5.0	1
	29	34.9	25.0	8.7	24.4	82	59	4.8	22.8	23.7	5.3	2
	30	32.3	24.0	3.5	48.0	88	74	4.0	22.9	24.6	3.7	3
	31	29.6	23.9	1.5	47.6	93	81	5.1	23.6	24.5	2.5	4
August	32	29.9	23.5	2.7	210.0	92	81	3.3	23.0	23.8	2.8	4
	33	28.6	22.9	2.9	302.1	91	83	3.2	22.4	22.9	1.9	4
	34	29.2	22.5	1.4	212.9	97	83	2.1	23.0	23.6	4.9	7
	35	30.9	23.4	3.3	57.2	93	75	0.7	23.5	24.5	3.2	4
September	36	31.6	23.4	3.8	185.0	94	79	1.8	23.9	25.0	4.9	5
	37	28.5	23.4	1.2	101.4	93	83	1.9	22.9	23.7	2.5	5
	38	31.7	22.7	4.5	53.1	91	78	1.1	22.7	22.5	3.5	3
	39	29.5	22.1	2.5	77.6	93	78	1.6	21.4	21.7	2.7	4
October	40	30.1	21.0	7.2	14.3	90	66	1.1	20.6	20.2	3.0	2
	41	30.3	18.0	8.4	0.0	91	56	0.6	17.7	17.9	3.3	0
	42	29.2	18.7	5.6	2.2	93	63	0.6	17.9	17.4	2.3	0
	43	27.1	19.1	0.9	1.0	92	60	2.0	17.5	16.2	1.8	0
	44	30.3	17.7	5.3	0.0	92	52	1.1	17.3	16.5	2.3	0

3.1.3 Experimental material

The experimental material consists of 96 soybean accessions with four checks. Details of germplasm lines and checks used in the study are given in Table 3.1.

3.1.4 Design of experiment

The experiment was laid out in Augmented Block Design (ABD) with 96 accessions along with four checks. The experimental details are as follows: -

Design	: Augmented Block design (ABD)
Net plot size	: 4 m X 0.5 m
Distance between rows	: 0.5 m
Distance between plants	: 7 cm

3.2. Observations recorded

Observations were recorded based on five random competitive plants selected from each line for the evaluation of yield and yield contributing traits. Observations regarding morphological characteristics were recorded on individual plant as well as net plot basis. For quantitative observations, mean of large, medium and smallest value of each traits like number of primary branches/plant, number of pods/plant, number of nodes per plant, number of seeds/plant, 100 seed weight (g), Biological yield/plant (g), harvest index, seed yield/plant from each of the five randomly selected plants were used to record the observations of proposed genotypes in this investigation.

3.2.1 Morphological traits

1. Hypocotyl colour

Hypocotyl colour as the presence or absence of anthocyanin was observed in the field, visually in bright sunlight when cotyledons are completely unfolded.

2. Growth type

The plant growth type was observed at time of flowering/ maturity stage visually as determinate, semi-determinate and indeterminate.

Table 3.1: Experimental material

S. No	Germplasm	S. No	Germplasm	S. No	Germplasm	S. No	Germplasm
1	K-53	26	UGM 75	51	JS 20-34	76	EC 468597
2	EC-389153	27	MACS 303	52	SL (E)1	77	EC 572160
3	UPSL 152	28	NRC 2006M	53	PK 701	78	SL 682
4	EC 389179B	29	EC16213	54	PK 1038	79	PI 204336
5	UPSM 77	30	JS 20-52	55	RKS 54	80	UGM 70
6	EC 391181	31	PS 1475	56	EC 33940	81	LEE 96
7	VGM 70	32	NRC 37	57	G2225	82	TG X 1488-9-1D
8	VLS 75	33	MACS 171	58	JS 20-29	83	GP566
9	EC 391316	34	SL 2951	59	G4P15	84	PS1421
10	JS 97-52	35	EC 389099	60	GP 465	85	VLS 11
11	NRC 2007A	36	JS 20-69	61	TGX 849-D-13-4	86	PS 1467
12	NRC 80-1	37	JSM 195	62	JSM 227	87	EC 350664
13	JS 20-01	38	EC 291397	63	JS 20-98	88	EC 377883B
14	EC 396065	39	PS 1336	64	TG X 849-813	89	JS 20-34
15	DCB 137	40	EC 294003	65	KB-17	90	GC 84051-32-1
16	EC 457214	41	EC 291451	66	KDS 256	91	JS 20-50
17	DE 201	42	EC 24091	67	LEE-54	92	MACS-7102
18	EC 457336	43	RSC 14	68	JS 96-31	93	20-40B(Z-9)
19	AGS 12	44	EC 325103	69	TNAU 20024	94	20-148 (Z-15)
20	F4P20	45	JSM 285	70	SQL 37	95	23-10B(Z-17)
21	EC 103336	46	EC 33872B	71	WT 88	96	23-11A(Z-18)
22	NRC 86	47	SQL 1	72	TNAU 20022	C1	JS 20-34
23	EC 106998	48	JSM 232	73	EC 528640	C2	JS 335
24	SL 752	49	JSM 222	74	EC 538830	C3	JS 20-98
25	EC 109540	50	JSM 245	75	PK 258	C4	NRC 86

3. Growth habit

The plant growth habit was recorded at full flowering stage visually as erect, semi-erect and semi-erect to horizontal.

4. Leaf shape

Shape of the lateral leaflets was observed visually at full flowering stage to be either Lanceolate, triangular, pointed ovate or rounded ovate.

5. Leaf size of lateral leaflet

It was observed visually at full flowering stage to be either small, medium or large.

6. Leaf intensity of green colour

The leaf intensity of green colour were observed visually at full flowering stage and recorded to be as light, medium and dark green.

7. Flower colour

The colour of fully developed freshly open flowers was observed visually in morning hours as white or violet.

8. Pod: presence of hairs

It was observed at advanced pod filling stage when about 70% of the pods have reached final length (15-20 mm) to be either present or absent.

9. Pod: colour of hairs

The pod colour was observed at advanced pod filling stage as grey or tawny.

10. Pod: intensity of brown colour

The intensity of brown colour were observed at advanced ripening stage and recorded to be either light, medium or dark brown.

11. Ripened seed: seed size

The size of seed was observed as the weight of randomly selected 100 ripe seeds (12-14% moisture) as small (<10 g), medium (10-13 g) and bold/ large (> 13 g).

12. Ripened seed: seed shape

Fully developed and matured seeds were visually observed to classify genotypes based on seed shape as spherical, spherical-flattened, elongated and elongated-flattened.

13. Ripened seed: ground colour of testa

The colour of testa excluding hilum were observed of the randomly selected ripe seeds (12-14 % moisture) as yellow, yellow-green, green and black.

14. Ripened seed: seed coat lusture

The luster of randomly selected ripe seeds was visually observed as shiny, intermediate and dull.

15. Ripened seed: hilum colour

Hilum colour of all the genotypes was visually observed after the seed threshing as grey, yellow, brown, imperfect black and black.

16. Ripened seed: colour of hilum funicle

The colour of hilum funicle were observed of the randomly selected ripe seeds as either same as testa or different from testa.

17. Ripened seed: colouration due to peroxidase activity

The seed coat of the genotypes was chemically tested for the presence or absence of peroxidase activity and allotted diverse scores based on the color gradient obtained. The intensity of the color developed on the seed is observed as absence (0), light red (1), red (2), medium red (3), dark red (4), very dark red (5).

3.2.2 Quantitative traits

1. Days to flower initiation

Days to flower initiation taken from the date of sowing to the date when plants have at least one flower.

2. Days to maturity

Number of days taken from the date of sowing to the date when 95% pods turn yellow or brown.

3. Plant height (cm)

The height of five plants was measured at physiological maturity in centimeters from the ground level to the tip of the plant and averaged

4. Number of primary branches per plant

The number of primary branches of five tagged plants from each line was recorded and mean was calculated.

5. Number of nodes per plant

The total number of nodes per plants of five plants was counted from the base of the plant above ground from first node to the top most node and mean was calculated

6. Number of pods per plant

The total numbers of pods per plant at maturity were counted on five plants and averaged to obtain mean.

7. Number of seeds per plant

Number of seeds per plant was counted from five random plants and averaged.

8. 100 seed weight (g)

Weight of 100 seeds drawn randomly from each genotype was taken in gram.

9. Biological yield per plant (g)

Dry weight of five tagged plants harvested above the ground level from each genotype was taken before threshing.

10. Harvest index (%)

It is also known as partitioning efficiency and was calculated by taking the % ratio of Seed yield to Biological yield. Harvest index was worked out from the following formula:

$$\text{Harvest Index} = \frac{\text{Seed yield}}{\text{Biological yield}} \times 100$$

11. Seed Yield per plant (g)

The tagged five plants were harvested and threshed separately. The seed yield of individual plant was weighed in gram and averaged to obtain mean yield per plant.

3.2.3 Physiological traits

1. Chlorophyll Content index (SPAD)

Chlorophyll content which is expressed as grams of chlorophyll per unit ground area (Nishimura, 1964; Okubo et al. (1968) and was determined in the 4th leaf of five weeks old plant using a non-destructive method that uses an optical instrument called chlorophyll meter (Model: CCM 200 Made in USA).

2. Leaf area index (LAI)

LAI expresses the ratio of leaf surface (One side only) to the ground area occupied by the plant or a crop stand worked out as per specifications of Gardner et al. (1985).

$$LAI = \frac{\text{Total leaf area}}{\text{Land area}} \times 100$$

3. Leaf Area Duration (LAD)

Leaf area duration expresses the magnitude and persistence of leaf area of leafiness during the period of crop growth. It reflects the extent of seasonal integral of light interaction and correlates with yield. LAD was computed as follows: (Watson, 1952)

$$LAD = \frac{(LA_1 + LA_2) \times T_2 - T_1}{2}$$

4. Specific leaf area (SLA)

The specific leaf area expresses the ratio between the leaf area (LA) and leaf dry weight (LW) (Gardner et al., 1985).

$$SLA = \frac{(LA_2/LW_2 + LA_1/LW_1)}{2} \text{ (cm}^2\text{/g)}$$

3.2.4 Biochemical estimations

The soybean seed were analyzed for the biochemical constituents as follows:

S. No.	Biochemical contents	Plant parts	Stages
1	Protein	Seed	Maturity
2	Fat	Seed	Maturity

3.2.4.1 Estimation of protein % in seeds

The nitrogen content was estimated by micro kjeldhal method (A.O.A.C., 1965) as per method suggested by Gopalan *et al.* (1985). For estimation, 0.1 gm of sample was digested with concentrated sulphuric acid (10 ml) in 9 digestion of (CuSO_4 , 5 H_2O and 0.34 g solution selenate). After digestion for about 3 hours till liquid becomes colourless, the digestion tube was allowed to cool and the contents carefully diluted to 100 ml with distilled water. The solution is then transferred quantitatively to a distillation apparatus, 15 ml of 40% of sodium hydroxide was added and the liberating ammonia was collected in a flask containing 10 ml of 2 percent boric acid with two drops of mixed indicator (Bromocresol green + methyl red). Distillation was continued for 5-minute appearance of green colour to ensure the complete evaluation of ammonia. After distillation solution was titrated with 0.1N H_2SO_4 .

Nitrogen and protein percent were calculated by the following formula:

$$\text{Nitrogen} = \frac{14 \times \text{Normality of } \text{H}_2\text{SO}_4 \times \text{Vol. of } \text{H}_2\text{SO}_4 \times 100}{\text{Weight of sample} \times 100}$$

Protein percent in the sample was estimated multiplying nitrogen percent of sample by factor 6.25. Protein (%) = Nitrogen % $\times$ 6.25

3.2.4.2 Estimation of fat content

The fat content in the sample was estimated by pelican equipment socs plus based on principle of Soxhlet's extraction method as described in AOAC (1980). The extract method used for this purpose is given below.

Procedure

2 g sample was weighed accurately into a thimble and plugged with fat free cotton. The extraction flask (A). Fat content was determined by extracting the sample with solvent, petroleum ether (A) Grade 60-80 fraction, for 6 hours by Soxhlet's extraction procedure. After extraction excess of ether is evaporated until no colour of ether remained. Cooled at room temperature and weighed the flask (B). The percent of fat was calculated by using formula: -

$$\text{Fat \% in ground sample} = \frac{\text{Wt. of flask B} - \text{Wt. of flask A}}{\text{Wt. of sample}} \times 100$$

3.3 Statistical analysis

Statistical analysis was performed for following parameters:

3.3.1 Analysis of variance

3.3.2 Parameters of genetic variability

3.3.3 Correlation coefficient analysis

3.3.4 Path coefficient analysis

3.3.5 Genetic divergence using Mahalanobis D^2 analysis

3.3.1 Analysis of variance

The mean data on five plants were subjected to variance analysis and test of significance as per the method of Sharma (1999).

The data on quantitative characters were statistically analyzed on the basis of model described for Augmented randomized block design.

$$Y_{ij} = (\mu + b_i + t_j + e_{ij}) n_{ij}$$

Where,

Y_{ij} = Performance of j^{th} genotype in i^{th} block

μ = General mean

b_i = True effect of i^{th} block

t_j = True effect of j^{th} treatment

e_{ij} = Random errors which are supposed to be identically and independently distributed with normal distribution having mean zero and variance σ^2_e .

Table 3.2 Skeleton of Anova for Augmented Randomized Block Design

Source of Variation	d.f.	Sum of Squares	Mean Squares	F value	Expected mean squares
Blocks	(b-1)	bSS	bMS	bMS/EMS	
Entries	(e-1)	eSS	eMS	eMS/EMS	$\sigma^2_g = MS_g - MS_e/r$
Checks	(c-1)	cSS	cMS	cMS/EMS	
Varieties	(v-1)	vSS	vMS	vMS/EMS	
Checks vs. varieties	1	cvSS	cvMS	cvMS/EMS	
Error	(c-1)(b-1)	ESS	EMS		
Total	(N-1)	TSS			

$$1. \text{Genotypic variance } (\sigma^2_g) = \frac{M_2 - M_3}{R}$$

$$2. \text{Phenotypic variance } (\sigma^2_p) = \frac{M_2 - M_3}{R} + M_3$$

$$3. \text{Environmental variance } (\sigma^2_e) = M_3$$

Where,

r = Number of replications

g = Number of genotypes

M₁ = Mean square due to replication

M₂ = Mean square due to genotype

M₃ = Mean square due to error

A significant value of F-test 5% and 1% level indicates that the genotypes differ significantly among themselves, which requires computing the critical difference (CD).

$$\text{Standard error of difference of mean SE (d)} = \sqrt{\frac{2 \text{ EMS}}{r}}$$

$$\text{Critical difference (CD)} = \text{SE}_{(d)} \times t_{\alpha}$$

Where,

t_α = t-value at 5% and 1% probability level

EMS = Error mean square from Anova

The significance of the computed mean squares was tested making ratio of respective mean square against error mean square. The calculated value of F(Fc) compared with table value of F(Ft) at n₁ and n₂ (error d.f.) degrees of

freedom. If calculated value is >F tabulated at given probability level is said to be significant.

3.3.2 Parameters of genetic variability

3.3.2.1 Mean

The average of recorded observation was calculated as follows:-

$$Mean(\bar{X}) = \frac{\sum x_i}{n}$$

Where,

$\sum X_i$ = Summation of all values of observation

n = Number of observed values

3.3.2.2 Range

Range is the difference between the smallest and the greatest term of a series of observation and thus provides the information about the variability present in the genotypes.

3.3.2.3 Phenotypic coefficient of variation (PCV)

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

$$P C V = (\sigma p / \bar{X}) \times 100$$

Where, $\sigma p = \sqrt{\sigma^2 p}$

3.3.2.4 Genotypic Coefficient of Variation (GCV)

$$GCV = (\sigma g / \bar{X}) \times 100$$

Where, $\sigma g = \sqrt{\sigma^2 g}$

Where,

- $\sigma^2 p$ = Phenotypic variance
- σp = Phenotypic standard deviation
- $\sigma^2 g$ = Genotypic variance
- σg = Genotypic standard deviation
- $\sigma^2 e$ = Environment variance
- $\bar{X}$ = General Mean

3.3.2.5 Heritability

Heritability in broad sense was estimated by the following formula given by Hanson (1956):

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

The range of heritability was categorized as low (below 50 per cent), moderate (50-70 per cent) and high (above 70 per cent) as followed by Johnson *et al.* (1955).

3.3.2.6 Genetic advance

The estimates of expected genetic advance from selection, $G(s)$, was obtained by the formula suggested by Johnson (1955).

$$G(s) = K \times h^2 \times \sigma_p$$

Where,

K = Selection intensity (value of K at 5% 2.06),

h^2 = Heritability in broad sense, and

σ_p = Phenotypic standard deviation

3.3.2.7 Genetic advance as percentage of mean

It was calculated by the following formula:

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

The range of genetic advance as percent of mean is classified as suggested by Johnson *et al.* (1955).

< 10 per cent = low

10-20 per cent = moderate

> 20 per cent = high

3.3.3 Correlation coefficients analysis

Correlation coefficients were calculated for combination of all characters under study at genotypic, phenotypic and environmental levels with the help of formula suggested by Miller et al. (1958).

$$r_{ij} = \frac{Cov(ij)}{\sqrt{(\sigma^2 i)(\sigma^2 j)}}$$

Where,

r_{ij} = Correlation coefficient between i^{th} and j^{th} traits

$Cov (ij)$ = Covariance between i^{th} and j^{th} traits

$\sigma^2 i$ = Variance of i^{th} trait

$\sigma^2 j$ = Variance of j^{th} trait

To test the significance of phenotypic correlation coefficients, the estimated values were compared with the tabulated values of Fisher and Yates (1963) at $n-2$ d.f. at two levels of probability, viz., 5% and 1%.

$$T_{cal.} = \frac{r}{\sqrt{(1 - r^2)}} \times \sqrt{n - 2} \quad \text{at } (n - 2) \text{ d. f.}$$

3.3.4 Path coefficient analysis

It is a simple standardized partial coefficient method to detect the direct and indirect effects of the independent variable on dependent variable. It permits separation of correlation into components of direct and indirect effects.

The method of path coefficient was developed by Wright (1921) and modified by Dewey and Lu (1959). The following set of simultaneous equations were formed and used for estimation of direct and indirect effects on seed longevity.

Path coefficients were obtained by simultaneous equations which express basic relationship between correlation and path coefficient.

$$r_{1y} = P_{1y} + P_{2y}r_{12} + P_{3y}r_{13} + \dots P(n-1)_y r_1 (n-1)$$

$$r_{2y} = P_{2y} + P_{1y}r_{21} + P_{3y}r_{23} + \dots P(n-1)_y r_2 (n-1)$$

$$r_{3y} = P_{3y} + P_{2y}r_{32} + P_{1y}r_{31} + \dots P(n-1)_y r_3 (n-1)(n-1) r(n-1)$$

$$y = P(n-1)y + P(n-2)y r(n-1)(n-3)y r(n-1)(n-3) + \dots + P(n-(n-1))y r_1(n-1)$$

Where,

y = is the dependent variable i.e. yield per plant

r = Genotypic or phenotypic correlation coefficients between a pair of character

n = Total number of characters under study

Apart from these variations, unexplained residual variation is also there, which is an account of residual factor which is calculated by following formula.

Residual effect:

$$1 = R^2 + P_1y^2 + P_2y^2 + \dots + [p(n-1)y]^2 + 2\{p_1yP_2y r_{12} + P_1y P_3y r_{13} + P_1y P_4y r_{14} + \dots + p(n-2)y p(n-1)y r(n-2)\}$$

$$1 = R^2 + X$$

Where,

X is equal to sum of all terms of right hand side of equation except R^2 .

$$\text{Or } R^2 = (1-X)$$

Therefore,

$$R = \sqrt{(1-X)}$$

Later the path coefficients were rated based on the scales given below (Lenka and Mishra, 1973).

>1.00 = Very high

0.3-0.99 = High

0.2-0.29 = Moderate

0.1-0.19 = Low

0.0-0.09 = Negligible

3.3.6: Principle component analysis

PCA is a well-known method of dimension reduction (Massy, 1965; Jolliffe, 1986), which seeks linear combinations of the columns of X with maximal variance, or equivalently, high information. It is routinely applied in chemometrics

with the goal of providing the most compact representation of the data. The original p variables $\mathbf{X} = [\mathbf{x}_1 \dots \mathbf{x}_p]$ are transformed in a new predictor set $\mathbf{T} = [\mathbf{t}_1 \dots \mathbf{t}_k]$, with $k \leq \min(n-1, p)$. The new variables $\mathbf{t}_j$, called *scores*, are a weighted average of the original $\mathbf{X}$ variables. The *principal components* are the eigenvectors, $\mathbf{u}_j$ from the eigen decomposition of $\mathbf{X}'\mathbf{X}$ (and of the sample covariance matrix $\mathbf{S}$, up to a constant). PCA sequentially maximises the variance of a linear combination of the original predictor variables

$$\mathbf{U}_j = \arg \max \text{Var}(\mathbf{X}\mathbf{u}),$$

$$\mathbf{u}=1$$

Subject to the constraint that $\mathbf{u}' \mathbf{S} \mathbf{u}_j = 0$ for all $1 \leq i < j$. This ensures that $\mathbf{t}_j = \mathbf{X}\mathbf{u}_j$ is uncorrelated with all the previous linear combinations $\mathbf{t}_i = \mathbf{X}\mathbf{u}_i$. The principal components are ordered in terms of the amount of variation of the original data they account for. The first principal component direction has the property that $\mathbf{t}_1 = \mathbf{X}\mathbf{u}_1$ has the largest sample variance among all normalized linear combinations of the columns of $\mathbf{X}$. Each subsequent component gives combinations with the largest possible variance which is uncorrelated with those that have been taken earlier.

There are various standard approaches to find the principal components, e.g. taking the singular value decomposition of $\mathbf{X}$. In chemometrics, it is common to estimate the principal components using the nonlinear iterative partial least-squares (NIPALS) algorithm (Wold, 1966). This is because the number of required components is usually much less than the total possible number ($k \ll p$). In fact, the NIPALS algorithm does not calculate all the principal components at once, but it first calculates $\mathbf{t}_1$ and $\mathbf{u}_1$ from the $\mathbf{X}$ matrix. Then the outer product $\mathbf{t}_1 \mathbf{u}_1'$ is subtracted from $\mathbf{X}$ and the residual $\mathbf{X}_2$ is calculated. In turn, this residual can be used to calculate $\mathbf{t}_2$ and $\mathbf{u}_2$.

3.3.5 Genetic divergence using Mahalanobis D^2 analysis

3.4.5.1 Genetic divergence

D^2 analysis: Mahalanobis (1928) defines D^2 analysis as follows.

$$D^2P = b_1d_1 + b_2d_2 + \dots + b_p d_p$$

A resource for group distance based on multiple characters with $X_1, X_2, X_3, \dots, X_p$ as the multiple measurements available on each individual and $d_1, d_2, \dots, d_p$ as $\bar{x}_{1_1}, \bar{x}_{2_2}, \dots, \bar{x}_{1_p}, \bar{x}_{2_p}$, respectively is the difference in the means of two populations. The 'P' values are to be estimated that the ratio of variance between the populations to the variance within the populations is maximized. Taking variance and covariance under consideration, the D^2 value may be estimated by this formula. 2

$$D^2 = \sum w_{ij} \sum \left(\frac{1}{\bar{x}} - \frac{2}{\bar{x}} \right) \left(\frac{1}{\bar{x}} - \frac{2}{\bar{x}} \right)$$

Where, W_{ij} is the inverse of estimated variance and covariance matrix

3.4.5.2 Steps to estimate D^2 value

3.4.5.2.1 Collection of data:

Data were collected considering "V" population and "P" characters which have ed on each individual.

3.4.5.2.2 Test of significance

According to Wilk's criteria, a simultaneous test of difference between mean values of number of correlated variances is done (Rao, 1948). Using pivotal condensation method, the determinant of error and error variety matrix will be calculated.

$$A = \left| \begin{array}{c} W \\ S \end{array} \right| = \frac{\text{Determinant of error matrix}}{\text{Determinant of error + variety matrix}}$$

$$V(\text{State}) = -m \log \frac{(p+g+1)}{2} e = -[n] \log e$$

Where

$$M = n - (p+q+1)/2$$

P = Number of variance or character

Q = Degree of freedom for population

N = Degree of freedom for error + variety

E = Constant (2.7183)

V (state) is distributed as X^2 with Pq degree of freedom.

The tabulated value of X^2 for Pq degree of freedom at 5% level is compared with the X^2 value for testing the significance.

3.4.5.2.3 Transformation of correlated values

Transformation is done by using pivotal consideration method. The correlated variables are first transformed into uncorrelated once and D^2 values are calculated.

3.4.5.2.4 Computation of D^2 values

The D^2 value obtained for a pair of population is taken as the calculated value of X^2 and is tested against the tabulated value of X^2 at “P” degree of freedom, where “P” is the number of characters considered.

3.4.5.2.5 Contribution of individual characters towards divergence

In all combination, each character is ranked on the basis of $d_i = Y_{ij} - Y_{ik}$ values. Rank 1 is given to the highest mean difference where “P” is the total number of characters.

3.4.5.2.6 Grouping of varieties into various clusters by Tocher's method

Populations are grouped in order to their relative genetic distance from each other in the first step grouping of different varieties into distinct clusters. The two population having the least distance from each other are considered first to which a third population having the smallest D^2 value from the first two population is added, then comes the fourth population and so on. There is disrupt increase in the average D^2 at certain stage by adding a particular population, then this population is not added in the cluster.

Similarly, second cluster is formed. The process is continued till all the populations are included into one or other cluster.

3.4.5.2.7 Average intra cluster distance

The formula is used for measuring the intra cluster distance is as follow

$$\sum D_i^2/n$$

Where,

$\sum D_i^2/n$ is the sum of distance between all possible contributions (n) of the population included in the cluster.

3.4.5.2.8 Average inter-cluster distance

First of all, the distance clusters are measured. The clusters are taken one by one and their distances from another cluster are calculated.

3.4 Screening for multiple disease resistance

To evaluate resistance in different germplasm accessions of soybean, the lines were also screened against biotic stresses like Charcoal rot, YMV, Bacterial pustules and *Rhizoctonia* aerial blight diseases. Each genotype was observed critically for the appearance, progress and severity of single or complex of the diseases throughout the cropping season. Different ratings or grades were assigned to each genotype for Charcoal rot, YMV, Bacterial pustules and *Rhizoctonia* aerial blight based on their severity (Anonymous, 2012) as per the following scales:

A. Scale for classifying reaction of Charcoal rot: Per cent mortality was recorded and genotypes were classified as given below:

Rating	Descriptions	Category
0	No mortality	Absolutely resistant
1	1 % mortality	Highly resistant
3	1.1 to 10 % mortality	Moderately resistant
5	10.1 to 25 % mortality	Moderately susceptible
7	25.1 to 50 % mortality	Susceptible
9	More than 50 % mortality	Highly susceptible

B. Scale for classifying reaction of *rhizoctonia* aerial blight and bacterial pustule:

Each infected plant was observed and 0-9 ratings/ grades were assigned based on the per cent leaf area infected.

Table 3.3. Rating description for *Rhizoctonia* aerial blight and bacterial pustule

Rating	Descriptions
0	No lesions/spots
1	1% leaf area covered with lesions/spots
3	1.1 to 10% leaf area covered with lesions/spots, no spots on stem
5	10.1 to 25% of leaf area covered, no defoliation; little damage
7	25.1 to 50% leaf area covered; some leaves drop; death of few plant, damage conspicuous
9	More than 50% area covered, lesions/spots very common on all plants, defoliation common; death of plants common; damage more than 50%

Table 3.4. Wheeler's scale for Per cent Diseases Index (PDI)

PDI	Category
0.0	Absolutely resistant
0.1 – 1.0	Highly resistant
1.1-10.0	Moderately resistant
10.1- 25.0	Moderately susceptible
25.1 - 50.0	Susceptible
> 50.0	Highly susceptible

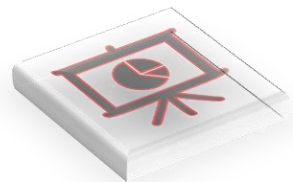
C. Scale for classifying reaction of Yellow mosaic disease:

This screening method is based on per cent incidence (number of plant infected) and their interaction with per cent disease severity (number of leaves infected in a plant).

Based on the disease severity, symptom severity grades (0-4) and response values (0-1) corresponding to such grades were assigned. The coefficient of infection (CI) was calculated by multiplying the percent disease incidence to the response value assigned for each severity grade following standard methodology (Singh and Singh, 2000).

Symptoms	Severity grade	Response value	Coefficient of Infection (CI)	Disease reaction
Symptoms absent	0	0	0-4	Highly resistant
Very mild symptoms up to 25% leaves	1	0.25	5-9	Resistant
Appearance of symptoms in 26-50% leaves	2	0.50	10-19	Moderately resistant
Appearance of symptoms in 51-75% leaves	3	0.75	20-39	Moderately susceptible
Severe disease infection in symptoms (>75% leaves)	4	1.00	40-69	Susceptible
			70-100	Highly susceptible

Chapter-4



RESULTS

RESULTS

The present investigation was carried out on 96 germplasm accessions of soybean along with four checks in Augmented Block Design at Seed Breeding Farm, JNKVV, Jabalpur, during *Kharif*, 2019.

To get a clear picture of variability in the accessions, the genetic parameters of variability were studied. Correlation analysis among traits was performed to find out the degree of relationship between yield and its attributing characters. Path coefficient analysis was carried out to have an idea of direct and indirect effects of various independent traits on yield. D^2 analysis was performed to find out the inter and intra cluster distances between germplasm lines of soybean to select best divergent parents for further hybridization programme.

The experimental results of the present investigation have been mentioned under following sub-heads.

- 4.1 Morphological characterization
- 4.2 Analysis of variance
- 4.3 Parameters of genetic variability
 - 4.3.1 Mean and range
 - 4.3.2 Genotypic and phenotypic coefficient of variation
 - 4.3.3 Heritability
 - 4.3.4 Genetic advance
- 4.4 Correlation coefficient analysis
- 4.5 Path coefficient analysis
- 4.6 Principal component analysis
- 4.7 Genetic divergence using Mahalanobis D^2 analysis
- 4.8 Physiological growth parameters
- 4.9 Biochemical estimations
- 4.10 Screening against multiple disease resistance

4.1 Morphological characterization of genotypes

In this experiment, hundred soybean genotypes were characterized on the basis of morphological traits viz., hypocotyl colour, growth type, growth habit, leaf shape, leaf size, leaf intensity of green colour, flower colour, pod: presence

of hairs, pod : colour of hairs , pod: intensity of brown colour, ripe seed : seed size, ripe seed : seed shape, ripe seed : ground colour of testa, ripe seed : seed coat lusture, ripe seed : colouration due to peroxidase activity, ripe seed : hilum colour, ripe seed: colour of hilum funicle. The categorization of different genotypes based on seventeen morphological traits is mentioned in table 4.1 (A) and 4.1 (B)

Table: 4.1 (A)- Frequency distribution of visual and morphological traits in soybean germplasm

Trait	Classes	Number of genotypes	Frequency (%)
1. Hypocotyl colouration	Present	63	63
	Absent	37	37
2. Growth habit	Determinate	1	1
	Semi-determinate	99	99
	Indeterminate	00	00
3. Growth type	Erect	01	01
	Semi-erect	99	99
	Semi erect to horizontal	00	00
4. Leaf shape	Lanceolate	00	00
	Pointed ovate	76	76
	Round ovate	34	34
5. Leaf size	Small	14	14
	Medium	75	75
	Large	11	11
6. Leaf intensity of green	Light	15	15
	Medium	48	48
	Dark	37	37
7. Flower colour	White	37	37
	Violet	63	63
8. Pods: presence of hairs	Present	82	82
	Absent	18	18
9.Pod: Colour of hairs	Tawny	67	67
	Grey	22	22
	Absent	11	11
10. Pod: Intensity of brown color at maturity	Light	24	24
	Medium	52	52
	Dark	24	24
11. Seed : ground colour of testa	Yellow	90	90
	Yellow green	02	02
	Green	02	02
	Black	04	04
	Brown	02	02

12. Seed size	Small	13	13
	Medium	81	81
	Bold	06	06
13. Seed shape	Spherical	16	16
	Spherical flattened	46	46
	Elongated	20	20
	Elongated flattened	18	18
14. Seed coat lusture	Shiny	26	26
	Intermediate	56	56
	Dull	18	18
15. Hilum colour	Grey	14	14
	Brown	46	46
	Intermediate black	08	08
	Black	32	32
16. Colour of Hilum funicle	Same as testa	90	90
	Different to testa	10	10
17. Seed : Peroxidase activity	0	12	12
	1	24	24
	2	23	23
	3	20	20
	4	11	11
	5	10	10

Expressions of following morphological traits were observed visually for distinctiveness and variations

4.1.1 Morphological traits:

1. Hypocotyl colour

Hypocotyl colour as the presence [9] or absence [1] of anthocyanin was observed in the field. Sixty-three genotypes showed presence of colouration and thirty-seven with no colouration.

2. Growth type

On the basis of plant growth type, genotypes were categorized in two groups i.e. determinate [1], semi-determinate [2] and indeterminate [3]. Ninety-nine genotypes were semi determinate and one genotype was found determinate.

3. Growth habit

The plant growth habit was recorded as erect [1], semi-erect [2] and semi-erect to horizontal [3]. Ninety- nine genotypes were semi erect and one genotypes was of erect growth habit.

4. Leaf shape

Based on shape of lateral leaflet, genotypes were categorized into three groups i.e. lanceolate [1]; pointed ovate [2]; and rounded ovate [3]. Four genotypes had lanceolate, seventy-six with pointed ovate and remaining thirty-four were with rounded ovate shape of leaves.

5. Leaf size of lateral leaflet

Based on size of lateral leaflet, the genotypes were categorized into three groups i.e. small [1]; medium [2] and large [3]. Seventy- five genotypes were having medium sized leaf, eleven genotypes had larger leaves and fourteen were small sized leaf.

6. Leaf intensity of green colour

The leaf intensity of green colour was observed as light [1], medium [2] and dark green [3]. Forty- eight genotypes were medium coloured leaf, thirty-seven were dark leaf and remaining fifteen had light coloured leaves.

7. Flower colour

Only two types of flower colour are found in soybean i.e. white [1] and violet [2]. Sixty- three genotypes showed violet coloured flowers and remaining thirty- seven genotypes had white flowers.

8. Pod: presence of hairs

On the basis of presence or absence of hair on pod, genotypes were categorized in two groups i.e. pubescent (presence of hairs) [1] and glabrous (absence of hairs) [2]. Eighty-two genotypes had pubescence (either grey or tawny) and remaining eighteen genotypes were glabrous.

9. Pod: colour of hairs

The pod colour was observed at advanced pod filling stage as grey [1]; tawny [2] or absent [3]. Out of hundred, sixty-seven genotypes reported tawny

Plate 1: Field conditions during Kharif, 2019



Field conditions at different crop growth stage



Characterization of Soybean Genotypes

Plate 2: Variation in Hypocotyl Colour

Hypocotyl: Anthocyanin colouration



Plate 3: Variation in Flower Colour, Leaf Colour and Leaf Shape

Flower Colour



White Flower



Violet Flower

Leaf Shape



Pointed Ovate



Round Ovate

Leaf Colour



Light green

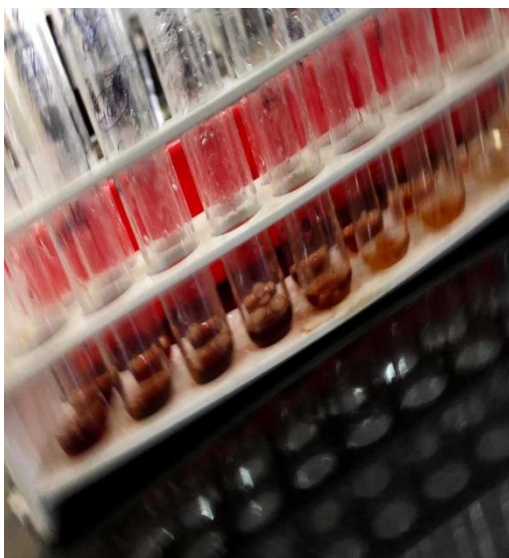


Medium green



Dark green

Plate 4: Intensity of the colour due to peroxidase activity



Colour gradient developed on the seed coat due to peroxidase activity

pubescence, twenty-two were observed with grey coloured pubescence and in eleven remaining genotypes pod hairs were absent.

10. Pod: intensity of brown colour

The soybean genotypes on the basis of pod colour are categorized as light [1]; medium [2] and dark [3]. Twenty-four genotypes showed light intensity of brown colour, fifty-two genotypes showed medium intensity of brown colour and remaining twenty-four had dark brown coloured pod.

11. Ripe seed: seed size

On the basis of seed size, genotypes are categorized in three groups i.e. small (<10 g) [1]; medium (10-13 g) [2] and bold/ large (>13 g) [3]. Thirteen genotypes were of small sized seeds, eighty-one were medium and remaining six had bold sized seeds.

12. Ripe seed: seed shape

On the basis of seed shape, genotypes were categorized in four groups i.e. spherical [1], spherical flattened [2], elongated [3] and elongated flattened [4]. Seeds of sixteen genotypes were found of spherical shape, forty-six were spherical flattened, twenty were elongated and remaining eighteen genotypes was elongated flattened.

13. Ripe seed: ground colour of testa

The colour of testa excluding hilum were observed as yellow [1], yellow-green [2], green [3] black [4] and brown [5]. Out of hundred genotypes, ninety genotypes were having yellow seed coat colour, two were having yellow-green colour, two were having green seed coat colour, four were having black seed coat colour and remaining two had brown colour.

14. Ripe seed: seed coat lusture

The lusture of randomly selected ripe seeds were visually observed as shiny [1], intermediate [2] and dull [3]. Twenty-six genotypes had shiny seed coat lusture, fifty-six had intermediate and remaining eighteen were of dull seed coat lusture.

15. Ripe seed: hilum colour

On the basis of hilum colour, genotypes were categorized in four groups i.e. Grey [1], Yellow [2], brown [3], Imperfect black [4] and black [5]. Fourteen genotypes exhibited grey hilum, thirty-two brown hilum, eight imperfect black and remaining forty-six had black colour of hilum.

16. Ripe seed: colour of hilum funicle

The colour of hilum funicle were observed as either same as testa [1] or different from testa [2]. Ninety genotypes were reported to have hilum funicle colour same as testa and remaining ten were having hilum funicle colour different to testa.

17. Ripe seed: colouration due to peroxidase activity

The seed coat of the genotypes was chemically tested for the presence [1] or absence [2] of peroxidase activity of which ten genotypes were observed with the presence of coloration in seed coat with a score of 5, eleven with a score of 4, twenty with a score of 3, twenty three with a score of 2 and twenty four with a score of 1 and remaining twelve genotypes had no coloration due to peroxidase activity i.e. had score 0.

Table. 4.1 (B): Categorization of soybean genotype based on morphological traits

Character	Classes	Genotypes
1. Hypocotyl colouration	Present	K-53, EC-389153, UPSL 152, EC 389179B, UPSM 77, EC 391181, VGM 70, EC 391316, JS 20-01, EC 396065, EC 457214, DE 201, AGS 12, EC16213, EC 103336, NRC 86, EC 106998, SL 752, EC 109540, MACS 171, SL 2951, EC 389099, EC 325103, JSM 285, EC 33872B, SQL 1, JSM 222, SL (E)1, PK 701, PK 1038, EC 291397, SQL 37, WT 88, TNAU 20022, EC 528640, EC 538830, PK 258, EC 468597, EC 572160, SL 682, PI 204336, UGM 70, LEE 96, TG X 1488-9-1D, JS 335, TNAU 20024, NRC 86, EC 350664, EC 377883B, TGX 849-D-13-4, LEE-54, PS1421, VLS 11, EC 33940, G2225, GC 84051-32-1, G4P15, TG X 849-813, KB-17, MACS-7102, EC 294003, EC 291451, EC 24091.
	Absent	VLS 75, JS 97-52, NRC 2007A, NRC 80-1, DCB 137, EC 457336, F4P20, UGM 75, MACS 303, NRC 2006M, JS 20-52, PS 1475, NRC 37, JS 20-69, JSM 195, PS 1336, RSC 14, JSM 232, JSM 245, JS 20-34, RKS 54, JS 20-29, GP 465, JSM 227, JS 20-98, KDS 256, JS 96-31, GP566, PS 1467, JS 20-34, JS 20-50, 20-40B(Z-9), 20-148 (Z-15), 23-10B(Z-17), 23-11A(Z-18), JS 20-34, JS 20-98.
2. Growth habit	Determinate	JS 20-34
	Semi-determinate	K-53, EC-389153, UPSL 152, EC 389179B, UPSM 77, EC 391181, VGM 70, EC 391316, JS 20-01, EC 396065, EC 457214, DE 201, AGS 12, EC16213, EC 103336, NRC 86, EC 106998, SL 752, EC 109540, MACS 171, SL 2951, EC 389099, EC 325103, JSM 285, EC 33872B, SQL 1, JSM 222, SL (E)1, PK 701, PK 1038, EC 291397, SQL 37, WT 88, TNAU 20022, EC 528640, EC 538830, PK 258, EC 468597, EC 572160, SL 682, PI 204336, UGM 70, LEE 96, TG X 1488-9-1D, JS 335, TNAU 20024, NRC 86, EC 350664, EC 377883B, TGX 849-D-13-4, LEE-54, PS1421, VLS 11, EC 33940, G2225, GC 84051-32-1, G4P15, TG X 849-813, KB-17, MACS-7102, EC 294003, EC 291451, EC 24091, VLS 75, JS 97-52, NRC 2007A, NRC 80-1, DCB 137, EC 457336, F4P20, UGM 75, MACS 303, NRC 2006M, JS 20-52, PS 1475, NRC 37, JS 20-69, JSM 195, PS 1336, RSC 14, JSM 232, JSM 245, JS 20-34, RKS 54, JS 20-29, GP 465, JSM 227, JS 20-98, KDS 256, JS 96-31, GP566, PS 1467, JS 20-34, JS 20-50, 20-40B(Z-9), 20-148 (Z-15), 23-10B(Z-17), 23-11A(Z-18), JS 20-98.
	Indeterminate	Nil

3. Growth type	Erect	JS 20-34
	Semi- erect	K-53, EC-389153, UPSL 152, EC 389179B, UPSM 77, EC 391181, VGM 70, EC 391316, JS 20-01, EC 396065, EC 457214, DE 201, AGS 12, EC16213, EC 103336, NRC 86, EC 106998, SL 752, EC 109540, MACS 171, SL 2951, EC 389099, EC 325103, JSM 285, EC 33872B, SQL 1, JSM 222, SL (E)1, PK 701, PK 1038, EC 291397, SQL 37, WT 88, TNAU 20022, EC 528640, EC 538830, PK 258, EC 468597, EC 572160, SL 682, PI 204336, UGM 70, LEE 96, TG X 1488-9-1D, JS 335, TNAU 20024, NRC 86, EC 350664, EC 377883B, TGX 849-D-13-4, LEE-54, PS1421, VLS 11, EC 33940, G2225, GC 84051-32-1, G4P15, TG X 849-813, KB-17, MACS-7102, EC 294003, EC 291451, EC 24091, VLS 75, JS 97-52, NRC 2007A, NRC 80-1, DCB 137, EC 457336, F4P20, UGM 75, MACS 303, NRC 2006M, JS 20-52, PS 1475, NRC 37, JS 20-69, JSM 195, PS 1336, RSC 14, JSM 232, JSM 245, JS 20-34, RKS 54, JS 20-29, GP 465, JSM 227, JS 20-98, KDS 256, JS 96-31, GP566, PS 1467, JS 20-34, JS 20-50, 20-40B(Z-9), 20-148 (Z-15), 23-10B(Z-17), 23-11A(Z-18), JS 20-98.
	Semi – erect to horizontal	Nil
4. Leaf shape	Lanceolate	Nil
	Pointed ovate	EC-389153, EC 389179B, UPSM 77, EC 391181, VLS 75, EC 391316, JS 97-52, NRC 2007A, NRC 80-1, JS 20-01, EC 396065, DCB 137, EC 457214, DE 201, EC 457336, EC 103336, NRC 86, EC 106998, EC 109540, NRC 2006M, EC16213, JS 20-52, PS 1475, NRC 37, SL 2951, EC 389099, JS 20-69, JSM 195, EC 291397, PS 1336, EC 294003, EC 291451, EC 24091, RSC 14, EC 33872B, SQL 1, JSM 222, SL (E)1, PK 1038, RKS 54, EC 33940, G2225, JS 20-29, G4P15, GP 465, TGX 849-D-13-4, JSM 227, JS 20-98, TG X 849-813, KB-17, KDS 256, LEE-54, JS 96-31, TNAU 20022, EC 528640, EC 538830, PK 258, EC 468597, EC 572160, SL 682, PI 204336, UGM 70, LEE 96, TG X 1488-9-1D, GP566, PS1421, VLS 11, PS 1467, EC 350664, EC 377883B, GC 84051-32-1, 20-148 (Z-15), 23-10B(Z-17), 23-11A(Z-18), JS 20-98, NRC 86.
	Round ovate	K-53, UPSL 152, VGM 70, AGS 12, F4P20, SL 752, UGM 75, MACS 303, MACS 171, EC 325103, JSM 285, JSM 232, JSM 245, JS 20-34, PK 701, TNAU 20024, SQL 37, WT 88, JS 20-34, JS 20-50, MACS-7102, 20-40B(Z-9), JS 20-34, JS 335.

5. Leaf size	Small	VGM 70, JS 97-52, JS 20-01, EC 396065, EC 457336, EC16213, JS 20-52, SL 2951, EC 389099, JS 20-69, EC 291397, TNAU 20022, PK 258, JS 20-34.
	Medium	K-53, EC-389153, UPSL 152, EC 389179B, UPSM 77, EC 391181, VLS 75, EC 391316, NRC 2007A, NRC 80-1, DCB 137, EC 457214, DE 201, AGS 12, F4P20, EC 103336, NRC 86, EC 106998, SL 752, EC 109540, MACS 303, NRC 2006M, PS 1475, NRC 37, MACS 171, JSM 195, PS 1336, EC 294003, EC 291451, RSC 14, JSM 285, EC 33872B, SQL 1, JS 20-34, PK 701, PK 1038, RKS 54, EC 33940, G2225, JS 20-29, G4P15, TGX 849-D-13-4, JSM 227, JS 20-98, TG X 849-813, KB-17, KDS 256, LEE-54, JS 96-31, TNAU 20024, SQL 37, WT 88, EC 528640, EC 538830, EC 468597, EC 572160, SL 682, PI 204336, UGM 70, LEE 96, GP566, PS1421, VLS 11, EC 350664, EC 377883B, GC 84051-32-1, JS 20-50, MACS-7102, 20-148 (Z-15), 23-10B(Z-17), 23-11A(Z-18), JS 20-34, JS 335, JS 20-98, NRC 86.
	Large	UGM 75, EC 24091, EC 325103, JSM 232, JSM 222, JSM 245, SL (E)1, GP 465, TG X 1488-9-1D, PS 1467, 20-40B(Z-9).
6. Leaf intensity of green	Light	EC 391316, NRC 2007A, DE 201, EC 106998, SL 752, NRC 37, SL 2951, EC 389099, PK 1038, KB-17, LEE 96, PS1421, JS 20-34, JS 20-50, 20-40B(Z-9), 20-148 (Z-15).
	Medium	K-53, EC-389153, UPSL 152, EC 389179B, UPSM 77, EC 391181, VGM 70, VLS 75, NRC 80-1, EC 396065, EC 457214, F4P20, EC 109540, UGM 75, NRC 2006M, EC16213, JS 20-52, PS 1475, MACS 171, JS 20-69, EC 291397, PS 1336, EC 294003, EC 291451, EC 33872B, SQL 1, PK 701, EC 33940, TGX 849-D-13-4, JSM 227, LEE-54, WT 88, TNAU 20022, EC 528640, EC 538830, EC 468597, EC 572160, TG X 1488-9-1D, GP566, VLS 11, EC 377883B, GC 84051-32-1, MACS-7102, 23-10B(Z-17), 23-11A(Z-18), JS 20-34, JS 20-98,
	Dark	JS 97-52, JS 20-01, DCB 137, EC 457336, AGS 12, EC 103336, NRC 86, MACS 303, JSM 195, EC 24091, RSC 14, EC 325103, JSM 285, JSM 232, JSM 222, JSM 245, JS 20-34, SL (E)1, RKS 54, G2225, JS 20-29, G4P15, GP 465, JS 20-98, TG X 849-813, KDS 256, JS 96-31, TNAU 20024, SQL 37, PK 258, SL 682, PI 204336, UGM 70, PS 1467, EC 350664, JS 335, NRC 86.
7. Flower colour	White	VLS 75, JS 97-52, NRC 2007A, NRC 80-1, DCB 137, EC 457336, F4P20, UGM 75, MACS 303, NRC 2006M, JS 20-52, PS 1475, NRC 37, JS 20-69, JSM 195, PS 1336, RSC 14, JSM 232, JSM 245, JS 20-34, RKS 54, JS 20-29, GP 465,

		JSM 227, JS 20-98, KDS 256, JS 96-31, JS 20-98, GP566, PS 1467, JS 20-34, JS 20-50, 20-40B(Z-9), 20-148 (Z-15), 23-10B(Z-17), 23-11A(Z-18), JS 20-34.
	Violet	K-53, EC-389153, UPSL 152, EC 389179B, UPSM 77, EC 391181, VGM 70, EC 391316, JS 20-01, EC 396065, EC 457214, DE 201, AGS 12, EC 103336, NRC 86, EC 106998, SL 752, EC 109540, EC16213, MACS 171, SL 2951, EC 389099, EC 291397, EC 294003, EC 291451, EC 24091, EC 325103, JSM 285, EC 33872B, SQL 1, JSM 222, SL (E)1, PK 701, PK 1038, EC 33940, G2225, G4P15, TGX 849-D-13-4, TG X 849-813, KB-17, LEE-54, TNAU 20024, SQL 37, WT 88, TNAU 20022, EC 528640, EC 538830, PK 258, EC 468597, EC 572160, SL 682, PI 204336, UGM 70, LEE 96, TG X 1488-9-1D, PS1421, VLS 11, EC 350664, EC 377883B, GC 84051-32-, 1MACS-7102, JS 335, NRC 86
8. Pods: presence of hairs	Present	K-53, EC-389153, UPSL 152, EC 389179B, UPSM 77, EC 391181, VGM 70, VLS 75, EC 391316, JS 97-52, NRC 2007A, NRC 80-1, JS 20-01, EC 396065, DCB 137, EC 457214, DE 201, EC 457336, F4P20, EC 103336, NRC 86, EC 106998, EC 109540, MACS 303, NRC 2006M, EC16213, JS 20-52, PS 1475, NRC 37, SL 2951, EC 389099, JS 20-69, JSM 195, EC 291397, PS 1336, EC 294003, EC 291451, EC 24091, RSC 14, EC 325103, EC 33872B, SQL 1, JSM 222, SL (E)1, PK 1038, RKS 54, EC 33940, G2225, JS 20-29, GP 465, TGX 849-D-13-4, JSM 227, JS 20-98, TG X 849-813, KB-17, KDS 256, LEE-54, JS 96-31, TNAU 20022, EC 528640, EC 538830, PK 258, EC 468597, EC 572160, SL 682, PI 204336, UGM 70, LEE 96, TG X 1488-9-1D, GP566, PS1421, VLS 11, PS 1467, EC 350664, EC 377883B, GC 84051-32-1, 20-40B(Z-9), 20-148 (Z-15), 23-10B(Z-17), 23-11A(Z-18), NRC 86, JS 20-98.
	Absent	AGS 12, SL 752, UGM 75, MACS 171, JSM 285, JSM 232, JSM 245, JS 20-34, PK 701, G4P15, TNAU 20024, SQL 37, WT 88, JS 20-34, JS 20-50, MACS-7102, JS 20-34, JS 335.
9.Pod: Colour of hairs	Tawny	K-53, EC-389153, UPSL 152, EC 389179B, UPSM 77, EC 391181, VGM 70, EC 391316, JS 97-52, NRC 80-1, JS 20-01, EC 396065, EC 457214, DE 201, EC 457336, EC 103336, NRC 86, EC 106998, MACS 303, NRC 2006M, EC16213, JS 20-52, PS 1475, MACS 171, SL 2951, EC 389099, EC 291397, PS 1336, EC 294003, EC 291451, EC 24091, RSC 14, EC 325103, EC 33872B, SQL 1, SL (E)1, PK 701, PK 1038, EC 33940, G2225, GP 465, TGX 849-D-13-4, JS 20-98, TG X 849-813, KB-17, LEE-54, JS 96-31, TNAU 20024, TNAU 20022, EC 528640, EC 538830, EC 572160, PI 204336, LEE 96, PS1421, VLS 11, PS 1467, EC 350664, EC 377883B, JS 20-50, 20-40B(Z-9), 20-148 (Z-15), 23-10B(Z-17), 23-11A(Z-18), JS 20-34, JS 20-98, NRC 86.

	Grey	VLS 75, NRC 2007A, DCB 137, F4P20, EC 109540, NRC 37, JS 20-69, JSM 195, JSM 285, JSM 232, JSM 222, RKS 54, JS 20-29, JSM 227, KDS 256, PK 258, EC 468597, SL 682, UGM 70, TG X 1488-9-1D, GP566, GC 84051-32-1.
	Absent	AGS 12, SL 752 UGM 75, JSM 245, JS 20-34, G4P15, SQL 37, WT 88, JS 20-34, MACS-7102, JS 335.
10. Pod: Intensity of brown colour at maturity	Light	K-53, EC-389153, UPSL 152, EC 391316, JS 97-52, NRC 2007A, JS 20-01, DE 201, EC 457336, EC 103336, EC 109540, UGM 75, NRC 2006M, EC16213, JS 20-52, NRC 37, SL 2951, JS 20-69, JSM 195, EC 291397, EC 294003, EC 24091, RSC 14, EC 33872B, SQL 1, PK 1038, EC 33940, JS 20-29, G4P15, TGX 849-D-13-4, KB-17, LEE-54, JS 96-31, SQL 37, TNAU 20022, EC 528640, PK 258, EC 572160, PI 204336, UGM 70, TG X 1488-9-1D, GP566, PS1421, PS 1467, EC 350664, JS 20-50, 20-40B(Z-9), 20-148 (Z-15), 23-10B(Z-17), 23-11A(Z-18), JS 20-34, JS 20-98.
	Medium	EC 391181, DCB 137, F4P20, NRC 86, EC 106998, MACS 303, MACS 171, EC 389099, EC 291451, JSM 285, SL (E)1, RKS 54, G2225, JS 20-98, TG X 849-813, KDS 256, EC 538830, EC 468597, LEE 96, VLS 11, EC 377883B, GC 84051-32-1, JS 335.
	Dark	EC 389179B, UPSM 77, VGM 70, VLS 75, NRC 80-1, EC 396065, EC 457214, AGS 12, SL 752, PS 1475, PS 1336, EC 325103, JSM 232, JSM 222, JSM 245, JS 20-34, PK 701, GP 465, JSM 227, TNAU 20024, WT 88, SL 682, JS 20-34, MACS-7102, NRC 86.
11. Seed: ground colour of testa	Yellow	K-53, EC 389179B, VGM 70, VLS 75, EC 391316, NRC 2007A, DCB 137, NRC 80-1, JS 97-52, JS 20-01, EC 396065, EC 457214, AGS 12, F4P20, EC 103336, NRC 86, EC 106998, SL 752, EC 109540, UGM 75, MACS 303, NRC 2006M, EC16213, JS 20-52, PS 1475, NRC 37, MACS 171, SL 2951, EC 389099, JS 20-69, JSM 195, EC 291397, PS 1336, EC 291451, EC 24091, RSC 14, EC 325103, JSM 285, EC 33872B, SQL 1, JSM 232, JSM 222, JSM 245, JS 20-34, SL (E)1, PK 701, PK 1038, RKS 54, EC 33940, G2225, G4P15, GP 465, JSM 227, JS 20-98, TG X 849-813, KB-17, KDS 256, LEE-54, JS 96-31, TNAU 20024, SQL 37, WT 88, TNAU 20022, EC 528640, EC 538830, PK 258, EC 468597, EC 572160, SL 682, PI 204336, UGM 70, LEE 96, TG X 1488-9-1D, GP566, PS1421, VLS 11, PS 1467, EC 350664, EC 377883B, JS 20-34, GC 84051-32-1, JS 20-50, MACS-7102, 20-40B(Z-9), 20-148 (Z-15), 23-10B(Z-17), JS 20-34, JS 335, JS 20-98, NRC 86.
	Yellow green	JS 20-29, EC 391181.
	Green	EC-389153, UPSL 152.
	Black	EC 294003, UPSM 77, TGX 849-D-13-4, DE 201.

	Brown	23-11A(Z-18), EC 457336.
12. Seed size	Small	EC-389153, EC 391316, DCB 137, EC 457214, SL 752, MACS 303, SL 2951, JS 20-69, JSM 222, RKS 54, SQL 1, G2225, SL 682.
	Medium	K-53, UPSL 152, EC 389179B, UPSM 77, EC 391181 JS 97-52, NRC 2007A, VGM 70, VLS 75, NRC 80-1, JS 20-01, EC 396065, DE 201, AGS 12, F4P20, EC 103336, NRC 86, EC 106998, EC 109540, JS 20-52, PS 1475, UGM 75, NRC 2006M, EC16213, NRC 37, MACS 171, EC 389099, JSM 195, EC 291397, PS 1336, EC 294003, EC 291451, EC 24091, RSC 14, EC 325103, JSM 285, EC 33872B, JSM 232, JSM 245, JS 20-34, PK 701, PK 1038, EC 33940, JS 20-29, G4P15, GP 465, TGX 849-D-13-4, JSM 227, JS 20-98, TG X 849-813, KB-17, KDS 256, LEE-54, TNAU 20024, SQL 37, WT 88, TNAU 20022, EC 528640, EC 538830, PK 258, EC 468597, EC 572160, PI 204336, LEE 96, TG X 1488-9-1D, GP566, PS1421, VLS 11, PS 1467, EC 350664, JS 20-34, GC 84051-32-1, JS 20-50, MACS-7102, 20-40B(Z-9), 20-148 (Z-15), 23-10B(Z-17), 23-11A(Z-18), JS 20-34, JS 335, JS 20-98.
	Bold	NRC 86, EC 457336, EC 377883B, UGM 70, JS 96-31, SL (E)1.
13. Seed shape	Spherical	VGM 70, NRC 80-1, DCB 137, EC 457214, NRC 86, NRC 2006M, JS 20-52, JSM 195, JSM 222, JSM 227, JS 20-98, SQL 37, PK 258, SL 682, MACS-7102, JS 20-34.
	Spherical flattened	K-53, EC-389153, UPSM 77, EC 391181, VLS 75, NRC 2007A, DE 201, AGS 12, F4P20, EC 106998, SL 752, MACS 303, EC16213, NRC 37, JS 20-69, PS 1336, RSC 14, EC 325103, JSM 285, EC 33872B, JSM 232, JSM 245, JS 20-34, SL (E)1, PK 701, RKS 54, EC 33940, G2225, JS 20-29, G4P15, GP 465, TGX 849-D-13-4, TG X 849-813, TNAU 20024, WT 88, PI 204336, TG X 1488-9-1D, GP566, VLS 11, PS 1467, EC 350664, JS 20-34, 20-40B(Z-9), 23-11A(Z-18), JS 335, JS 20-98.
	Elongated	UPSL 152, EC 389179B, JS 97-52, PS 1475, MACS 171, EC 389099, EC 291397, EC 291451, SQL 1, KB-17, JS 96-31, TNAU 20022, EC 468597, EC 572160, UGM 70, LEE 96, EC 377883B, JS 20-50, 20-148 (Z-15), 23-10B(Z-17).
	Elongated flattened	EC 391316, JS 20-01, EC 396065, EC 457336, EC 103336, EC 109540, UGM 75, SL 2951, EC 294003, EC 24091, PK 1038, KDS 256, LEE-54, EC 528640, EC 538830, PS1421, GC 84051-32-1, NRC 86.
14. Seed coat lusture	Shiny	EC 33872B, JSM 232, JSM 245, JS 20-34, SL (E)1, PK 701, RKS 54, EC 33940, G2225, JS 20-29, G4P15,

		GP 465, TGX 849-D-13-4, TG X 849-813, TNAU 20024, WT 88, PI 204336, TG X 1488-9-1D, GP566, VLS 11, PS 1467, EC 350664, JS 20-34, 20-40B(Z-9), 23-11A(Z-18), JS 335, JS 20-98.
	Intermediate	20-148 (Z-15), 23-10B(Z-17), EC 391316, JS 20-01, EC 396065, EC 457336, EC 103336, EC 109540, UGM 75, SL 2951, EC 294003, EC 24091, PK 1038, KDS 256, LEE-54, EC 528640, EC 538830, PS1421, GC 84051-32-1, NRC 86, VGM 70, NRC 80-1, DCB 137, EC 457214, NRC 86, NRC 2006M, JS 20-52, JSM 195, JSM 222, JSM 227, JS 20-98, SQL 37, PK 258, SL 682, MACS-7102, JS 20-34, K-53, EC-389153, UPSM 77, EC 391181, VLS 75, NRC 2007A, DE 201, AGS 12, F4P20, EC 106998, SL 752, MACS 303, EC16213, NRC 37, JS 20-69, PS 1336, RSC 14, EC 325103, JSM 285.
	Dull	UPSL 152, EC 389179B, JS 97-52, PS 1475, MACS 171, EC 389099, EC 291397, EC 291451, SQL 1, KB-17, JS 96-31, TNAU 20022, EC 468597, EC 572160, UGM 70, LEE 96, EC 377883B, JS 20-50.
15. Hilum colour	Grey	EC 391316, EC 396065, EC 103336, EC 109540, EC 389099, EC 291397, EC 291451, EC 24091, EC 528640, EC 538830, EC 468597, EC 572160, LEE 96, PS1421, GC 84051-32-1.
	Brown	LEE-54, JS 96-31, TNAU 20024, SQL 37, TG X 849-813, KB-17, JSM 232, JSM 222, JSM 245, RSC 14, EC 325103, PS 1336, JSM 195, MACS 171, SL 2951, NRC 2006M, NRC 86, EC 106998, EC 391181, VGM 70, EC-389153, NRC 80-1, DCB 137, EC 457336, AGS 12, SL (E)1, PK 701, PK 1038, EC 33940, G2225, JS 20-29, G4P15, GP 465, JSM 227, TNAU 20022, PK 258, SL 682, UGM 70, TG X 1488-9-1D, GP566, VLS 11, PS 1467, S 20-50, MACS-7102, JS 335.
	Intermediate black	PI 204336, JS 20-01, EC 389179B, VLS 75, NRC 37, EC 350664, EC 377883B, NRC 86.
	Black	K-53, UPSL 152, UPSM 77, JS 97-52, NRC 2007A, EC 457214, DE 201, F4P20, SL 752, UGM 75, MACS 303, EC16213, JS 20-52, PS 1475, JS 20-69, EC 294003, JSM 285, EC 33872B, SQL 1, JS 20-34, RKS 54, TGX 849-D-13-4, JS 20-98, KDS 256, WT 88, JS 20-34, 20-40B(Z-9), 20-148 (Z-15), 23-10B(Z-17), 23-11A(Z-18), JS 20-34, JS 20-98
16.Colour of hilum funicle	Same as testa	EC-389153, UPSL 152, EC 389179B, UPSM 77, EC 391181, VGM 70, VLS 75, EC 391316, JS 97-52, NRC 2007A, NRC 80-1, JS 20-01, EC 396065, DCB 137, EC 457214, AGS 12, F4P20, EC 103336, NRC 86, EC 106998, SL 752, EC

		109540, UGM 75, NRC 2006M, EC16213, JS 20-52, NRC 37, MACS 171, SL 2951, EC 389099, JSM 195, EC 291397, PS 1336, EC 24091, RSC 14, EC 325103, JSM 285, EC 33872B, JSM 232, JSM 222, JSM 245, JS 20-34, SL (E)1, PK 701, PK 1038, RKS 54, EC 33940, G2225, JS 20-29, G4P15, GP 465, JSM 227, JS 20-98, TG X 849-813, KB-17, KDS 256, LEE-54, JS 96-31, TNAU 20024, SQL 37, WT 88, TNAU 20022, EC 528640, EC 538830, PK 258, EC 468597, EC 572160, SL 682, PI 204336, UGM 70, LEE 96, TG X 1488-9-1D, GP566, PS1421, VLS 11, PS 1467, EC 350664, EC 377883B, JS 20-34, GC 84051-32-1, JS 20-50, MACS-7102, 20-40B(Z-9), 20-148 (Z-15), 23-10B(Z-17), 23-11A(Z-18), JS 20-34, JS 335, JS 20-98, NRC 86.
	Different to testa	K-53, DE 201, EC 457336, MACS 303, PS 1475, JS 20-69, EC 294003, EC 291451, SQL 1, TGX 849-D-13-4.
17. Seed : Peroxidase activity	0	TNAU 20022, JS 20-34, DE 201, EC 457336, NRC 2006M, JSM 227, EC 294003, PS 1467, TGX 849-D-13-4, TG X 849-813, PI 204336, UPSM 77.
	1	DCB 137, EC 457214, F4P20, EC 106998, EC 538830, EC 389179B, EC 389099, JS 20-69, EC 291451, EC 24091, JSM 285, SQL 1, JSM 232, JSM 245, KB-17, EC 468597, EC 391181, UGM 70, LEE 96, PS1421, EC 377883B, GC 84051-32-1, JS 20-50.
	2	EC 109540, MACS 303, EC 528640, UPSL 152, EC 396065, AGS 12, EC 103336, SL 752, WT 88, EC16213, SL 2951, JSM 195, EC 291397, RSC 14, JSM 222, PK 701, EC 33940, G4P15, MACS 171, LEE-54, PK 258, EC 350664, MACS-7102, JS 20-98.
	3	K-53, EC-389153, JS 20-01, SQL 37, JS 20-52, PS 1336, EC 325103, SL (E)1, G2225, GP 465, JS 20-98, KDS 256, JS 96-31, EC 572160, NRC 37, VGM 70, GP566, VLS 11, JS 335, NRC 86
	4	UGM 75, JS 97-52, NRC 80-1, NRC 86, PS 1475, EC 33872B, RKS 54, TNAU 20024, VLS 75, SL 682, 20-148 (Z-15)
	5	NRC 2007A, PK 1038, JS 20-29, EC 391316, TG X 1488-9-1D, JS 20-34, 20-40B(Z-9), 23-10B(Z-17), 23-11A(Z-18), JS 20-34.

4.2 Analysis of variance

The ANOVA (Table 4.2) indicated that the mean sum of squares due to genotypes were highly significant for all the traits under study viz. days to flower initiation, days to maturity, plant height (cm), number of primary branches per plant, number of nodes per plant, number of pods per plant, number of seeds per plant, biological yield per plant (g), 100 seed weight (g), harvest index (%) and seed yield per plant (g).

4.3 Estimation of parameters of genetic variability

The parameters of genetic variability viz., mean, range, phenotypic and genotypic coefficient of variation (%), heritability in broad sense (%), genetic advance and genetic advance as percentage of mean for each trait are presented in table 4.3 and Fig 1.

4.3.1 Mean and Range

Estimates of mean and range for all the eleven characters along with the character and genotype wise mean values have been presented in table 4.2

Days to flower initiation

The degree of dispersion for flower initiation phase ranged from 28.00 days {JS 20-34} to 67.00 days {UPSM 77} with mean of 43.54 days.

Days to maturity

Days to maturity ranged from 88.50 {JS 20-34} days to 118.00 {UPSM 77} days with mean value of 102.64 days.

Plant height (cm)

The plant height ranged from 32.90 cm {JS 20-34} to 146.00 cm {TNAU 20024} with mean value of 73.60 cm.

Number of branches per plant

Number of branches per plant recorded minimum of 0.00 {JS 20-34} and maximum of 5.90 {JSM 232} with mean value of 2.65

Number of nodes per plant

Number of nodes per plant recorded minimum of 8.30 {JS 20-34} and maximum of 21.00 {JSM 222} with mean value of 13.70

Number of pods per plant

Number of pods per plant varied from 18.76 {JS 20-34} to 114.70 {G2225} with mean value of 51.30

Number of seeds per plant

Number of seeds per plant ranged from 16.00 {20-148 (Z-15)} to 223.00 {G2225} with mean value of 71.43

100 Seed weight (g)

The 100 seed weight varied from 15.10 g {23-11A(Z-18)} to 54.70 g {UPSL 152} with its mean value of 8.05

Biological yield per plant (g)

The average value of biological yield per plant was recorded 25.19 g with degree of dispersion from 7.50 {EC 33940} to 79.93 {NRC 86}

Harvest index (%)

Harvest index (%) had mean value of 30.25%, ranging from 1.90% {SL 2951} to 23.00% {NRC 86}.

Seed yield per plant (g)

The yield per plant recorded minimum of 2.20 g {GC 84051-32-1} while maximum of 15.20 g {EC 377883B} with mean value of 6.85 g.

Table 4.2 Mean squares from analysis of variance of 11 quantitative traits in 100 soybean germplasm

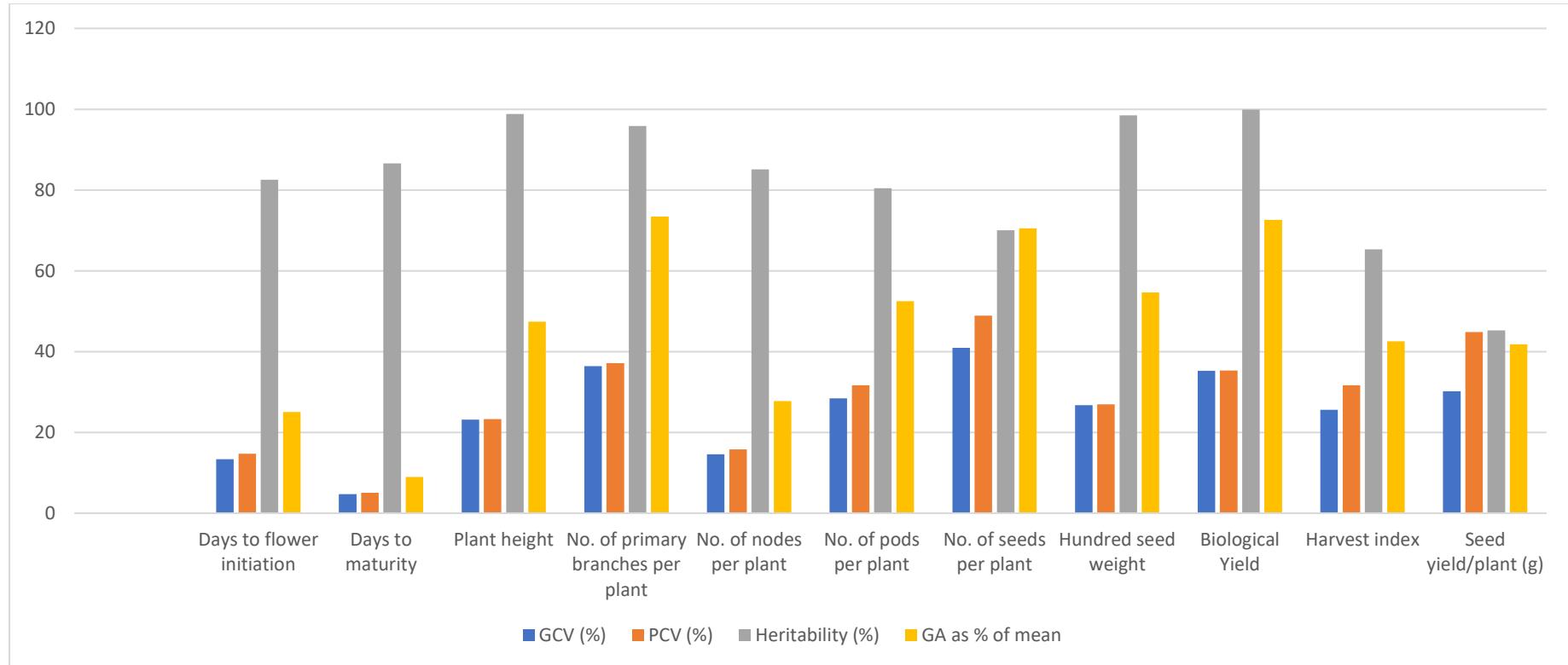
Source of variation	df	Mean sum of square										
		DFI	DM	HGT	NB	NN	NP	NS	100S	BY	HI	SY
Blocks	3	63.80	67.10	1054.50	1.02	9.80	1051.20	4769.28	1.01	175.20	93.20	28.12
Entries	99	57.10**	35.70**	336.14**	1.46*	5.40**	339.50**	1664.31**	5.20**	82.20**	402.61**	20.11**
Checks	3	521.60**	101.20**	1306.70**	4.96**	26.70**	2898.20**	15875.22**	15.80**	15.86**	220.34**	284.60**
Variety	95	41.20**	26.80**	293.90**	0.97*	4.70**	261.30**	1218.98**	4.70**	79.05**	91.68**	9.44**
Checks Vs varieties	1	174.10**	692.90**	1431.40**	37.94**	12.35**	96.02**	1338.44**	16.05**	581.59*	30487.5**	240.30**
Error	9	7.20	3.60	3.46	0.04	0.70	51.14	365.05	.70	.70	31.82	5.17

*Significant at probability level of 0.05 and **Significant at probability level 0.01.

Table 4.3- Genetic parameters of variability for yield and its component traits in soybean genotypes

Traits	Mean	Range		GCV (%)	PCV (%)	h ² b (%)	GA as % of mean 5%
		Mini	Maxi				
Days to flower initiation	43.54	28.00	67.00	13.39	14.74	82.52	25.06
Days to maturity	102.64	88.50	118.00	4.69	5.04	86.57	8.99
Plant height	73.60	32.90	146.00	23.16	23.29	98.82	47.42
No. of primary branches per plant	2.65	0.00	5.90	36.39	37.17	95.88	73.40
No. of nodes per plant	13.70	8.30	21.00	14.60	15.82	85.11	27.74
No. of pods per plant	51.03	18.76	114.70	28.41	31.68	80.43	52.48
No. of seeds per plant	71.43	16.00	223.00	40.91	48.88	70.05	70.54
Hundred seed weight	8.05	15.10	54.70	26.73	26.93	98.51	54.65
Biological Yield	25.19	7.50	79.93	35.28	35.30	99.91	72.64
Harvest index	30.25	1.90	23.00	25.58	31.65	65.29	42.57
Seed yield/plant (g)	6.85	2.20	15.20	30.17	44.85	45.23	41.79

Fig. 1 Graphical representation of GCV, PCV, Heritability (%) and GA as % of mean



4.3.2 Genotypic and phenotypic coefficient of variation

The genetic variability plays a significant role in evolving superior genotypes through various breeding approaches. Thus, higher the amount of variation present for a concerned character in the breeding materials, greater is the scope for its improvement through further selection. Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) are categorized as low (<10%), moderate (10-20%) and high (> 20%) as suggested by Sivasubramanian and Madhavamenon (1973). The phenotypic coefficient of variation was significantly higher in magnitude than that of genotypic coefficient of variation for all the characters under study. Number of seeds per plant recorded the highest PCV (48.88%) and GCV (40.91%) followed by seed yield per plant (44.85% and 30.17%), number of primary branches per plant (37.17% and 36.39%), biological yield per plant (35.30% and 35.28%), number of pods per plant (31.68% and 28.41%), harvest index (31.65% and 25.58%), plant height (23.29% and 23.16%); moderate for number of nodes per plant (15.82% and 14.60%), days to flower initiation (14.74% and 13.39%), and low PCV and GCV is of trait days to maturity (5.04% and 4.69%).

4.3.3 Heritability in Broad Sense (%)

Heritability was estimated for all the quantitative characters under study. Heritability estimates were classified as high (> 70%), moderate (50- 70%) and low (< 50%). The heritability estimates varied for different morphological and quantitative traits (Table 4.3). Most of the characters expressed high estimates of heritability. The highest heritability (99.91%) was obtained for biological yield followed by plant height (98.82%), 100 seed weight (98.51%), number of primary branches per plant (95.88%), days to maturity (86.57%), number of nodes per plant (85.11%), days to flower initiation (82.52%), number of pods per plant (80.43%), number of seeds per plant (70.05%), harvest index (65.29%) and seed yield per plant (45.23%).

4.3.4 Genetic advance as percentage of mean

The highest genetic advance as percentage of mean (at 5% selection intensity) were recorded for number of primary branches per plant (73.40%) followed by biological yield (72.64%), number of seeds per plant (70.54%), 100 seed weight (54.65%), number of pods per plant (52.48%), plant height (47.42%),

harvest index (42.57%), seed yield per plant (41.79%), number of nodes per plant (27.74%), days to flower initiation (25.06%) and days to maturity (8.99%).

4.4 Correlation coefficient analysis

Phenotypic correlations between seed yield per plant and various yield traits viz. days to flower initiation, days to maturity, plant height, number of primary branches per plant, number of nodes per plant, number of pods per plant, number of seeds per plant, biological yield per plant, 100 seed weight and harvest index. Estimates of phenotypic correlation are mentioned in table 4.4.

Study revealed that seed yield per plant showed highly significant positive correlation with number of seeds per plant (0.873) followed by harvest index (0.685), hundred seed weight (0.553), number of pods per plant (0.534), biological yield (0.456) and number of nodes per plant (0.452) and significant positive association with days to maturity (0.331), days to flower initiation (0.308), number of primary branches per plant (0.305), and plant height (0.290).

Significant phenotypic correlations among different traits are described as under;

4.4.1 Days to flower initiation

Days to flower initiation exhibited highly significant positive association with number of nodes per plant (0.447), number of seeds per plant (0.419), plant height (0.411), number of pods per plant (0.402) and number of primary branches per plant (0.323) whereas, a negative association with 100 seed weight (-0.066).

4.4.2 Days to maturity

Days to maturity showed highly significant positive association with biological yield per plant (0.505) followed by number of primary branches per plant (0.452), seed yield per plant (0.331) and number of nodes per plant (0.330). Whereas, it showed negative association with harvest index (-0.078).

4.4.3 Plant height

Plant height revealed highly significant positive association with number of nodes per plant (0.501) followed by number of primary branches per plant (0.450), number of seeds per plant (0.360), number of pods per plant (0.334) and seed yield per plant (0.290)

4.4.4 Number of primary branches per plant

Number of primary branches per plant showed highly significant positive association with biological yield per plant (0.494) followed by number of pods per plants (0.418) and number of nodes per plants (0.354). Whereas, it showed negative association with harvest index (-0.098).

4.4.5 Number of nodes per plant

This character showed highly significant positive association with number of seeds per plant (0.510) followed by number of pods per plant (0.460), and significant association with seed yield/plant (0.452).

4.4.6 Number of pods per plant

This character showed highly significant positive association with number of seeds per plant (0.656) followed by seed yield per plant(0.534), biological yield per plant (0.325) and significant association with harvest index (0.200) .

4.4.7 Number of seeds per plant

Association of this trait was found to be highly significantly positive with seed yield per plant (0.873), harvest index (0.608) and biological yield per plant (0.387).

4.4.8 100 seed Weight

100 seed weight showed highly significant positive association with seed yield per plant (0.553), biological yield pre plant (0.357) and harvest index (0.338).

4.4.9 Biological yield per plant

Biological yield established highly significant positive association with seed yield per plant (0.456) and negative significant association with harvest index (-0.165).

4.4.10 Harvest Index

It showed the highest significant positive association with seed yield per plant (0.685).

Table 4.4 Correlation coefficient analysis for yield and its contributing trait in soybean germplasm

Character	Days to flower initiation	Days to maturity	Plant height	No. of primary branches/plant	No. of nodes/plant	No. of pods/plant	No. of seeds/plant	100 seed weight	Biological yield/plant	Harvest index	Seed yield/plant
Days to flower initiation	1.00	0.318 **	0.411* *	0.323**	0.447**	0.402**	0.419**	-0.066	0.214*	0.031	0.308**
Days to maturity		1.00	0.288**	0.452**	0.330**	0.304**	0.314**	0.226*	0.505**	-0.078	0.331**
Plant height			1.0	0.452**	0.501**	0.334**	0.360**	0.005	0.145	0.120	0.290**
No. of primary branches/plant				1.00	0.354**	.418**	0.370**	0.094	0.494**	-0.098	0.305**
No. of nodes/plant					1.00	.460**	0.510**	0.094	0.385**	0.120	0.452**
No. of pods/plant						1.00	0.656**	0.069	0.325**	0.200*	0.534**
No. of seeds/plant							1.00	0.135	0.387**	0.608**	0.873**
100 seed weight								1.00	0.357**	0.338**	0.553**
Biological yield/plant									1.00	-0.165	0.456**
Harvest index										1.00	0.685**
Seed yield/ plant											1.00

(* Significant at probability level of 0.05 and * * significant at probability level 0.01)

4.5 Path coefficient analysis

Path coefficient analysis measures direct and indirect contribution of various independent characters on the dependent characters. It reveals the association of these independent characters with yield, whether the dependent character is due to their direct effect on yield or is consequence of their indirect effect via other component characters. In the present study, path coefficient analysis was carried out using seed yield/plant as a dependent variable.

4.5.1 Direct effect

The path coefficient analysis of different yield and its contributing traits on seed yield per plant revealed that harvest index (1.3194) and biological yield per plant (0.7877) recorded considerably very high estimates of positive direct effect. Substantial higher positive direct effect was recorded for days to maturity (0.2497), days to flower initiation (0.2167), number of pods per plant (0.1928). Whereas, high negative direct effect on seed yield per plant was observed by number of seeds per plant (-0.5433) followed by negative direct effect via hundred seed weight (-0.5263), number of primary branches per plant (-0.1363) and plant height (-0.0804). (Table 4.5)

4.5.2 Indirect Effects

4.5.2.1 Days to flower initiation

Days to flower initiation showed positive indirect effect on seed yield per plant via number of seeds per plant (0.1535) followed by number of nodes per plant (0.1414), biological yield (0.1392) and negligible positive indirect effect via harvest index (0.0082) and days to maturity (0.0940). However, it had negative indirect effects on seed yield per plant via 100 seed weight (-0.0026)

4.5.2.2 Days to maturity

Days to maturity exhibited lower positive indirect effect on seed yield per plant via biological yield (0.2142), number of primary branches (0.1149) and days to flower initiation (0.1083). However, it had negative indirect effects on seed yield per plant via Harvest index (-0.0212)

Table 4.5 Path coefficient analysis for yield and its component traits in soybean germplasm

Characters	Days to flower initiation	Days to maturity	Plant height	No of primary branches/plant	No .of nodes/ plant	No of pods/plant	No.of seeds/plant	100 seed weight	Biological yield/plant	Harvest index
Days to flower initiation	0.2167	0.0940	0.1169	0.1186	0.1414	0.1244	0.1535	-0.0026	0.1392	0.0082
Days to maturity	0.1083	0.2497	0.0709	0.1149	0.0942	0.0765	0.0961	0.0893	0.2142	-0.0212
Plant height	-0.0434	-0.0228	-0.0804	-0.0325	-0.0543	-0.0278	-0.0191	0.0061	-0.0298	0.0103
No. of primary branches/plant	-0.0746	-0.0627	-0.0551	-0.1363	-0.0441	0.0011	-0.0377	0.0402	-0.0821	0.0571
No. of nodes/pod	-0.0106	-0.0062	-0.0110	-0.0053	-0.0163	-0.0108	-0.0092	-0.0021	-0.0086	-0.0024
No. of pods/plant	0.1107	0.0591	0.0666	-0.0015	0.1272	0.1928	0.1662	0.0512	0.0799	0.0949
No. of seeds/ plant	-0.3848	-0.2092	-0.1293	-0.1504	-0.3068	-0.4682	-0.5433	-0.1568	-0.3316	-0.2850
100 seed weight	0.0063	-0.1882	0.0398	0.1551	-0.0675	-0.1398	-0.1519	-0.5263	-0.1721	-0.3978
Biological yield/plant	0.5058	0.6759	0.2922	0.4748	0.4155	0.3266	0.4808	0.2575	0.7877	-0.0036
Harvest index	0.0520	-0.1122	-0.1685	-0.5524	0.1938	0.6494	0.6921	0.9972	-0.0060	1.3194
Seed yield/ plant	0.4847	0.4775	0.1420	-0.0150	0.4831	0.7242	0.8275	0.7536	0.5908	0.7799

Fig.2 Correlation Coefficient of ten characters with seed yield



4.5.2.3 Plant height

Plant height showed positive indirect effect on seed yield per plant through harvest index (0.0103) and 100 seed weight (0.0061). Whereas, it showed negligible amount of negative indirect effect via all other characters viz., number of nodes per plant (-0.0543), days to flower initiation (-0.0434), number of primary branches per plant (-0.0325), biological yield per plant (-0.0298), number of pods per plant (-0.278), days to maturity (-0.0228) and number of seeds per plant(-0.0191).

4.5.2.4 Number of primary branches per plant

Number of primary branches per plant showed positive indirect effect on seed yield per plant *via* harvest index (0.0571) and 100 seed weight (0.0402) whereas of negligible magnitude *via* number of pods per plant (0.0011). However, it showed negligible negative indirect effect *via* biological yield (-0.0821), days to flower initiation (-0.0746), days to maturity (-0.0627), plant height (-0.0551), number of nodes per plant (-0.0441) and number of seeds per plant (-0.0377).

4.5.2.5 Number of nodes per plant

Number of nodes per plant had moderate negative indirect effect on seed yield per plant *via* plant height (-0.0110), number of pods per plant (-0.0108) and days to flower initiation(-0.0106) whereas negligible negative indirect effect on seed yield per plant were shown by number of seeds per plant(-0.0092), biological yield (-0.0086), days to maturity (-0.0062), number of primary branches per plant (-0.0053), harvest index (-0.0024) and 100 seed weight (-0.0021).

4.5.2.6 Number of pods per plant

Number of pods per plant showed lower magnitude of positive indirect effect on seed yield per plant *via* number of seeds per plant (0.1662) followed by number of nodes per plant (0.1272, days to flower initiation (0.1107) while negligible positive indirect effect were revealed by days to maturity (0.0519) followed by 100 seed weight (0.0512). Whereas, negligible negative indirect effect on seed yield per plant was noted by number of primary branches per plant (-0.0015).

4.5.2.7 Number of seeds per plant

Number of seeds per plant had lower negative indirect effect on seed yield per plant *via* number of pods per plant (-0.4682) followed by days to flower initiation(-0.3848), biological yield (-0.3316) and number of nodes per plant (-0.3068) Whereas, moderate negative indirect effect on seed yield per plant were shown harvest index(-0.2850), days to maturity (-0.2092), 100 seed weight (-0.1568), number of primary branches per plant (-0.1504) and plant height (-0.1293).

4.5.2.8 100 seed weight

100 seed weight had lower positive indirect effect on seed yield per plant *via* number of primary branches per plants (0.1551). The indirect effect of 100 seed weight on seed yield per plant *via* all the traits irrespective of sign under study were found to be of negligible magnitude.

4.5.2.9 Biological yield per plant

Biological yield per plant had high positive indirect effect on seed yield per plant *via* days to maturity (0.6759) followed by days to flower initiation (0.5058), moderate positive indirect effect on seed yield per plant *via* number of seeds per plant (0.4808) followed by number of primary branches per plant (0.4748), number of nodes per plant (0.4155) and number of pods per plant (0.3266) and lower positive indirect effect were exhibited by plant height (0.2922) and 100 seed weight (0.2572). Negligible negative indirect effect on seed yield per plant was recorded by harvest index (-0.0036).

4.5.2.10 Harvest index

Harvest index recorded high positive indirect effect on seed yield per plant *via* 100 seed weight (0.9972), number of seeds per plant (0.6921), number of pods per plant (0.6494), while moderate positive indirect effect were found *via* number of nodes per plant (0.1938) . However, high negative indirect effect on seed yield per plant were found *via* number of primary branches per plant (-0.5524) while moderate negative indirect effect were found *via* plant height (-0.1685). Moreover, its other indirect effects either of the sign manifested *via* others characters on seed yield per plant were found to be of negligible magnitude.

4.6 Principal Components Analysis

PCA is a well-known method of dimension reduction that can be used to reduce a large set of variables to a small set that still contains most of the information in the large set (Massay, 1965; Jolliffe, 1986). It is a mathematical procedure that transforms a number of (possibly) correlated variables into a (smaller) number of uncorrelated variables called principal components. The first principal component accounts for as much of the variability in the data as possible and each succeeding component accounts for as much of the remaining variability as possible.

In the present investigation Eigen values, % variance and cumulative eigen values are mentioned in table 4.6. Out of twelve, only 6 principal components (PCs) exhibited more than 0.5 Eigen value and showed about 87.78% variability among the traits studied. Hence, these four principal components were given due importance for further explanation. The PC1 had the highest variability (40.380 %) followed by PC2 (16.833%), PC3 (12.464%) and PC4 (6.917 %) for traits under study.

Scree plot explained the percentage of variance associated between eigen values and the principal components with each PC obtained by drawing a graph. First principal component recorded the highest variation PC1 (40.380 %) followed by PC2 (16.833%), PC3 (12.464%) and PC4 (6.917%). Total variation of four PCs was recorded to be 87.78%. Semi curve line obtained after eighth PC with little variation observed in each PC indicated that maximum variation was found in PC1; therefore, selection of genotypes for traits under PC1 may be desirable (Figure 3).

Table 4.6 Eigen values, percentage of total variation and cumulative percentage for corresponding traits in soybean genotypes

Characters	Principal component (PC)	Eigen value	Variability (%)	Cumulative %
Days to flower initiation	PC 1	4.442	40.380	40.380
Days to maturity	PC 2	1.852	16.833	57.213
Plant height	PC 3	1.371	12.464	69.676
No. of primary branches/plant	PC 4	0.761	6.917	76.593
No. of nodes/plant	PC 5	0.649	5.900	82.493
No. of pods/plant	PC 6	0.582	5.287	87.780
No. of seeds/ plant	PC 7	0.491	4.462	92.242
100 seed weight	PC 8	0.432	3.926	96.168
Biological yield/plant	PC 9	0.310	2.817	98.985
Harvest index	PC 10	0.090	0.821	99.806
Seed yield/ plant	PC 11	0.021	0.194	100.00

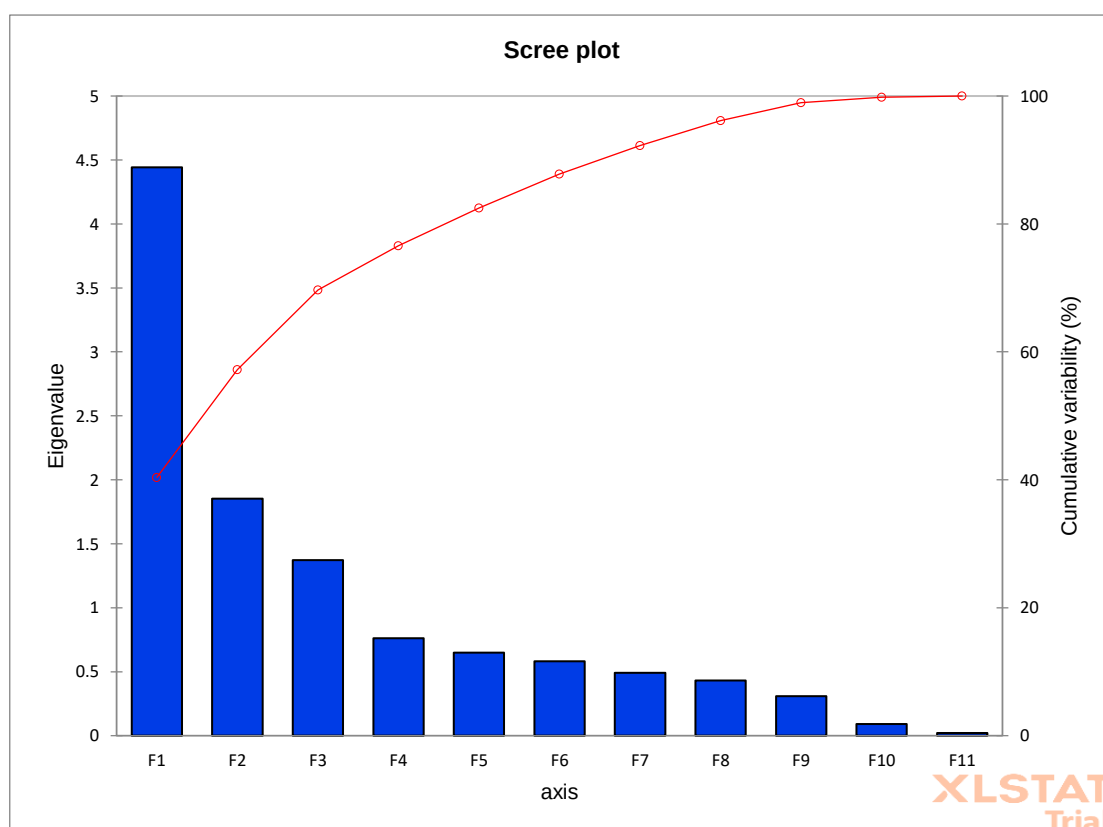


Fig. 3 Scree plot between Eigen value and Principal Components

Rotated component matrix revealed that first four PCs are representing maximum variability (76.59%) hence, the traits falling in these PCs may be given due importance in soybean breeding programme. (table 4.7) Results revealed that the first principal component (PC1) which accounted for the highest variation (40.380%) was mostly related with yield and its contributing traits such as days to flower initiation, days to maturity, number of pods per plant, number of nodes per plant, number of seeds per plant, biological yield per plant, and seed yield/plant. The second principal component (PC2) consisted of harvest index. Third principal component was related to 100 seed weight and fourth principal component with plant height (Table 4.8). On the basis of PCA, most of the important yield attributing traits were present in PC1.

Table 4.7 Rotated component matrix for different traits of soybean genotypes

Traits	Principal Components			
	PC1	PC2	PC3	PC4
Days to flower initiation	0.572	-0.307	-0.357	-0.036
Days to maturity	0.574	-0.361	0.368	0.055
Plant height	0.569	-0.267	-0.364	0.596
No. of primary branches/plant	0.616	-0.453	0.129	0.058
No. of nodes/pod	0.700	-0.188	-0.197	0.147
No. of pods/plant	0.721	-0.036	-0.213	-0.393
No. of seeds/ plant	0.852	0.306	-0.211	-0.241
Biological yield/plant	0.347	0.433	0.671	0.325
100 seed weight	0.608	-0.288	0.567	-0.208
Harvest index	0.384	0.842	-0.213	0.118
Seed yield/ plant	0.841	0.491	0.114	-0.037

Extraction Method: Principal Component Analysis.

A bold value represents more related traits in each principal component

PC scores of genotypes

The PC scores of each component (PC1, PC2, PC3 and PC4) had positive and negative values (Table 4.9, Table 4.10, Table 4.11, and Table 4.12). These scores can be utilized to propose precise selection indices whose intensity can be decided by variability explained by each of principal component. High PC

score for a particular genotype in a particular component denotes high values for the variables in that particular genotype. In PC1, the positive scores ranged from 7.583 (G2225) to 0.074(PK 701) while negative value ranged from -4.429 (JS 20-34) to -0.040 (KB-17). In PC2, the positive value of the component ranged from 5.569 (UGM75) to 0.002 (RKS54) and negative value ranged from -3.104(SL 752) to -0.004 (EC 468597). In PC3, the positive value of the components ranged from 3.466 (NRC86) to 0.015 (RSC14) and negative from -2.830 (PS1467) to -0.008(EC391181). In PC4, the positive value of the components ranged from 2.658 (GP566) to 0.001(TGX894-813) while negative value ranged from -2.118 (SL (E) 1) to -0.025 (MACS-7102).

In PC1, the higher value for traits viz., days to flower initiation, days to maturity, number of pods per plant, number of nodes per plant, number of seeds per plant, biological yield per plant, and seed yield/plant were present in genotype G225 (7.583) followed by TGX 849-D-13-4 (6.128) NRC-86 (5.029), TNAU 20024 (4.663), UPSL125 (4.135), PK1038 (3.983), EC-389353(3.660), JSM232 (3.195), JSM 222 (3.168), NRC2007A (3.064), NRC 2006M (2.789), SL(E)1 (2.628), PS 1467 (2.279), RKS54 (2.121), UGM75 (2.110), EC377883B (2.054), JSM245 (1.928), PK258 (1.867), SL 682 (1.851) JSM227 (1.823), GP465 (1.809) VGM70 (1.785), RSC14(1.345), JSM285 (1.258), JS20-98 (1.209), WT88 (1.134) JS 20-01 (1.038) UGM70 (0.801) VLS75 (0.725), NRC86 (0.659) and UPSM77 (0.659). Maximum negative values were recorded by JS 20-34 (-4.429), SL 2951 (-2.962), 20-148 (Z-15) (-2.825), JS 20-34 (-2.718), GC 84051-32-1 (-2.539), GC 84051-32-1 (-2.539), EC 16213 (-2.342), EC 389099 (-2.332), PS 1475 (-2.298), EC291397 (-2.208), PS1421 (-2.171), JS 20-98 (-2.115), LEE 96 (-2.121), 23- 11A (Z-18) (-2.097), EC 109540 (-2.038), 20-40B (Z-19) (-2.034), PS 1336 (-2.010), JS 20-52 (-1.992), EC 33940 (-1.963), JS 20-69 (-1.946), SQL1 (-1.854), EC391316 (-1.837), EC291451 (-1.668), JS 20-29 (-1.648), JS 20-50 (-1.578), EC 103336 (-1.565), JS 96-31 (-1.502), EC 572160 (-1.429), JSM 195 (-1.411), K-53 (-1.281), EC 106998 (-1.275), EC389179B (-1.236), EC 325103 (-1.092), EC 294003 (-1.073), EC 468597 (-1.051), EC 396065 (-1.024), GP 566 (-0.872), EC 538830 (-0.855), DE 201 (-0.787), EC 24091 (-0.744), TGX 1488-9-1D (-0.744), MACS 303 (-0.614), MACS 171 (-

0.588), KDS 256 (-0.577), JS 335 (-0.566), VLS 11 (-0.533), F4P20 (-0.522) and NRC37 (-0.518).

In PC2, higher value of trait viz., harvest index present in genotypes UGM75 (5.569) followed by JS335 (4.596), JS 20-98 (3.979), NRC86 (3.876), EC 291451(2.536), EC 528640 (2.098) JS 20-34 (1.668), EC 106998 (1.607), TGX 849-D-13-4 (1.599) KDS256 (1.582), EC 24091 (1.532), EC 389179B (1.516), PK1038 (1.458), EC391316 (1.310), EC 457214 (1.176), JSM 227 (0.918), GP 465 (0.899), EC377883 (0.889), NRC 2007A (0.817), EC 350664 (0.774), KB-17 (0.616), G2225 (0.591), MACS303 (0.570), WT88 (0.550) and JS 20-29 (0.531). Maximum negative values were recorded by SL 752 (-3.104), UPSM 77 (-2.734), EC33872B (-2.079), JS 96-31 (-1.982), MACS-7102 (-1.974), DE 201 (-1.808), F4P20 (-1.643), PI 204336 (-1.438), K-53 (-1.411), EC 457336 (-1.397), JSM 285 (-1.246), TNAU 20024 (-1.243), GP566 (-1.211), JSM 195 (-1.181), JS 20-69 (-1.153), PS 1336 (-1.097), JS 20-01 (-1.054), RSC 14 (-1.011), JS 20-50 (-1.000), EC 572160 (-0.974), EC 291397 (-0.952), EC 16213 (-0.950), DCB 137 (-0.853), JS 20-52 (-0.832), MACS 171 (-0.759), G4P15 (-0.751), JS 20-34 (-0.663), EC389153 (-0.612), EC 389099 (-0.609), JS 97-52 (-0.604), PK258 (-0.597), JSM 222 (-0.597) and NRC 80-1 (-0.507).

In PC3, highest PC scores were obtained by genotypes NRC 86 (3.466) 2.212), JS 20-29 (2.145), JSM222 (1.859), 23-11A(Z-18) (1.652), NRC 2007A (1.613), 20-40B(Z-9) (1.568), EC572160 (1.456) JSM232 (1.434) NRC2006M (1.268), PI204336 (1.167), 20-148(Z-15) (1.707), EC325103 (1.019), EC350664 (0.973), TGX 849-D-13-4 (0.937), GC84051-32-1 (0.885), EC 24091 (0.882), SQL37 (0.873), AGS12 (0.817), MACS-7102 (0.728), RKS 52 (0.695), JSM 227 (0.694), KDS256 (0.665), MACS 030 (0.646), PS1336 (0.634), EC 109540 (0.691), WT 88 (0.610) And JS 20-34 (0.592). Maximum negative values were recorded in PKS 1467 (-2.830) followed by PK 1038 (-2.464), GP566 (-2.240), G4P15 (-1.873), LEE 54 (-1.749), JS 20-50 (-1.626), LEE 96 (-1.501), UGM 75 (-1.474), EC33872B (-1.455), EC 389099 (-1.454), PS 1475 (-1.389), JS 20-34 (-1.289), VLS 75 (-1.237), JS 96-31 (-1.237), EC 391316 (-1.232), UPSM 77 (-1.213), TNAU 20024 (-1.208), TGX849-813 (-0.951), PS1421 (-0.929), EC294003 (-0.912), NRC 86 (-0.871), KB-17 (-0.871), JS 20-01 (-0.860), SL 2951 (-0.853), SL (E)1 (-0.735), EC 10336 (-0.693), EC 291451 (-0.680), EC 291397

(-0.679), JS 20-52 (-0.651), JSM 285 (-0.612), DCB 137 (-0.568), DE201 (-0.567), VLS11 (-0.551), PK258 (-0.543), GP465 (-0.530) and JS 20-69 (-0.502) for the trait 100 seed weight.

In PC4, the highest value plant height was obtained by GP566 (2.658) followed by LEE-54 (2.426), EC391316 (1.560), EC468597 (1.539), EC 24091 (1.531), JS 20-98 (1.493, EC 377883B (1.394), EC 33872B (1.225), UPSM 77 (1.183), EC 457336 (1.135), NRC2007A (1.121), EC 391181 (1.076), TGX849-D-13-4 (0.990), UGM70 (0.937), EC291451 (0.897), JSM 245 (0.808), NRC 37 (0.787), RKS54 (0.744), MACS171 (0.698), JSM195 (0.618), KDS256 (0.604), NRC86 (0.574), 20-148(Z-15)(0.568) and DCB 137 (0.548). Maximum negative values were recorded in SL (E) 1 (-2.118), JS 20-52 (-1.823), F4P20 (-1.648), PKS 1475 (-1.358), JSM 285 (-1.354), JS 96-31 (-1.339), EC-389179B (-1.300), G4P15 (-1.229), UPSL 152 (-1.160), EC-538830 (-1.141), JS 20-50 (-1.067), JS 20-34 (-1.033), JSM 227 (-0.971), NRC 2006M (-0.940), GC 84051-32-1 (-0.852), JS 20-69 (-0.802), EC109540 (-0.755), EC 389099 (-0.713), EC16213 (-0.649), EC325103 (-0.604), PI 204336 (-0.586), LEE 96 (-0.537), JS335 (-0.535) and EC 389153 (-0.519).

Table 4.8: Interpretation of rotated component matrix for the traits having maximum values >0.5 in each PCs

CHARACTERS	PC 1	PC 2	PC 3	PC 4
	Days to flower initiation	Harvest Index	100 seed weight	Plant height
	Days to maturity			
	Number of pods per plant			
	Number of nodes per plant			
	Number of seeds per plant			
	Biological yield per plant			
	Harvest Index			
	Seed yield per plant			

Table 4.9: PC scores of soybean germplasm having positive values >0.5 in each PCs.

S. No.	Genotypes	PC1 score	PC2 score	PC3 score	PC4 score
1	K-53	-1.281	-1.411	-0.320	0.350
2	EC 109540	-2.038	-0.094	0.619	-0.755
3	UGM 75	2.110	5.569	-1.474	-0.406
4	MACS 303	-0.614	0.570	0.646	-0.278
5	TNAU 20022	-0.252	-0.315	-0.405	0.026
6	EC 528640	-0.192	2.098	0.505	0.284
7	EC-389153	3.660	-0.612	-0.489	-0.519
8	UPSL 152	4.135	0.002	0.230	-1.160
9	JS 20-34	-2.718	-0.663	-1.289	-1.033
10	JS 97-52	-0.096	-0.604	-0.435	-0.407
11	NRC 2007A	3.064	0.817	1.613	1.121
12	NRC 80-1	0.093	-0.507	0.183	0.304
13	JS 20-01	1.038	-1.054	-0.860	-0.192
14	EC 396065	-1.024	0.165	-0.425	0.368
15	DCB 137	0.429	-0.853	-0.568	0.548
16	EC 457214	-0.354	1.176	0.482	0.074
17	DE 201	-0.787	-1.808	-0.567	0.370
18	EC 457336	-0.081	-1.397	-0.465	1.135
19	AGS 12	0.503	0.100	0.817	0.426
20	F4P20	-0.522	-1.643	2.907	-1.648
21	EC 103336	-1.565	-0.483	-0.693	0.478
22	NRC 86	0.659	0.097	3.466	-0.363
23	EC 106998	-1.275	1.607	-0.341	-0.543
24	SL 752	-0.096	-3.104	2.212	0.280
25	SQL 37	0.395	-0.432	0.873	-0.084
26	WT 88	1.134	0.550	0.601	-0.319
27	EC 538830	-0.855	0.152	-0.305	-1.141
28	NRC 2006M	2.789	0.482	1.268	-0.940
29	EC16213	-2.342	-0.950	-0.089	-0.649
30	JS 20-52	-1.992	-0.832	-0.651	-1.823
31	PS 1475	-2.298	0.210	-1.389	-1.358
32	EC 389179B	-1.236	1.516	0.136	-1.300
33	JSM 227	1.823	0.918	0.694	-0.971
34	SL 2951	-2.962	0.178	-0.853	-0.063
35	EC 389099	-2.332	-0.609	-1.454	-0.713
36	JS 20-69	-1.946	-1.153	-0.502	-0.802
37	JSM 195	-1.411	-1.181	0.136	0.618
38	EC 291397	-2.208	-0.952	-0.679	0.328
39	PS 1336	-2.010	-1.097	0.634	-0.329
40	EC 294003	-1.073	0.375	-0.912	-0.111
41	EC 291451	-1.668	2.536	-0.680	0.897

S. No.	Genotypes	PC1 score	PC2 score	PC3 score	PC4 score
42	EC 24091	-0.744	1.532	0.882	1.531
43	RSC 14	1.345	-1.011	0.015	0.086
44	EC 325103	-1.092	0.079	1.019	-0.604
45	JSM 285	1.258	-1.246	-0.612	-1.354
46	EC 33872B	-0.112	-2.079	-1.455	1.225
47	SQL 1	-1.854	0.025	-0.230	0.115
48	JSM 232	3.195	-0.310	1.434	-0.118
49	JSM 222	3.168	-0.597	1.859	0.235
50	JSM 245	1.928	-0.267	-0.012	0.808
51	PS 1467	2.279	0.061	-2.830	0.323
52	SL (E)1	2.628	-0.094	-0.735	-2.118
53	PK 701	0.074	-1.510	0.133	-0.488
54	PK 1038	3.983	1.458	-2.464	-1.574
55	RKS 54	2.121	0.002	0.695	0.744
56	EC 33940	-1.963	0.202	0.456	-0.146
57	G2225	7.583	0.591	0.160	0.434
58	JS 20-29	-1.648	0.531	2.145	-0.121
59	G4P15	-0.421	-0.751	-1.873	-1.229
60	GP 465	1.809	0.899	-0.530	0.117
61	TGX 849-D-13-4	6.128	1.599	0.937	0.990
62	MACS 171	-0.588	-0.759	0.504	0.698
63	JS 20-98	1.209	-0.339	0.293	1.493
64	TG X 849-813	-0.099	-0.349	-0.951	0.001
65	KB-17	-0.040	0.616	-0.871	-0.229
66	KDS 256	-0.577	1.582	0.665	0.604
67	LEE-54	0.081	-0.436	-1.749	2.426
68	JS 96-31	-1.502	-1.982	-1.237	-1.339
69	TNAU 20024	4.663	-1.243	-1.208	0.348
70	PK 258	1.867	-0.597	-0.543	0.111
71	EC 468597	-1.051	-0.004	-0.203	1.539
72	EC 572160	-1.429	-0.974	1.456	0.418
73	NRC 37	-0.518	0.425	-0.143	0.787
74	EC 391181	0.112	-0.013	-0.008	1.076
75	VGM 70	1.785	-0.018	2.246	-0.396
76	VLS 75	0.725	0.053	-1.237	0.087
77	EC 391316	-1.837	1.310	-1.232	1.560
78	SL 682	1.851	0.284	0.125	-0.072
79	PI 204336	0.179	-1.438	1.167	-0.586
80	UGM 70	0.801	-0.343	-0.265	0.937
81	LEE 96	-2.121	-0.228	-1.501	-0.537
82	TG X 1488-9-1D	-0.744	-0.385	0.328	-0.357
83	GP566	-0.872	-1.211	-2.240	2.658
84	PS1421	-2.171	0.166	-0.929	0.219
85	VLS 11	-0.533	-0.182	-0.551	0.033
86	UPSM 77	0.659	-2.734	-1.213	1.183

S. No.	Genotypes	PC1 score	PC2 score	PC3 score	PC4 score
87	EC 350664	0.448	0.774	0.973	-0.221
88	EC 377883B	2.054	0.889	3.426	1.394
89	JS 20-34	-3.212	1.668	0.592	-1.318
90	GC 84051-32-1	-2.539	0.196	0.885	-0.852
91	JS 20-50	-1.578	-1.000	-1.626	-1.067
92	MACS-7102	-0.159	-1.974	0.728	-0.025
93	20-40B(Z-9)	-2.034	0.239	1.568	0.233
94	20-148 (Z-15)	-2.825	-0.284	1.070	0.568
95	23-10B(Z-17)	-0.055	-0.319	0.226	-0.241
96	23-11A(Z-18)	-2.097	-0.006	1.652	0.153
97	JS 20-34	-4.429	-0.314	-0.165	-0.247
98	JS 335	-0.566	4.596	-0.162	-0.535
99	JS 20-98	-2.155	3.979	-0.168	0.370
100	NRC 86	5.029	3.876	-0.871	0.574

Table 4.10: List of selected genotypes in each principal component having positive values

PC1	PC2	PC3	PC4
UGM75	UGM75	EC 109540	NRC 2007A
EC389153	MACS 303	MACS 303	DCB137
UPSL 152	EC 528640	NRC 2007A	EC 457336
NRC2007A	NRC2007A	AGS12	JSM 195
JS 20-01	EC 457214	F4P20	EC291451
NRC 86	EC 106998	NRC 86	EC24091
WT 88	WT 88	SL 752	EC 33872B
NRC 2006M	EC 389179B	SQL 37	JSM 245
JSM227	JSM227	WT 88	RKS 54
RSC 14	EC291451	NRC 2006M	TGX 849-D-13-4
JSM285	EC24091	JSM 227	MACS 171
JSM232	PK 1038	PS 1336	JS 20-98
JSM 222	G2225	EC 24091	KDS 256
JSM 245	JS 20-29	EC 325103	LEE-54
PS 1467	GP 465	JSM 232	EC 468597
SL (E)1	TGX 849-D-13-4	JSM 222	NRC37
PK 1038	KB-17	RKS 54	EC 391181
RKS 54	KDS 256	JS 20-29	EC 391316
G2225	EC 391316	TGX 849-D-13-4	UGM70
GP 465	EC 350664	KDS256	GP 566

TGX 849-D-13-4	EC 377883B	EC 572160	UPSM 77
JS 20-98	JS 20-34	VGM 70	EC 377883B
TNAU 20024	JS 335	PI 204336	20-148(Z-15)
PKS 258	JS 20-98	EC 350664	NRC 86
VGM 70	NRC 86	EC 377883B	
VLS 75		JS 20-34	
SL 682		GC 84051-32-1	
UGM 70		MACS 7102	
UPSM77		20-40B (Z-9)	
EC377883B		20-148 (Z-15)	
NRC 86		23-11A (Z-18)	

Germplasm having common PC scores with positive value

On the basis of PC scores, maximum positive values were recorded in genotype G2225 (7.583) followed by TGX 849-D-13-4 (6.128), UGM75 (5.569), PK1038 (3.983), EC377883B (3.426), JSM232 (3.195), JSM 222 (3.168), NRC 2007A (3.064), NRC 2006M (2.789), EC 291451 (2.536), VGM 70 (2.246), JS 20-29 (2.145), RKS 54 (2.121), JSM 245 (1.928), JSM 227 (1.832), GP465 (1.809), JS 20-34 (1.668), KDS 256 (1.582), EC391316 (1.560), EC24091 (1.532), JS 20-98 (1.493), UPSM 77 (1.183), WT88 (1.134), 20-148(Z-15) (1.070), EC 350664 (0.973), JSM 227 (0.918), EC291451 (0.897), EC 350664 (0.774), and NRC 86 (0.659) which fell in more than one PCs.

Germplasm having common PC scores with negative value

Maximum negative values were recorded in JS 20-34 (-3.212), SL2951 (-2.962), UPSM77 (-2.734), JS 20-34 (-2.718), GC84051-32-1 (-2.539), PK1038 (-2.464), EC16213 (-2.342), EC389099 (-2.332), PS1475 (-2.298), GP556 (-2.240), EC 29397 (-2.208), PS1421 (-2.171), LEE 96 (-2.121), SL (E)1 (-2.118), EC 109540 (-2.038), PS1336 (-2.010), JS 20-52 (-1.992), JS 20-69 (-1.946), G4P15 (-1.873), EC391316 (-1.837), DE201 (-1.808), EC291451(-1.668), F4P20 (-1.648), JS 20-50 (-1.626), EC 103336 (-1.565), JS 96-31(-1.502), EC 33872B (-1.455), PI 204336 (-1.438), EC 572160 (-1.429), JSM195 (-1.411), K-53 (-1.411), JSM 285 (-1.354), EC 106998 (-1.273), EC 389179B (-1.236), TNAU 20024 (-1.208), EC 538830 (-1.141), EC325103 (-1.092), EC 294003 (-1.073), JS 20-01 (-1.054), DCB137(-0.853), EC 389153 (-0.759), EC389153 (-0.612), JS 335 (-0.566) and VLS 11 (-0.551) which are common in more than one PCs.

Table 4.11: PC scores of sesame germplasm having negative values >0.5 in each PCs.

S. No.	Genotypes	PC1 score	PC2 score	PC3 score	PC4 score
1	K-53	-1.281	-1.411	-0.320	0.350
2	EC 109540	-2.038	-0.094	0.619	-0.755
3	UGM 75	2.110	5.569	-1.474	-0.406
4	MACS 303	-0.614	0.570	0.646	-0.278
5	TNAU 20022	-0.252	-0.315	-0.405	0.026
6	EC 528640	-0.192	2.098	0.505	0.284
7	EC-389153	3.660	-0.612	-0.489	-0.519
8	UPSL 152	4.135	0.002	0.230	-1.160
9	JS 20-34	-2.718	-0.663	-1.289	-1.033
10	JS 97-52	-0.096	-0.604	-0.435	-0.407
11	NRC 2007A	3.064	0.817	1.613	1.121
12	NRC 80-1	0.093	-0.507	0.183	0.304
13	JS 20-01	1.038	-1.054	-0.860	-0.192
14	EC 396065	-1.024	0.165	-0.425	0.368
15	DCB 137	0.429	-0.853	-0.568	0.548
16	EC 457214	-0.354	1.176	0.482	0.074
17	DE 201	-0.787	-1.808	-0.567	0.370
18	EC 457336	-0.081	-1.397	-0.465	1.135
19	AGS 12	0.503	0.100	0.817	0.426
20	F4P20	-0.522	-1.643	2.907	-1.648
21	EC 103336	-1.565	-0.483	-0.693	0.478
22	NRC 86	0.659	0.097	3.466	-0.363
23	EC 106998	-1.275	1.607	-0.341	-0.543
24	SL 752	-0.096	-3.104	2.212	0.280
25	SQL 37	0.395	-0.432	0.873	-0.084
26	WT 88	1.134	0.550	0.601	-0.319
27	EC 538830	-0.855	0.152	-0.305	-1.141
28	NRC 2006M	2.789	0.482	1.268	-0.940
29	EC16213	-2.342	-0.950	-0.089	-0.649
30	JS 20-52	-1.992	-0.832	-0.651	-1.823
31	PS 1475	-2.298	0.210	-1.389	-1.358
32	EC 389179B	-1.236	1.516	0.136	-1.300
33	JSM 227	1.823	0.918	0.694	-0.971
34	SL 2951	-2.962	0.178	-0.853	-0.063
35	EC 389099	-2.332	-0.609	-1.454	-0.713
36	JS 20-69	-1.946	-1.153	-0.502	-0.802
37	JSM 195	-1.411	-1.181	0.136	0.618
38	EC 291397	-2.208	-0.952	-0.679	0.328
39	PS 1336	-2.010	-1.097	0.634	-0.329

S. No.	Genotypes	PC1 score	PC2 score	PC3 score	PC4 score
40	EC 294003	-1.073	0.375	-0.912	-0.111
41	EC 291451	-1.668	2.536	-0.680	0.897
42	EC 24091	-0.744	1.532	0.882	1.531
43	RSC 14	1.345	-1.011	0.015	0.086
44	EC 325103	-1.092	0.079	1.019	-0.604
45	JSM 285	1.258	-1.246	-0.612	-1.354
46	EC 33872B	-0.112	-2.079	-1.455	1.225
47	SQL 1	-1.854	0.025	-0.230	0.115
48	JSM 232	3.195	-0.310	1.434	-0.118
49	JSM 222	3.168	-0.597	1.859	0.235
50	JSM 245	1.928	-0.267	-0.012	0.808
51	PS 1467	2.279	0.061	-2.830	0.323
52	SL (E)1	2.628	-0.094	-0.735	-2.118
53	PK 701	0.074	-1.510	0.133	-0.488
54	PK 1038	3.983	1.458	-2.464	-1.574
55	RKS 54	2.121	0.002	0.695	0.744
56	EC 33940	-1.963	0.202	0.456	-0.146
57	G2225	7.583	0.591	0.160	0.434
58	JS 20-29	-1.648	0.531	2.145	-0.121
59	G4P15	-0.421	-0.751	-1.873	-1.229
60	GP 465	1.809	0.899	-0.530	0.117
61	TGX 849-D-13-4	6.128	1.599	0.937	0.990
62	MACS 171	-0.588	-0.759	0.504	0.698
63	JS 20-98	1.209	-0.339	0.293	1.493
64	TG X 849-813	-0.099	-0.349	-0.951	0.001
65	KB-17	-0.040	0.616	-0.871	-0.229
66	KDS 256	-0.577	1.582	0.665	0.604
67	LEE-54	0.081	-0.436	-1.749	2.426
68	JS 96-31	-1.502	-1.982	-1.237	-1.339
69	TNAU 20024	4.663	-1.243	-1.208	0.348
70	PK 258	1.867	-0.597	-0.543	0.111
71	EC 468597	-1.051	-0.004	-0.203	1.539
72	EC 572160	-1.429	-0.974	1.456	0.418
73	NRC 37	-0.518	0.425	-0.143	0.787
74	EC 391181	0.112	-0.013	-0.008	1.076
75	VGM 70	1.785	-0.018	2.246	-0.396
76	VLS 75	0.725	0.053	-1.237	0.087
77	EC 391316	-1.837	1.310	-1.232	1.560
78	SL 682	1.851	0.284	0.125	-0.072
79	PI 204336	0.179	-1.438	1.167	-0.586
80	UGM 70	0.801	-0.343	-0.265	0.937

S. No.	Genotypes	PC1 score	PC2 score	PC3 score	PC4 score
81	LEE 96	-2.121	-0.228	-1.501	-0.537
82	TG X 1488-9-1D	-0.744	-0.385	0.328	-0.357
83	GP566	-0.872	-1.211	-2.240	2.658
84	PS1421	-2.171	0.166	-0.929	0.219
85	VLS 11	-0.533	-0.182	-0.551	0.033
86	UPSM 77	0.659	-2.734	-1.213	1.183
87	EC 350664	0.448	0.774	0.973	-0.221
88	EC 377883B	2.054	0.889	3.426	1.394
89	JS 20-34	-3.212	1.668	0.592	-1.318
90	GC 84051-32-1	-2.539	0.196	0.885	-0.852
91	JS 20-50	-1.578	-1.000	-1.626	-1.067
92	MACS-7102	-0.159	-1.974	0.728	-0.025
93	20-40B(Z-9)	-2.034	0.239	1.568	0.233
94	20-148 (Z-15)	-2.825	-0.284	1.070	0.568
95	23-10B(Z-17)	-0.055	-0.319	0.226	-0.241
96	23-11A(Z-18)	-2.097	-0.006	1.652	0.153
97	JS 20-34	-4.429	-0.314	-0.165	-0.247
98	JS 335	-0.566	4.596	-0.162	-0.535
99	JS 20-98	-2.155	3.979	-0.168	0.370
100	NRC 86	5.029	3.876	-0.871	0.574

Table 4.12: List of selected genotypes in each principal component having negative values

PC 1	PC2	PC3	PC4
K53	K53	UGM 75	EC 109540
EC 109540	EC 389153	JS 20-34	EC 389153
MACS 303	JS 20-34	JS 20-01	UPSL 152
JS 20-34	JS 97-52	DCB 137	JS 20-34
EC 396065	NRC 80-1	DE201	F4P20
DE201	JS 20-01	EC 103336	EC106998
F4P20	DCB 137	JS 20-52	EC 538830
EC 103336	DE201	PS 1475	NRC 2006M
EC106998	EC 457336	SL 2951	EC 16213
EC 538830	F4P20	EC 389099	JS 20-52
EC 16213	SL752	JS 20-69	PS 1475E
JS 20-52	EC 16213	EC 291397	EC 389179B
PS 1475	JS 20-52	EC 294003	JSM 227
EC 389179B	EC 389099	EC 291451	EC 389099
SL 2951	JS 20-69	JSM 285	JS 20-69
EC 389099	JSM 195	EC 33872B	EC 325103
JS 20-69	EC 291397	PS 1467	JSM 285
JSM 195	PS 1336	SL (E)1	SL (E)1
EC 291397	RSC 14	PK 1038	PK 1038
PS 1336	JSM 285	G4P15	G4P15
EC 294003	EC 33872B	G 465	JS 96-31
EC 291451	JSM 222	TGX 849-813	PI 204336
EC 24091	PK 701	KB 17	LEE 96
EC 325103	G4P15	LEE 54	JS 20-34
SQL 1	MACS 171	JS 96-31	GC 84051-32-1
EC 33940	JS 96-31	TNAU 20024	JS 20-50
JS 20-29	TNAU 20024	PK 258	JS 335
MACS 171	PK 258	VLS 75	
KDS 256	EC 572160	EC 391316	
JS 96-31	PI 204336	LEE 96	
EC 468597	GP 566	GP 566	
EC 572160	UPSM 77	PS 1421	

NRC 37	JS 20-50	UPSM 77	
EC 391316	MACS 7102	JS 20-50	
LEE 96		NRC 86	
TG X 1488-9-1D			
GP 566			
PS 1421			
JS 20-34			
GC 84051-32-1			
JS 20-50			
20-40B (Z-9)			
20-148 (Z-15)			
23-11A (Z-18)			
JS 20-34			
JS 335			
JS 20-98			

4.7 Genetic Divergence:

To estimate D^2 values, correlated means of characters were transformed to standard uncorrelated means using Tocher's method. The statistical distance between pair of genotypes were obtained as the sum of squares of the difference between the pairs of corresponding uncorrelated value of any two genotypes considered at a time. The genetic divergence has been studied using Mahalanobis' D^2 statistics on 100 genotypes over 11 yield and yield contributing characters. The results obtained are presented below:

4.7.1 Contribution of individual characters towards genetic divergence

The percentage contribution towards genetic divergence by all the characters is presented in table 4.13. The traits, number of seeds per plant (56.89%) by 2816 times contributed most towards genetic divergence followed by plant height (20.14%) by 997 times, number of pods per plant (12.00%) by 594 times, harvest index by 239 times (4.83%), biological yield per plant by 208 times (4.2%), days to flower initiation (1.29%) by 64 times, whereas, magnitude of genetic divergence was less than one per cent for days to maturity (0.65%) by 32 times rank first.

4.7.2 Grouping of genotypes into different clusters

In the present study, 100 genotypes were grouped into nine clusters based on divergence analysis (D^2 values) using Tocher's method. (Table 4.14). Clustering of genotypes was not associated with the geographical distribution and were mainly grouped due to their morphological differences. Cluster 1 was the largest among all clusters comprising 87 genotypes, Cluster II had 10 genotypes, Cluster IV had 2 genotypes and Cluster III, V, VI, VII, VIII and IX were mono genotypic.

Table No. 4.13 Percent contribution of characters towards divergence in 100 genotypes of soybean

S. No	Characters	Times Ranked 1 st	% contribution of traits towards divergence
1	Number of seeds per plant	2816	56.89%
2	Plant height (cm)	997	20.14%
3	Number of pods per plant (g)	594	12.00%
4	Harvest Index (%)	239	4.83%
5	Biological yield per plant (g)	208	4.2%
6	Days to flower initiation	64	1.29%
7	Days to maturity	32	0.65%
8	Number of nodes per plant	-	-
9	Number of primary branches per plant	-	-
10	100 seed weight (g)	-	-
11	Seed yield per plant (g)	-	-

Table 4.14 Distribution of soybean genotypes in different clusters

Cluster	Number of genotypes	Genotypes
I	87	K-53, UGM 70, TNAU 20022, EC 109540, MACS 303, DE 201, EC 528640, JS 20-34, JS 97-52, NRC 80-1, JS 20-01, DCB 137, EC 396065, AGS 12, F4P20, EC 457214, EC 457336, NRC 86, SL 752, SQL 37, WT88, JS 20-52, KB-17, PS1475, JSM 227, SL2951, JS 20-69, PS1336, JSM 195, RSC 14, EC103336, EC 106998, EC 538830, NRC 2006M, EC 16213, EC 389179B, EC 389099, EC291397, EC 294003, EC 291451, EC 24091, EC 325103, EC 33872B, SQL1, PS1467, SL (E)1, PK 701, EC 33940, JS 20-29, G2P15, GP 465, MACS 171, JS 20-98, TGX 849-813, KDS 256, LEE 54, JS 96-31, PK 258, EC 468597, EC 572160, NRC 37, EC 391181, UGM 70, VLS 75, EC 391316, PI 204336, UGM 70, LEE 96, TGX 1488-9-1D, PS 1421, VLS 11, UPSM 77, JS 20-34, JS 20-50, MACS 7102, EC 84051-32-1, EC 350664, EC 377883B, 20-40B (Z-9), 20-148(Z-15), 23-10B (Z-17), 23-11A (Z-18)
II	10	EC 389153, UPSL 152, NRC 2007A, JSM 285, JSM 232, JSM 222, JSM 245, PK 1038, RKS 54, SL 682
III	1	JS 335
IV	2	JS 20-34, JS 20-98
V	1	GP566
VI	1	TNAU 20024
VII	1	TGX 849-D-13-4
VIII	1	G2225
IX	1	NRC 86

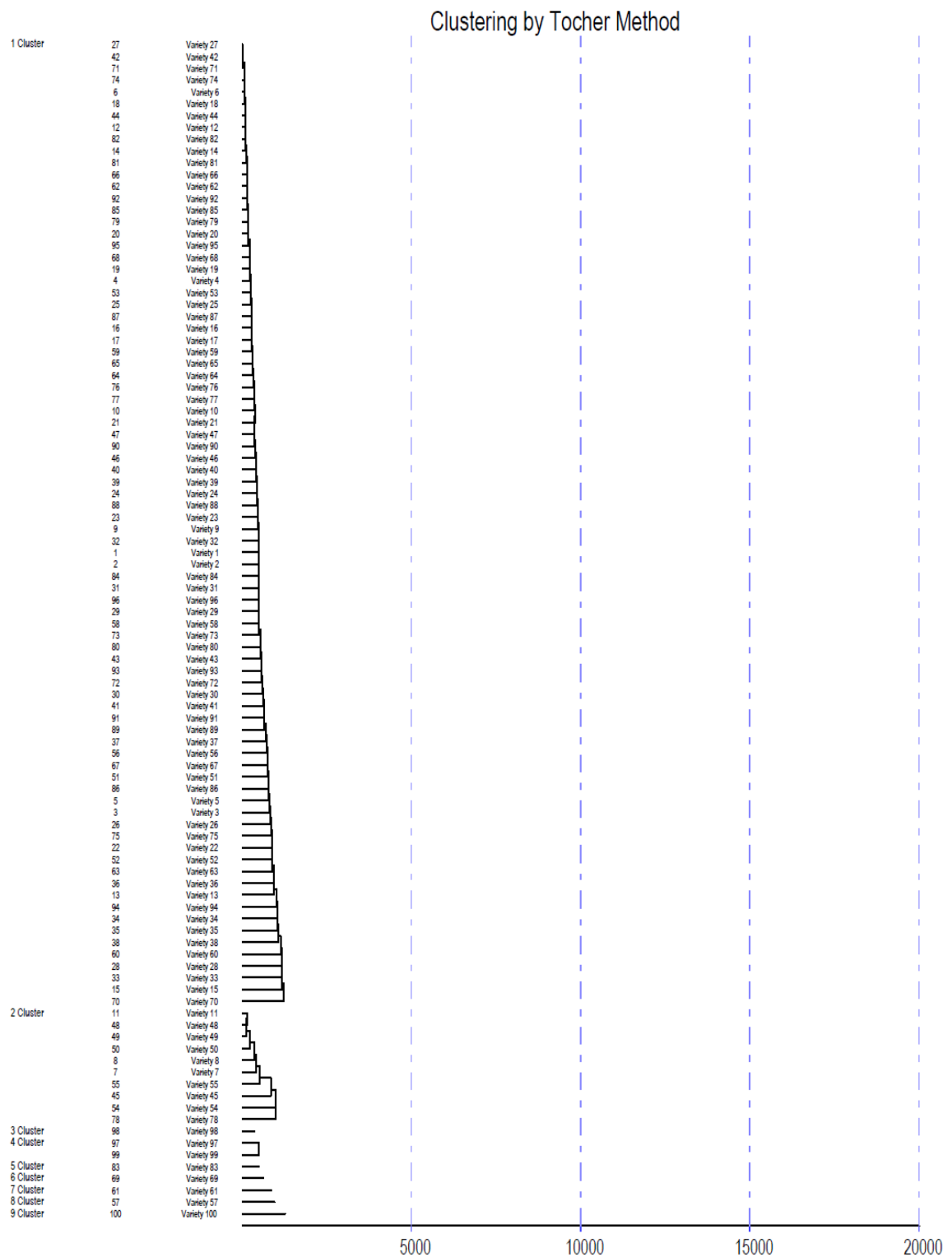
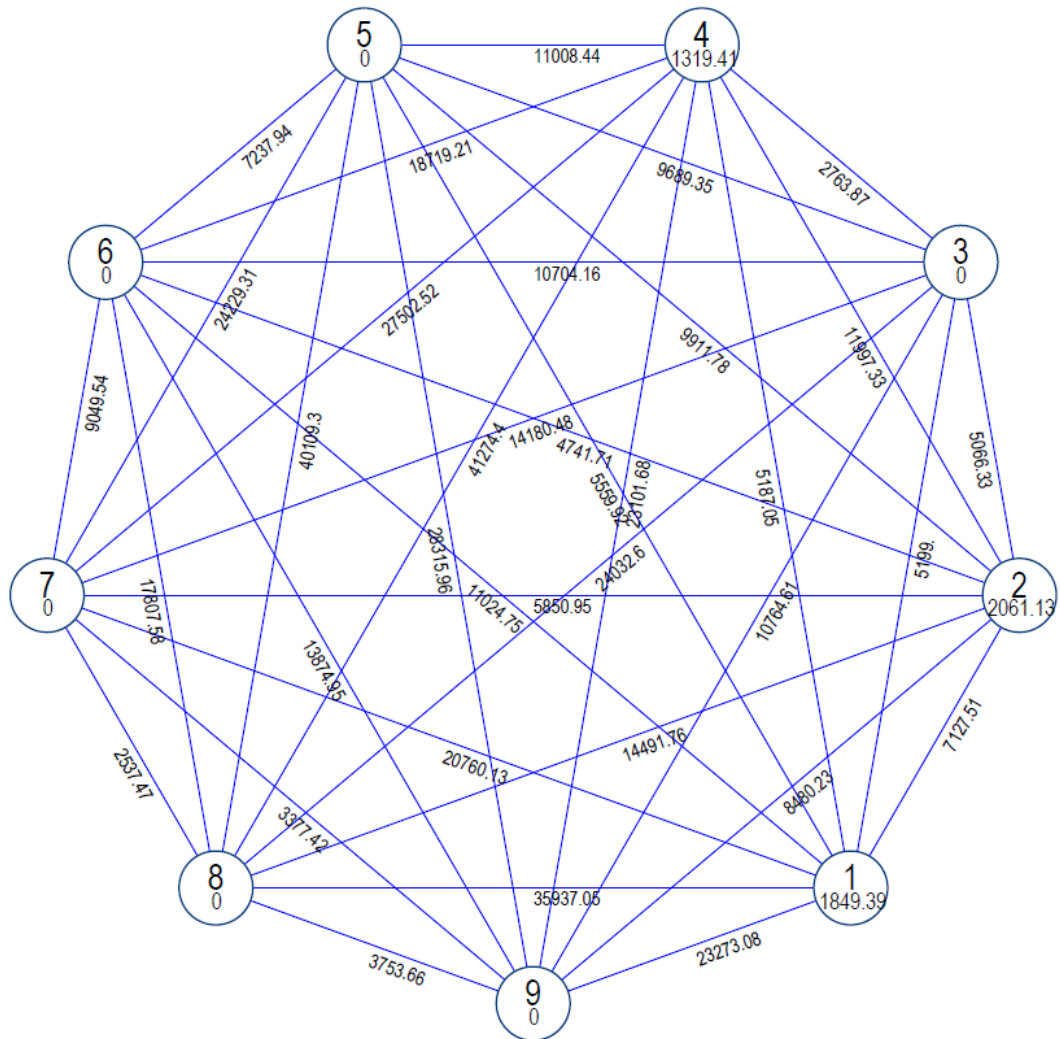


FIG.4: CLUSTERING BY TOCHER'S METHOD

Tocher Method



Mahalanobis Euclidean Disatnce (Not to the Scale)

FIG. 5: Mahalanobis Euclidean Distance

4.7.3 Intra and inter cluster divergence D^2 values

The average intra and inter-cluster D^2 values estimated as per the procedure given by Singh and Choudhary (1979) are presented in table 4.15

Cluster II showed maximum intra cluster D^2 value (2061.13) followed by cluster I (1834.39) and cluster VI (1319.41), while other clusters were mono-genotypic with no intra cluster divergence.

The highest inter cluster divergence was observed between genotypes of cluster IV and VIII (41274.40), followed by cluster V vs. VIII (40109.30), cluster I vs VIII (35937.05), cluster V vs IX (28315.96) whereas least inter cluster divergence was observed between genotypes of cluster IV vs. IV (1319.41).

Cluster I (1834.39) was poly-genotypic and was found nearest to cluster III (5199.00) followed in ascending order by cluster IV (5187.50), cluster V (5559.92), cluster II (7127.51), however, it was distantly placed to cluster VI (11024.75), cluster VII (20760.13), cluster XI (23273.08) and cluster VIII (35937.05).

Cluster II (2061.13) was poly genotypic and was found the nearest to cluster VI (4741.71) followed by cluster III (5066.33), cluster VII (5850.95), cluster IX (8480.23) and cluster V (9911.78), however, it was distantly placed to cluster VI (11997.33) and cluster VIII (14491.76).

Cluster III (0.00) was mono genotypic and was observed to be nearest to cluster IV (2763.87), followed by cluster V (9689.35), cluster VI (10704.16) and cluster IX (10764.61), while farthest to cluster VII (27502.52) and cluster VIII (24032.60).

Cluster IV (1319.41) was also poly genotypic and was observed to be nearest to cluster V (11008.44) followed by cluster VI (18719.21), cluster IX (23101.68) and cluster VII (27502.52), however, it was distantly placed to cluster VIII (40109.30).

Cluster V (0.00) was also mono-genotypic and was found to be nearest to cluster VI (7237.94) followed by cluster VII (24229.31) and cluster XI (28315.96), however, it was distantly placed to cluster VIII (40109.30).

Cluster VI (0.00) was also mono genotypic and was found be nearest to cluster VII (9049.54) followed by cluster VIII (17807.58), while farthest to cluster IX (13874.95).

Cluster VII (0.00) was also mono-genotypic and was found to be nearest to cluster VIII (2537.47), while farthest to cluster IX (3377.42).

Cluster VIII (0.00) was also mono-genotypic and was found to have cluster distance of 3753.66 with cluster IX.

Cluster IX (0.00) was found to be mono-genotypic and distance from other clusters has been described in the earlier clusters.

4.7.4 Cluster mean values

The cluster mean values of different characters are presented in Table 4.16

Cluster I

None of the characters had recorded the highest cluster mean value in this cluster but harvest index (21.45) had shown the lower cluster mean values.

Cluster II

The highest cluster mean value was recorded for the character biological yield per plant (33.62). While none of the characters had recorded the lowest cluster mean value.

Cluster III

None of the characters had recorded the highest and the lowest cluster mean value in cluster I. However, average values for all the characters under study were recorded

Cluster IV

Number of pods per plant (21.26), days to maturity (93.38), plant height (46.53), days to flower initiation (33.52), biological yield per plant (16.01), number of primary branches per plant (0.23) and number of nodes per pod (10.94) exhibited the lowest cluster mean values, whereas none of the characters showed the highest cluster mean value.

Cluster V

None of the characters had recorded the highest cluster mean value in this cluster but number of seeds per plant (51.70), 100 seed weight (5.22) and seed yield per plant (3.70) showed the lower cluster mean value.

Cluster VI

The highest cluster mean value were recorded for plant height (146.00), number of primary branches per plant (4.60) and number of nodes per plants (19.60), whereas the lowest cluster mean value were not recorded for any of the characters.

Cluster VII

The highest cluster mean value was recorded for days to maturity (118.00), whereas the lowest cluster mean value was recorded for none of the characters.

Cluster VIII

Cluster VIII recorded the highest cluster mean value for number of pods per plant (114.70) and days to flower initiation (66.00), whereas none of the characters exhibited the lowest cluster mean values.

Cluster IX

Number of seeds per plant (187.33), 100 seed weight (11.71), harvest index (79.93) and seed yield per plant (22.95) had shown the highest cluster mean values, while none of the character had recorded the lower cluster mean values.

Table 4.15 Intra and Inter-cluster divergence (D^2) for seed yield and associated traits

Cluster No.	I	II	III	IV	V	VI	VII	VIII	IX
I	1834.39	7127.51	5199.00	5187.05	5559.92	11024.75	20760.13	35937.05	23273.08
II		2061.13	5066.33	11997.3 3	9911.78	4741.71	5850.95	14491.76	8480.23
III			0.00	2763.87	9689.35	10704.16	14180.48	24032.60	10764.61
IV				1319.41	11008.44	18719.21	27502.52	41274.40	23101.68
V					0.00	7237.94	24229.31	40109.30	28315.96
VI						0.00	9049.54	17807.58	13874.95
VII							0.00	2537.47	3377.42
VIII								0.00	3753.66
IX									0.00

Table 4.16 Cluster means value for eleven traits in soybean

Clusters	Days to flower initiation	Days to maturity	Plant height	No of primary branches/ plant	No of nodes/ plant	No of pods/ plant	No.of seeds/ plant	100 seed weight	Biological yield/plant	Harvest index	Seed yield/plant
Cluster I	43.27	103.15	72.35	2.74	13.54	49.15	54.71	7.96	25.64	21.45	5.48
Cluster II	47.90	105.70	90.76	3.85	15.63	72.63	119.04	7.76	33.62	33.29	10.03
Cluster III	35.25	98.00	63.75	2.05	11.75	35.68	97.58	9.23	17.73	66.32	10.00
Cluster IV	33.25	93.38	46.53	0.23	10.94	21.26	54.38	7.51	16.01	68.32	5.12
Cluster V	49.00	101.00	136.00	2.60	11.60	29.60	51.70	5.22	17.00	21.76	3.70
Cluster VI	44.00	109.00	146.00	4.60	19.60	90.60	104.00	8.94	24.30	42.39	10.30
Cluster VII	64.00	118.00	95.30	3.60	19.30	99.00	180.30	6.38	32.90	37.99	12.50
Cluster VIII	66.00	117.00	95.70	3.60	18.00	114.70	221.00	7.47	28.20	62.06	17.50
Cluster IX	55.00	99.25	75.68	2.20	16.15	78.00	187.33	11.71	20.21	79.93	22.95

4.8 Physiological growth parameters

Characterization of growth rates and growth analysis parameters in diverse soybean genotypes

4.8.1 Leaf Area Index (LAI)

At 30 DAS

A significantly higher magnitude for LAI was recorded in genotypes MACS 303 (6.63) over the rest of the genotypes. It was followed by JSM 222 (5.79) and PK 701 (5.31). The minimum was found in genotype JS 20-98 (0.33) followed by KDS 256 (0.71).

At 45 DAS

The genotypes JSM 222 (11.28) possessed maximum LAI over remaining genotypes though they showed significant differences among all genotypes followed by JSM 232 (9.80) and JSM 222 (7.08). The lowest value was noted in EC 33872B (0.55) followed by PS 1336 (0.77).

At 60 DAS

The genotypes TNAU 20022 (71.08) possessed maximum LAI over remaining genotypes though they showed significant differences among all genotypes followed by LEE 54 (42.96) and SL682 (16.30). The lowest value was noted in EC 294003 (0.56) followed by EC 572160 (0.69).

4.8.2 Leaf Area Duration (LAD)

At 30-45 DAS

Significantly maximum LAD was noted in genotype JSM 222 (127.98) followed by JSM 232 (91.94) and LEE-54 (77.03) while least LAD value was EC 991397 (17.34) followed by PS 1336 (18.43).

At 45-60 DAS

Significantly maximum LAD was noted in genotype TNAU 20022 (551.31) followed by LEE-54 (375.32) and SL 682 (129.03) while least LAD value was PS 1336 (16.66) followed by JS 20-52 (17.39).

4.8.3 Specific Leaf Area (SLA)

At 30-45 DAS

Significantly maximum SLA was noted in genotype DCB 137 (1565.54) followed by MACS 303 (875.85) and EC 33940 (593.46) while least SLA value was SQL 1 (168.84) followed by NRC 86 (166.70).

At 45-60 DAS

Significantly maximum SLA was noted in genotype TNAU 20022 (2331.23) followed by LEE 54 (1246.37) and EC 389179B (510.20) while least SLA value was JS 20-34 (119.35) followed by PK 1038 (112.01).

4.8.4 Chlorophyll Content Index (SPAD)

The 100 genotypes exhibited an average magnitude of 31.61 chlorophyll content. Significantly higher magnitudes of chlorophyll content were recorded in EC 294003 (47.73) followed by SQL1 (46.07), JS 96-31 (44.57) and PS 1475 (42.33). These were further followed by PI 204336 (40.03) and MACS 7102 (40.03) and were found at par with each other. Whereas, significant lower magnitude of chlorophyll was reported by EC 291451 (13.43) followed by PS 1467 (13.10). (Table 4.17)

Table 4.17 General Mean Values of each genotype for Physiological traits

S. No	GENOTYPE	LAI 30	LAI 45	LAI 60	LAD 30-45	LAD 45-60	SLA 30-45	SLA 45-60	Chlorophyll content
1.	K-53	1.87	2.27	3.89	31.05	46.18	328.93	244.60	34.53
2.	EC 109540	2.28	1.65	2.29	29.46	29.55	313.79	250.31	35.90
3.	UGM 75	2.34	2.53	0.96	36.51	26.15	203.39	210.81	34.90
4.	MACS 303	6.63	2.06	1.08	65.16	23.51	875.85	194.74	31.80
5.	TNAU 20022	1.66	2.43	71.08	30.66	551.31	240.71	2331.23	28.13
6.	EC 528640	2.12	4.72	2.32	51.31	52.75	257.78	328.77	31.33
7.	EC-389153	2.14	3.92	4.04	45.46	59.71	219.94	375.53	17.13
8.	UPSL 152	1.81	4.53	3.18	47.50	57.77	238.89	248.12	26.07
9.	JS 20-34	2.77	1.77	3.24	34.10	37.62	236.53	187.51	28.07
10.	JS 97-52	1.78	2.44	2.55	31.66	37.44	236.60	193.55	33.57
11.	NRC 2007A	2.09	3.05	2.44	38.59	41.20	273.85	248.30	33.57
12.	NRC 80-1	2.32	3.87	4.26	46.44	60.96	236.63	299.09	26.73
13.	JS 20-01	1.52	2.75	2.58	32.09	39.97	188.23	221.73	23.03
14.	EC 396065	0.78	2.40	1.24	23.89	27.32	185.44	208.11	31.53
15.	DCB 137	2.12	4.39	1.44	48.78	43.73	1565.64	254.62	28.73
16.	EC 457214	2.27	4.07	4.95	47.51	67.58	384.71	307.64	24.93
17.	DE 201	1.01	3.74	1.64	35.62	40.34	227.54	267.48	31.37
18.	EC 457336	2.64	5.29	1.14	59.49	48.21	219.14	212.29	36.37
19.	AGS 12	2.36	2.61	1.44	37.26	30.34	233.06	225.60	33.43
20.	F4P20	2.18	4.81	2.22	52.36	52.69	238.24	214.36	25.57
21.	EC 103336	2.37	2.20	3.45	34.28	42.43	301.49	177.96	38.43
22.	NRC 86	3.61	4.36	3.17	59.73	56.48	250.81	236.63	32.93
23.	EC 106998	2.42	2.41	2.01	36.20	33.16	235.01	160.49	30.60

24.	SL 752	2.15	3.96	10.72	45.79	110.10	223.93	443.99	30.47
25.	SQL 37	1.70	3.59	3.95	39.68	56.57	244.09	258.10	31.27
26.	WT 88	1.81	4.65	1.94	48.41	49.38	263.74	227.19	24.17
27.	EC 538830	1.77	2.98	12.60	35.65	116.83	249.20	414.17	29.83
28.	NRC 2006M	2.16	4.27	3.39	48.26	57.49	322.71	225.63	32.67
29.	EC16213	2.10	2.50	1.08	34.53	26.84	226.99	242.81	26.43
30.	JS 20-52	1.41	1.14	1.18	19.10	17.39	226.03	191.25	34.53
31.	PS 1475	1.68	1.39	2.27	23.00	27.45	268.43	224.44	42.33
32.	EC 389179B	1.68	3.10	11.36	35.82	108.41	287.26	510.20	35.17
33.	JSM 227	1.31	3.40	1.75	35.31	38.60	226.76	278.59	34.50
34.	SL 2951	3.41	3.13	2.32	49.06	40.93	302.30	350.85	37.87
35.	EC 389099	1.63	1.73	1.14	25.25	21.58	272.48	197.76	26.87
36.	JS 20-69	0.88	1.92	2.37	20.99	32.17	223.57	242.84	31.27
37.	JSM 195	1.69	2.70	1.98	32.89	35.04	243.11	203.60	35.30
38.	EC 291397	1.01	1.31	1.46	17.34	20.72	170.58	179.79	30.97
39.	PS 1336	1.68	0.77	1.45	18.43	16.66	221.92	164.72	35.93
40.	EC 294003	2.09	6.27	0.56	62.69	51.26	289.28	275.69	47.73
41.	EC 291451	1.55	4.36	4.38	44.30	65.49	262.10	224.14	13.43
42.	EC 24091	1.84	5.73	2.39	56.76	60.87	200.82	202.36	27.10
43.	RSC 14	3.56	6.15	1.82	72.83	59.72	251.60	239.72	30.33
44.	EC 325103	2.46	3.27	1.88	42.93	38.60	217.35	201.49	37.80
45.	JSM 285	4.27	5.60	2.95	73.99	64.11	294.06	215.84	31.60
46.	EC 33872B	2.44	0.55	4.19	22.43	35.54	256.92	177.36	20.37
47.	SQL 1	1.64	4.51	2.91	46.09	55.67	168.84	244.21	46.07
48.	JSM 232	2.46	9.80	3.95	91.94	103.10	400.00	330.83	35.13
49.	JSM 222	5.79	11.28	2.31	127.98	101.88	319.09	258.63	38.30

50.	JSM 245	4.46	3.88	6.85	62.59	80.52	232.88	212.79	34.97
51.	PS 1467	2.12	5.09	2.98	54.11	60.50	400.28	234.47	13.10
52.	SL (E)1	3.08	6.46	2.14	71.58	64.55	343.02	247.38	35.00
53.	PK 701	5.31	2.35	2.73	57.47	38.12	324.99	270.53	23.40
54.	PK 1038	2.26	1.85	1.35	30.82	24.03	305.73	112.01	34.33
55.	RKS 54	3.07	2.25	3.75	39.89	44.98	468.14	454.78	33.50
56.	EC 33940	1.98	2.04	1.84	30.12	29.12	593.46	198.57	30.77
57.	G2225	1.13	3.04	5.55	31.30	64.43	435.57	380.10	28.07
58.	JS 20-29	2.31	3.22	1.03	41.48	31.87	223.51	210.28	34.63
59.	G4P15	0.85	3.50	1.35	32.67	36.38	368.83	282.62	27.80
60.	GP 465	3.16	5.38	2.33	64.04	57.84	391.53	220.59	32.73
61.	TGX 849-D-13-4	1.86	2.35	2.33	31.55	35.11	260.59	238.23	36.67
62.	MACS 171	2.83	5.37	2.86	61.51	61.74	247.98	200.21	30.57
63.	JS 20-98	0.33	6.25	2.87	49.33	68.34	253.74	298.40	31.13
64.	TG X 849-813	1.32	2.21	2.21	26.43	33.14	254.66	182.86	39.43
65.	KB-17	2.19	2.64	2.00	36.24	34.80	346.97	180.50	32.47
66.	KDS 256	0.71	3.03	1.04	28.10	30.58	218.01	205.55	29.20
67.	LEE-54	3.19	7.08	42.96	77.03	375.32	380.82	1246.37	30.37
68.	JS 96-31	3.28	2.96	1.34	46.87	32.30	238.05	170.45	44.57
69.	TNAU 20024	2.74	3.80	1.73	49.05	41.53	207.19	225.44	34.57
70.	PK 258	2.22	2.46	2.07	35.09	33.98	273.68	165.55	37.30
71.	EC 468597	4.45	4.96	3.65	70.59	64.56	216.76	177.70	36.13
72.	EC 572160	2.95	5.23	0.69	61.30	44.40	241.96	192.83	32.17
73.	NRC 37	3.08	2.64	2.51	42.92	38.61	342.16	187.63	30.33
74.	EC 391181	3.52	2.20	2.40	42.90	34.50	266.60	188.45	31.83
75.	VGM 70	2.38	2.57	3.43	37.12	45.01	312.70	201.43	22.63

76.	VLS 75	1.83	2.69	1.06	33.85	28.07	360.54	186.02	27.67
77.	EC 391316	1.20	1.93	1.88	23.43	28.57	187.17	145.64	25.40
78.	SL 682	4.45	0.90	16.30	40.15	129.03	302.86	403.30	29.87
79.	PI 204336	3.26	5.17	4.77	63.28	74.55	347.54	251.70	40.03
80.	UGM 70	1.79	4.48	3.17	47.04	57.33	285.77	231.70	23.77
81.	LEE 96	1.16	1.95	2.28	23.29	31.68	201.22	194.58	26.60
82.	TG X 1488-9-1D	1.58	3.36	1.30	37.04	34.93	267.08	178.83	27.47
83.	GP566	1.82	2.75	1.74	34.23	33.68	339.67	227.56	33.13
84.	PS1421	1.85	1.17	1.84	22.63	22.53	271.69	187.24	37.17
85.	VLS 11	0.82	2.87	1.63	27.64	33.74	209.48	270.56	34.50
86.	UPSM 77	3.29	3.37	1.35	49.94	35.35	240.30	147.17	31.27
87.	EC 350664	1.89	4.68	2.88	49.30	56.69	290.45	277.42	39.60
88.	EC 377883B	3.19	1.66	4.70	36.38	47.70	335.85	261.70	37.20
89.	JS 20-34	2.35	1.12	1.39	26.03	18.83	206.41	119.35	30.60
90.	GC 84051-32-1	1.35	2.63	5.78	29.88	63.14	258.48	374.33	26.20
91.	JS 20-50	3.15	1.34	1.11	33.68	18.37	265.52	181.98	32.20
92.	MACS-7102	3.11	2.54	3.07	42.34	42.05	338.97	249.42	40.03
93.	20-40B(Z-9)	2.75	1.82	0.71	34.26	19.00	388.63	148.59	35.10
94.	20-148 (Z-15)	2.53	2.07	1.51	34.55	26.90	388.86	198.19	31.80
95.	23-10B(Z-17)	3.84	3.59	1.83	55.74	40.66	366.20	187.26	35.97
96.	23-11A(Z-18)	1.88	2.13	1.08	30.11	24.09	292.48	197.69	31.37
97.	JS 20-34	1.87	2.64	3.10	33.87	43.10	229.56	209.86	23.17
98.	JS 335	1.34	1.50	1.05	21.24	19.13	261.93	132.66	19.20
99.	JS 20-98	1.62	1.46	3.92	23.10	40.38	330.25	251.95	27.20
100.	NRC 86	1.66	2.25	4.63	29.28	51.58	166.70	185.16	31.40

4.9 Biochemical estimations

4.9.1 Seed Protein Content (%)

The most noteworthy protein content (%) was recorded in JSM222 (41.89), trailed by JSM 245 (40.68) at standard with JS 20-34 (40.21) and UPSM 77 (40.15) while the least protein content (%) was evaluated in EC538830 (35.92). (Table 4.17)

4.9.2 Seed Oil (%)

The most extreme oil (%) was noted in NRC2007A (20.5) followed by TNAU 20022 and EC16213 (20.1) at standard with EC 389153, EC 325103, SQL1 and PK701(20.0) while EC 389179B (15.5) had the least incentive when contrasted with all others. (Table 4.17)

Table 4.18 Seed Oil and Protein Values of each genotype

S. No	Genotypes	Seed Oil %	Seed Protein N %
1.	K-53	17.2	38.27
2.	EC 109540	17.8	39.42
3.	UGM 75	18.8	36.21
4.	MACS 303	16.9	40.01
5.	TNAU 20022	20.1	37.22
6.	EC 528640	17.5	36.15
7.	EC-389153	20.0	38.62
8.	UPSL 152	17.1	37.27
9.	JS 20-34	18.5	40.21
10.	JS 97-52	19.1	38.19
11.	NRC 2007A	20.5	37.81
12.	NRC 80-1	17.5	38.29
13.	JS 20-01	18.3	37.13
14.	EC 396065	19.6	38.37
15.	DCB 137	18.5	37.73
16.	EC 457214	18.2	37.34
17.	DE 201	17.1	36.44
18.	EC 457336	16.9	38.64
19.	AGS 12	17.6	39.27
20.	F4P20	18.1	37.70
21.	EC 103336	16.8	40.01
22.	NRC 86	19.3	38.21
23.	EC 106998	17.2	37.15

24.	SL 752	18.4	36.49
25.	SQL 37	16.8	38.21
26.	WT 88	19.4	37.17
27.	EC 538830	16.0	35.92
28.	NRC 2006M	19.1	36.29
29.	EC16213	20.1	36.91
30.	JS 20-52	16.8	39.74
31.	PS 1475	19.5	37.46
32.	EC 389179B	15.5	38.12
33.	JSM 227	19.1	37.42
34.	SL 2951	19.7	38.01
35.	EC 389099	16.8	37.12
36.	JS 20-69	18.6	38.21
37.	JSM 195	17.5	37.71
38.	EC 291397	19.3	37.42
39.	PS 1336	16.8	37.21
40.	EC 294003	19.2	39.84
41.	EC 291451	16.8	37.42
42.	EC 24091	17.5	39.81
43.	RSC 14	18.7	37.19
44.	EC 325103	20.0	37.47
45.	JSM 285	18.6	37.71
46.	EC 33872B	17.6	36.19
47.	SQL 1	20.0	37.51
48.	JSM 232	16.3	37.39
49.	JSM 222	17.1	41.89
50.	JSM 245	19.8	40.68
51.	PS 1467	18.9	37.79
52.	SL (E)1	19.6	40.01
53.	PK 701	20.0	39.28
54.	PK 1038	16.9	36.43
55.	RKS 54	17.5	37.27
56.	EC 33940	18.4	40.07
57.	G2225	18.3	40.12
58.	JS 20-29	19.2	37.72
59.	G4P15	17.4	37.25
60.	GP 465	19.5	39.78
61.	TGX 849-D-13-4	16.5	40.12
62.	MACS 171	17.8	38.29
63.	JS 20-98	18.0	38.42
64.	TG X 849-813	19.1	37.22
65.	KB-17	16.9	39.71
66.	KDS 256	17.2	37.19

67.	LEE-54	18.3	36.92
68.	JS 96-31	19.0	38.17
69.	TNAU 20024	17.9	38.81
70.	PK 258	16.8	38.11
71.	EC 468597	18.7	37.75
72.	EC 572160	16.8	38.42
73.	NRC 37	19.5	39.21
74.	EC 391181	17.6	40.11
75.	VGM 70	16.5	37.54
76.	VLS 75	16.0	38.12
77.	EC 391316	18.9	37.27
78.	SL 682	17.6	36.72
79.	PI 204336	16.3	37.41
80.	UGM 70	16.5	38.14
81.	LEE 96	17.3	37.42
82.	TG X 1488-9-1D	19.1	39.29
83.	GP566	18.9	37.81
84.	PS1421	17.6	38.11
85.	VLS 11	19.1	36.45
86.	UPSM 77	17.1	40.15
87.	EC 350664	18.3	37.41
88.	EC 377883B	17.6	36.48
89.	JS 20-34	16.8	37.24
90.	GC 84051-32-1	19.0	37.12
91.	JS 20-50	18.7	39.60
92.	MACS-7102	16.8	38.16
93.	20-40B(Z-9)	17.3	37.96
94.	20-148 (Z-15)	16.6	36.61
95.	23-10B(Z-17)	19.2	39.81
96.	23-11A(Z-18)	16.5	38.45
97.	JS 20-34	19.4	39.56
98.	JS 335	19.8	39.85
99.	JS 20-98	19.2	38.12
100.	NRC 86	18.9	37.83

4.10 Field Screening for Multiple Disease Resistance

Jabalpur is a hotspot for charcoal rot bacterial pustules, YMV and *Rhizoctonia* aerial blight diseases. Therefore, it is necessary to have the genotypes capable of withstanding the uncertainty of biotic stresses. The genotypes under study were screened for the appearance of these major diseases at the field level.

Charcoal rot disease appeared during reproductive stages of crop. Out of hundred genotypes only forty five genotypes viz. VLS 11, EC389153, UPSL152, EC391181, DCB137, AGS12, SL752, EC109540, UGM75, MACS303, NRC2006M, EC16213, PS1475, EC389099, EC325103, JSM285, SQL1, JSM 232, JSM 222, JSM 245, JSM 20-34, SL(E)1, PK 701, PK 1038, RKS 54, EC 33940, G 2225, G4 P15, TGX849-D-13-4, JSM 227, JS 20-98, TGX849-813, KDS 256, SQL 37, WT 88, PK 258, PI 204336, UGM 270, PS 1467, EC 350664, EC 377883B, JS 20-34, 23-10B(Z-17), JS 20-34 and JS 2098 were found to be absolutely resistant, whereas six genotypes namely DE 201, EC 457336, MACS 171, SL2951, LEE96 and PS1421 were found to be highly susceptible to charcoal rot disease incidence. Table 4.18 depicts the percent mortality of soybean genotypes as a result of charcoal rot incidence.

Bacterial pustules appeared during the growing season of the crop. Out of 100 genotypes 54 viz K-53, UPSM 77, VLS 75, EC 391316, JS 97-52, NRC 2007A, NRC 80-1, JS 20-01, EC 457214, DE 201, EC 457336, AGS 12, NRC 86, MACS 303, NRC 2006M, JS 20-52, PS 1475, NRC 37, MACS 171, SL 2951, JSM 285, JSM 222, JSM 245, JS 20-34, SL (E)1, G2225, GP 465, TGX 849-D-13-4, JSM 227, JS 20-98, KB-17, SQL 37, WT 88, EC 538830, PI 204336, UGM 70, LEE 96, TG X 1488-9-1D, GP566, PS1421, VLS 11, PS 1467, EC 350664, EC 377883B, JS 20-34, GC 84051-32-1, JS 20-50, MACS-7102, 20-40B(Z-9), 20-148 (Z-15), 23-10B(Z-17), JS 20-34 (C), JS 20-98 (C) and NRC86 (C) were found to be absolutely resistant whereas 11 genotypes viz- EC 389179B, JS 20-69, JSM 195, PS 1336, EC 294003, RSC 14, G4P15, KDS 256, JS 96-31, SL 682, and JS 335 (C) were found to be highly resistant. However, the genotype EC 389099 was found to be susceptible to the disease incidence. (Table 4.19)

YMV incidence started 15th July onwards and it continued till August end. Here in percent disease severity and incidence were expressed in the form of the Coefficient of infection (CI). Among screened, genotypes EC33940 UPSL152, DCB137, JSM232, EC350664, EC457336, PS1336, EC294003, EC291451, EC24091, EC325103, G4PLS, GP465, TGX849-D-13-4, KDS256, PS1421, VLS11, JS20-98, DE201, EC106998, EC389099, JS20-69, EC291397, EC33872B, PK701, JS20-29, EC528640, EC103336, 20-40B(Z-9), 20-148(Z-17), and 23-10B(Z-17) exhibited highly resistant reaction against Yellow Mosaic Virus. However, seven genotypes viz EC391181, VLS75, NRC2007A, TNAU20022, UGM70, LEE96, and GP566 were found to be susceptible. (Table 4.20)

The appearance of aerial blight was observed during the month of August and continued till the harvesting of the crop. Among all, eleven genotypes namely UPSL152, DCB137, AGS12, F4P20, MACS303, JSM232, RKS54, G2225, PS1467, EC350664 exhibited highly resistant reaction against *Rhizoctonia* aerial blight. However, the genotypes EC103336, 20-40B (Z-9), 20-148(Z-15) and 23-10B (Z-17) were found to be susceptible for the disease incidence as mentioned in the table 4.21

Table 4.22 signifies that out of a hundred genotypes, one genotype viz. EC 350664 showed resistance against multiple diseases in the evaluation. Various other genotypes that demonstrated resistance to more than one disease referenced in the table.

Table 4.19 Field screening of soybean genotypes against Charcoal rot disease

Categories	Per Cent Mortality	TOTAL
Absolutely resistant	0	45
Highly resistant	0-1	--
Moderately resistant	1.1 to 10	29
Moderately susceptible	10.1 to 25	13
Susceptible	25.1 to 50	07
Highly susceptible	> 50	06

Table 4.20 Field screening of soybean genotypes against Bacterial pustule disease

Categories	Per Cent Mortality	TOTAL
Absolutely resistant	0	54
Highly resistant	0-1	11
Moderately resistant	1.1 to 10	23
Moderately susceptible	10.1 to 25	11
Susceptible	25.1 to 50	1
Highly susceptible	> 50	-

Table 4.21 Screening of soybean entries/genotypes against YMV disease

Symptoms	Severity grade	Response value	(CI)	Disease reaction	Genotypes
Symptoms absent	0	0	0-4	Highly resistant	33
Very mild symptoms up to 25% leaves	1	0.25	5-9	Resistant	20
Appearance of symptoms in 26-50% leaves	2	0.50	10-19	Moderately resistant	25
Appearance of symptoms in 51-75% leaves	3	0.75	20-39	Moderately susceptible	16
Severe disease infection in symptoms (>75% leaves)	4	1.00	40-69	Susceptible	6
			70-100	Highly susceptible	-

Table 4.22 Screening of soybean entries/genotypes against aerial blight disease

Categories	Per cent Disease Index	Germplasm lines
Absolutely resistant	0	-
Highly resistant	0-1	11
Moderately resistant	1.1 to 10	51
Moderately susceptible	10.1 to 25	34
Susceptible	25.1 to 50	04
Highly susceptible	> 50	-

Table 4.23 Germplasm showing multiple resistances against Charcoal rot, Bacterial pustules, Aerial blight and Yellow mosaic diseases of soybean

S. No	Diseases	Absolute /Highly resistant lines	Total
1.	Charcoal rot + Aerial blight	UPSL 152, DCB137, AGS12, MACS303, JSM 285, JSM 232, PKS54, G2225, PS1467, EC 350664	10
2.	Charcoal rot + YMV	JS 20-98*, 23-10B (Z-17), VLS11, TGX849-D-13-4, EC 350664, EC 377883B, KDS256, G4P15, PK701, EC 33940, JSM 232, UPSL 152, EC 325103, EC 389099, DCB 137.	15
3.	Charcoal rot + Bacterial pustules	AGS 12, MACS 303, NRC 2006M, PS1475, JSM 285, JSM 222, JSM 245, SL (E)1, JS 20-34, G2225, G4P15, TGX849-D-13-4, JSM227, JS 20-98, KDS 256, SQL 37, WT88, UGM70, VLS11, PI 204336, PS 1467, EC350664, EC377883B, JS 20-34, JS 20-34*, 23-10B (Z-17), JS 20-98*	27
4.	Aerial blight + Bacterial pustules	AGS 12, MACS 303, JSM 285, G2225, PS 1467, EC 350664	06
5.	Aerial blight + YMV	EC 350664, JSM 232, UPSL 152, DCB 137	04
6.	Bacterial pustules + YMV	DC101, EC 457336, JS 20-69, PS 1336, EC 294003, G4P15, GP465, TGX849-D-13-4, KDS 256, PS1421, VLS11, EC350664, EC377883B, GC84051-32-1, 20-40B(Z-9), 23-10B (Z-17), 20-148(Z-15), JS 20-98*	18
7.	Charcoal rot + Yellow Mosaic Viruses+ Bacterial pustules	JS 20-98*, 23-10B (Z-17), EC 377883B, VLS 11, EC 350664, G4P15, TGX849-D-13-4, KDS 256.	08
8.	Charcoal rot + Aerial blight + Yellow Mosaic Viruses	EC 350664, JSM 232, UPSL 125, DCB 137	04
9.	Aerial blight + Yellow Mosaic Viruses+ Bacterial pustules	EC 350664	01
10.	Charcoal rot + Aerial blight + Bacterial pustules	EC350664, PS1467, G2225, JS 285, MACS303, AGS 12	06
11.	Charcoal rot + Aerial blight + Yellow Mosaic Viruses+ Bacterial pustules	EC350664	01

Plate 5: Disease Reaction



Symptoms and reaction of charcoal rot disease of soybean



Symptoms and reaction of aerial blight disease of soybean

Plate 6: Disease Reaction



Symptoms and reaction of YMV disease of soybean



Symptoms and reaction of BP disease of soybean

Chapter-5



DISCUSSION

DISCUSSION

Plant genetic resources are considered as one of the most valuable and essential basic raw materials for any crop enhancement programme (Paroda and Arora,1991). The evidence on nature and magnitude of genotypic and phenotypic variability present in any crop species plays a vital role in articulating and designing successful breeding programmes. Greater genetic diversity in the germplasm for traits of interest such as yield, quality or resistance to both biotic and abiotic stresses will ensure greater chances of improvement for these traits in future breeding programmes. Morphological variability being highly influenced by the external environment, does not give a genuine picture of the potential genotypic variability. Thus, information about heritability and genetic advancement in yield and yield contributing characters are necessary for the crop improvement through selection and utilization. It is also known that yield is complex trait and influenced by many factors mainly environmental factors and qualitative traits are generally governed by polygenes that is by a large number of genes. Hence, selection of superior quality genotypes based on yield or single character as such is not very effective. Therefore, study among the different traits and correlation of direct and indirect effects should be taken into consideration. Assessment of genetic diversity among soybean genotypes from different groups is important because it allows plant breeders to select highly diverse genotypes for the further crop improvement programmes. Varietal development and release of promising lines in seed production chain which is the need of the hour could be achieved by way of utilizing superior genotypes in breeding and crossing activity and introducing background of diverse parents as source from the characterized material through introduction of new alleles and lines into breeding programme both from exotic and indigenous germplasm. Less diversity and narrow genetic base is one of the reason for only around hundred varieties being cultivated throughout the length and breadth of India.

Morphological characterization is essential for characterization of genotypes in a breeding programme, which depends upon the magnitude of genetic variability Zubair et al. (2007). Improvement of traits responsible for variability through selection and introduction of new alleles, lines and accessions

into breeding activity helps to broaden genetic base in turn helps future breeding activity and varietal development programmes.

Adaptation of improved material is also a barrier for crop breeder for its utilization in introgression of desirable genes present in the introduced material.

Characterization of germplasm resources available in crop species is very much essential for cultivar identification, avoiding duplications and protection of elite genotypes. Production of new varieties or hybrids could be achieved through introduction of new alleles in breeding programmes.

The study was carried out to estimate the extent of diversity present in soybean accessions. An attempt has been made to identify accessions with diverse genetic base and, the present investigation was subjected to different genetical studies viz., genetic variability, heritability, genetic advance, association analysis, path analysis, divergence and principal component analysis. The observations were recorded for hundred accessions of soybean. The experimental findings are discussed under following heads:

5.1 Morphological Characterization

5.2 Parameters of genetic variability

5.2.1 Genetic variability

5.2.2 Genotypic and phenotypic coefficient of variation

5.2.3 Heritability and genetic advance

5.3 Correlation coefficient analysis

5.4 Path coefficients analysis

5.5 Principal component analysis

5.6 Genetic divergence

5.7 Physiological growth parameters

5.8 Biochemical estimations

5.9 Screening for Multiple Disease Resistance

5.1 Morphological Characterization

Characterization with distinct morphological markers is essential for identification of genotypes and Intellectual property protection on phenotypic basis. India has enacted legislation for the Protection of Plant Varieties and Farmer's Right Act in 2001, in order to provide incentives for development and fulfil obligations under Trade Related Intellectual Property Right (TRIPs).

Novelty, Distinctiveness, Uniformity and Stability are the essential requirements for grant of protection to varieties/ germplasm / variation either. Genotypes are characterized on the basis of morphological traits viz., hypocotyl colour, growth habit, growth type, pubescence, pubescence colour, leaf shape, flower colour, pod colour, seed coat colour, seed size, seed shape, coloration due to peroxidase activity, hilum colour and colour of hilum funicle. From the study of these characters we can easily identify different genotypes of soybean. So, as to these characters as an identification key.

Similar, characterization pattern was adopted by Satyavathi *et al.* (2004), Sawarkar (2010), Badkul *et al.* (2014), Dubey (2015), Mishra (2016), Mehra (2019) and Saraswat (2019) taking distinguished morphological traits.

5.2 Parameters of genetic variability

5.2.1 Genetic variability

Variability refers to the presence of phenotypic differences among the individuals of plant population. Variability results due to differences either in the genetic constitution of the individuals of a population or in the environment in which they grown. Magnitude of genetic variability present in a population was of paramount importance to a plant breeder for starting a judicious breeding programme. The results obtained from present investigation are discussed here for pod and yield traits in all the genotypes used in the experiment.

The ANOVA exhibited highly significant mean sum of squares due to genotypes for all the traits viz., days to flower initiation, days to maturity, plant height, number of primary branches per plant, number of pods per plant, number of nodes per pod, number of seeds per plant, biological yield per plant, 100 seed weight, harvest index and seed yield per plant. This indicates that exploitable level of genetic variability is present and genetic base is broad for most of the important characters among different genotypes of soybean. This variation is useful in the initial breeding material as it offers opportunities for desired trait through phenotypic selection in the pre – breeding material for varietal development and crop improvement.

Similar results have been reported by Aditya *et al.* (2011) and Suresh Rao *et al.* (2014) for number of pods per plant and seed yield per plant, Athoni and

Basavaraja (2012) for plant height, Ghodrati (2013) for number of branches per plant, number of pods per plant and plant height, Mahbub *et al.* (2015) for seed yield per plant, number of branches per plant and plant height and Jha (2016) for the number of seeds per plant, number of pod clusters per plant, biological yield per plant, 100 seed weight and number of pods per plant.

5.2.2 Phenotypic and genotypic coefficient of variation

To obtain a clear picture about the variability present in all the genotypes, it is further split into phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV). In the present study, the phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the characters. High magnitudes of PCV and GCV was observed for the traits viz., number of seeds per plant, seed yield per plant, number of primary branches per plant, biological yield per plant, number of pods per plant, harvest index and plant height.

Number of seeds per plant recorded the highest PCV (48.88%) and GCV (40.91%) followed by seed yield per plant (44.85% and 30.17%), number of primary branches per plant (37.17% and 36.39%), biological yield per plant (35.30% and 35.28%), number of pods per plant (31.68% and 28.41%), harvest index (31.65% and 25.58%), plant height (23.29% and 23.16%); moderate for number of nodes per plant (15.82% and 14.60%), days to flower initiation (14.74% and 13.39%), and low PCV and GCV is of trait days to maturity (5.04% and 4.69%)

In agreement with the present findings, Chandel *et al.* (2013) for number of primary branches per plant and number of pods/plant, Ghodrati (2013) for number of pods per plant and plant height, Osekit and Ajayi (2013) for seed yield per plant and number of seeds/plant, Reni and Rao (2013) for seed yield/plant, number of pods/plant and biological yield/plant, Hakim *et al.* (2014) for seed weight/plant, number of pods/plant and days to maturity, Pawar *et al.* (2014) for seed yield/plant and number of pods/plant, Mahbub *et al.* (2015) for seed yield/plant, Akram *et al.* (2016) for harvest index, Jain *et al.* (2017) for number of pods per plant and harvest index, Neelima *et al.* (2018) for number of pods per plant, number of seeds per plant, biological yield per plant and harvest index,

Shruti *et al.* (2019) for pod weight per plant and seed yield per plant, Bhairwa *et al.* (2020) for days to flowering, days to maturity, plant height, number of nodes per plant, number of pods per plant, 100 seed weight, dry matter weight per plant, plant population per plot and harvest index

The PCV and GCV were found moderate for number of nodes per plant and days to flower initiation which were in confirmation with the findings of Chandel *et al.* (2013) for plant height, Pawar *et al.* (2014) for plant height, Bhairwa *et al.* (2020) plant population per plot. Low PCV and GCV were recorded for days to maturity indicating that they are very difficult to improve *via* selection programme. These results are in confirmation with the findings of Patil *et al.* (2011) for days to 50% flowering and days to maturity, Malek *et al.* (2014) for days to maturity, Pawar *et al.* (2014) for days to 50 per cent flowering and days to maturity, Bhairwa *et al.* (2020) days to 50% flowering and days to maturity.

5.2.3 Heritability and genetic advance

Heritability and genetic advance are important selection parameters in breeding programme. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone. The estimate of heritability can be utilized for the prediction of genetic gain, which indicates the genetic improvement that would result from the selection of best individuals. Hence, estimate of heritability is an essential prerequisite for formation of an effective selection method for genetic improvement.

Genetic advance is an indicator of improvement in the mean genotypic value of selected individual over the parental population. High heritability accompanied with high genetic advance indicates that the heritability is due to additive gene effect and selection may be effective, while high heritability coupled with low genetic advance indicates predominance of non-additive gene action, while low heritability is exhibited due to influence of environmental interaction rather than genotypes. Selection for such characters may not be rewarding.

Heritability estimates along with high genetic advance as percentage of mean was observed by biological yield per plant, number of primary branches

per plant, 100 seed weight, plant height per plant, number of seeds per plant, number of nodes per plant, number of pods per plant and harvest index which gives an indication that these traits might be governed by additive genes indicating that direct selection would be effective. High heritability with moderate genetic advance was recorded for days to flower initiation. High heritability with low genetic advance was recorded for days to maturity.

In agreement with the present investigation, high heritability coupled with high genetic advance have also been reported by Ghodatri *et al.* (2013) for plant height, Badkul *et al.* (2014) for number of pods per plant, biological yield per plant and seed yield per plant, Mahbub *et al.* (2015) for number of pods per plant, number of seeds per plant and primary branches. Tantway (2015) for number of pods per plant, biological yield per plant, number of seed per plant and seed yield per plant, Adsul *et al* (2016) for 100 seed weight, yield per plant and number of primary branches per plant, Akram *et al.* (2016) for plant height, yield per plant, number of pods per plant and number of seeds per plant , Mahbub and Shirazy (2016) for plant height, number of seeds per plant, number of pods per plant and 100-seed weight, Chandel *et al* (2017) for biological yield per plant , pods per plant and harvest Index, Jain *et al* (2017) for number of pods per plant, harvest index and plant height, Neelima *et al.* (2018) for plant height, number of branches per plant, number of pods per plant and seed yield per plant, Bhairwa *et al.* (2020) for plant height, number of pods per plant, dry matter weight per plant, plant population per plot and harvest index %.

Contradictory results were obtained by Hakim *et al.* (2014) for genetic advance for days to maturity, Sureshrao *et al.* (2014) for genetic advance of seed yield per plant, Akram *et al* (2016) and Mahbub and Shirazy (2016) for number of branches per plant, Getnet *et al.* (2019) for days to 50% flowering and days to maturity.

On the basis of heritability and genetic advance the present investigation suggests that selection may be effective from early generation for the improvement of traits *viz.* biological yield per plant, number of primary branches per plant, 100 seed weight, plant height per plant, number of seeds per plant, number of nodes per plant, number of pods per plant and harvest index, because these traits are governed by additive gene action.

5.3 Correlation coefficient analysis

Correlations indicate the magnitude of linear association between different pair of characters and form the basis of selection index, thereby aiding the breeder in crop improvement programmes. It will help to know how the improvement in one character will bring simultaneous changes in other characters. Yield is a complex quantitative character governed by large number of genes and is highly influenced by environment. Hence, the selection of superior genotypes based on yield as such is not effective and desirable. For a rational approach towards improvement of yield, selection has to be made for the component characters of yield. Association of yield components and yield thus assumes special importance on the basis of indirect selection. Genetic correlation between different characters of plant often arises because of linkage or pleiotropy.

Correlation coefficient studies revealed that the degree of association between yield and its components provides mutual relationship between the yield components. It helps in direct selection of associated characters for the improvement of desirable traits.

In biological system most of the characters are associated with each other by one or more paths. In the present investigation, seed yield per plant showed highly significant positive correlation with number of seeds per plant followed by harvest index, hundred seed weight, number of pods per plant, biological yield and number of nodes per plant and significant positive association with days to maturity, days to flower initiation, number of primary branches per plant and plant height.

Days to flower initiation exhibited highly significant positive association with number of nodes per plant, number of seeds per plant, plant height, number of pods per plant and number of primary branches per plant whereas, a negative association with 100 seed weight.

Days to maturity showed highly significant positive association with biological yield per plant followed by number of primary branches per plant, seed yield per plant and number of nodes per plant. Whereas, it showed negative association with harvest index.

Plant height revealed highly significant positive association with number of nodes per plant followed by number of primary branches per plant, number of seeds per plant , number of pods per plant and seed yield per plant.

Number of primary branches per plant showed highly significant positive association with biological yield per plant followed by number of pods per plants and number of nodes per plants. Whereas, it showed negative association with harvest index.

Number of nodes per plant showed highly significant positive association with number of seeds per plant followed by number of pods per plant, and significant association with seed yield/plant.

Number of pods per plant showed highly significant positive association with number of seeds per plant followed by seed yield per plant, biological yield per plant and significant association with harvest index.

Number of seeds per plant was found to be highly significantly positive association with seed yield per plant , harvest index and biological yield per plant.

100 seed weight showed highly significant positive association with seed yield per plant, biological yield pre plant and harvest index.

Biological yield established highly significant positive association with seed yield per plant and negative significant association with harvest index.

Harvest Index has the highest significant positive association with seed yield per plant.

Significant positive correlation of different traits with seed yield per plant have also been reported by Badkul *et al.* (2014) for biological yield, number of pods per plant, number of seeds per plant, plant height, harvest index and number of seeds per pod, Koraddi *et al.* (2015) for days to 50% flowering, plant height, number of branches per plant, number of pods per plant, 100 seed weight and harvest index, Alpna *et al.* (2015) for number of pods per plant, 100 seed weight and harvest index , Mahbub and Shirazy (2016) for plant height, number of seeds per pod, number of pods per plant, 100 seed weight, primary branches per plant and number of seeds per pod, Dessia D. H. and Gemechu H. L. (2018) for number of pod per plant, number of seed per pod, biological yield, hundred

seed weight, and number of branch per plant, Li M. *et al.* (2020) plant height, nodes of main stem, branches, pods, grains, and 100-grain weight.

5.4 Path coefficient analysis

Estimation of correlation coefficient indicates only the extent and nature of association between yield and its attributes, but does not show direct and indirect effects of different yield attributes on yield *per se*. Seed yield is dependent on several component characters which are mutually associated. The path analysis first suggested by Wright (1921) and later by Dewey and Lu (1959) provides an effective measure of direct and indirect cause of association and depicts the relative importance of each factor involved in contributing the final product.

If the correlation between yield and character is due to the direct effects of character, it reflects true relationship between them, selection can be practiced for such a character in order to improve yield. However, if correlation is due to indirect effect of the character through another component trait, the breeder has to select for the latter trait through which indirect effect is exerted.

The path coefficient analysis of different physiological and yield traits on seed yield per plant revealed that harvest index and biological yield per plant recorded considerably very high estimates of positive direct effect. Substantial higher positive direct effect was recorded for days to maturity , days to flower initiation, number of pods per plant .Whereas, high negative direct effect on seed yield per plant was observed by number of seeds per plant followed by negative direct effect via hundred seed weight, number of primary branches per plant and plant height.

Similar findings have also been reported by Badkul *et al.* (2014), Chandel *et al.* (2017) for biological yield, and, Badkul *et al.* (2014) for harvest index. Barnabas *et al* (2016) for pod number per plant, 100 seed weight and days to 50% flowering, Balla *et al.* (2017) for days to maturity, Chandel *et al.* (2017) for biological yield per plant and harvest index, Dessia *et al.* (2018) for number of pods per plant, number of seeds per pod and biological yield per plant.

Contradictory findings have been reported by Mahbub *et al.* (2015) for 100 seed weight, Akram *et al.* (2016) for number of seeds per plant and pods

per plant, 100 seed weight and plant height, Barnabas *et al.* (2016) and Balla *et al.* (2017) for plant height, Mishra *et al.* (2015) for number of seed per plant, 100 seed weight and number of pods per plant, Mahbub *et al.* (2015) for number of seeds per pod, 100 seed weight and plant height, Chavan *et al.* (2016) for 100 seed weight, Mishra (2019) for 100 seed weight and number seeds per plant.

On the basis of path analysis, traits viz., harvest index, biological yield per plant days to maturity, days to flower initiation and number of pods per plant have been found most important in the improvement of seed yield as they exhibited substantial direct effect.

5.5 Principal component analysis

Principal component analysis is a simple non parametric method for extracting relevant information from confusing data sets. With minimal efforts PCA provides a roadmap for how to reduce a complex data set to a lower dimension. The principal component may then be used as predictor or criterion variables in subsequent analysis.

In present investigation first four principal components were identified as important because they have more than 0.5 Eigen value that showed total variation among hundred genotypes of soybean under study. Out of twelve, only six principal components (PCs) exhibited more than 0.5 Eigen value and showed 87.78% variability among the traits studied. Hence, out of six four principal components were given due importance for further explanation. The PC1 had the highest variability (40.380 %) followed by PC2 (16.833%), PC3 (12.464%) and PC4 (6.917 %) for traits under study.

In hundred genotypes, the top principal component scores (PC score) for all the traits were estimated in these four components. These scores can be utilized to propose precise selection indices whose intensity can be decided by variability exhibited by each of principal component. High PC score for a particular genotype in a particular component denotes high values for the variables in that particular genotype.

The PC1 showed positive effect for the specific traits under study that is as days to flower initiation, days to maturity, number of pods per plant, number

of nodes per plant, number of seeds per plant, biological yield per plant and seed yield/plant.

The second principal component (PC2) consisted of harvest index. Third principal component was related to 100 seed weight and fourth principal component with plant height (Table 4.8). On the basis of PCA, most of the important yield attributing traits was present in PC1.

G 225 (7.583) had the highest PC score followed by TGX 849-D-13-4 (6.128) NRC 86 (5.029), TNAU 20024 (4.663), UPSL125 (4.135), PK1038 (3.983), EC 389353(3.660), JSM 232 (3.195), JSM 222 (3.168), NRC 2007A (3.064), NRC 2006M (2.789), SL (E)1 (2.628), PS 1467 (2.279), RKS 54 (2.121), UGM 75 (2.110), EC 377883B (2.054), JSM 245 (1.928), PK 258 (1.867), SL 682 (1.851), JSM 227 (1.823), GP 465 (1.809) VGM 70 (1.785), RSC 14(1.345), JSM 285 (1.258), JS 20-98 (1.209), WT 88 (1.134) JS 20-01 (1.038) UGM 70 (0.801) VLS 75 (0.725), NRC 86 (0.659) and UPSM 77 (0.659) in PC1 indicating that these genotypes possess high values of traits viz., days to flower initiation, days to maturity, number of pods per plant, number of nodes per plant, number of seeds per plant, biological yield per plant, and seed yield/plant. The highest PC score of UGM 75 (5.569) followed by JS335 (4.596), JS 20-98 (3.979), NRC 86 (3.876), EC 291451(2.536), EC 528640 (2.098) JS 20-34 (1.668), EC 106998 (1.607), TGX 849-D-13-4 (1.599) KDS 256 (1.582), EC 24091 (1.532), EC 389179B (1.516), PK 1038 (1.458), EC 391316 (1.310), EC 457214 (1.176), JSM 227 (0.918), GP 465 (0.899), EC 377883 (0.889), NRC 2007A (0.817), EC 350664 (0.774), KB-17 (0.616), G2225 (0.591), MACS 303 (0.570), WT 88 (0.550) and JS 20-29 (0.531) of PC2 was mainly related with harvest index .The highest PC score was obtained by in PC3 for NRC 86 (3.466) followed by , JS 20-29 (2.145), JSM 222 (1.859), 23-11A(Z-18) (1.652), NRC 2007A (1.613), 20-40B(Z-9) (1.568), EC572160 (1.456) JSM232 (1.434) NRC 2006M (1.268), PI 204336 (1.167), 20-148 (Z-15) (1.707), EC 325103 (1.019), EC 350664 (0.973), TGX 849-D-13-4 (0.937), GC 84051-32-1 (0.885), EC 24091 (0.882), SQL 37 (0.873), AGS 12 (0.817), MACS-7102 (0.728), RKS 52 (0.695), JSM 227 (0.694), KDS 256 (0.665), MACS 030 (0.646), PS 1336 (0.634), EC 109540 (0.691), WT 88 (0.610) and JS 20-34 (0.592) trait viz.,100 seed weight. PC scores in PC4 were recorded the highest value for character; plant height was obtained by GP

566 (2.658) followed by LEE 54 (2.426), EC 391316 (1.560), EC 468597 (1.539), EC 24091 (1.531), JS 20-98 (1.493), EC 377883B (1.394), EC 33872B (1.225), UPSM 77 (1.183), EC 457336 (1.135), NRC 2007A (1.121), EC 391181 (1.076), TGX849-D-13-4 (0.990), UGM 70 (0.937), EC 291451 (0.897), JSM 245 (0.808), NRC 37 (0.787), RKS 54 (0.744), MACS 171 (0.698), JSM 195 (0.618), KDS 256 (0.604), NRC 86 (0.574), 20-148 (Z-15) (0.568) and DCB 137 (0.548).

Similar findings have been reported by Ojo *et al.* (2012) for pods per plant and seed yield per plant, Shaahu *et al.* (2013) for pods per plant, seed yield and plant height, Badkul *et al.* (2014), Tantway (2015), Mishra (2015), Birla and Ramgiri (2015) and Jha (2016) for plant height, number of branches per plant, number of pods per plant, number of seeds per plant, biological yield per plant and seed yield per plant in PC1, Manav *et al.* (2017) for pods per plant and seed yield per plant, Singh *et al.* (2020) for days to maturity, number of pods per plant and grain yield.

Characters identified on the basis of principal component analysis in soybean genotypes

It can be concluded from the above results that yield contributing traits having the highest variation in PC1 followed by PC2. The above results revealed that genotypes namely G 2225, UGM 75, NRC 86, GP 566, TG X 849D-13-4, JS 20-34, SL 752, PKS 1467 and SL (E) 1 were found promising because they fall in more than one PCs. The most important characters were identified as harvest index, number of pods per plant, number of seeds per plant, seed yield per plant, number of nodes per plant, biological yield per plant, 100 seed weight and number of primary branches per plant. In soybean breeding programmes, these genotypes and traits may be utilized for incorporation of desirable traits to improve the existing cultivars or as donors.

5.6 Genetic divergence analysis

The choice of parents is of paramount importance in any breeding programme. It is rather a difficult task for a plant breeder. Selection of parents on the basis of *per se* performance is good but there is a possibility of related lines being chosen resulting in limited or no advances under selection and therefore, there is a need for emphasis to broader genetic base. Selection of the parents

on the basis of geographical diversity is another way of choosing parents, but this needs to be supplemented with the information on genetic diversity. In formulating successful breeding programme for evolving superior cultivars, knowledge of genetic divergence among parents is of utmost importance since a cross involving genetically diverse parents is likely to produce high heterotic effect as well as broad range of variability could be expected in the segregating generations.

The present study was also aimed at analyzing the genetic divergence among the hundred genotypes of soybean and to identify the superior and divergent parental genotypes for formulating the crossing programme. Mahalanobis D^2 Statistics is a powerful tool, widely used by the breeders in quantifying the degree of divergence at genotypic level.

Group Constellations

On the basis of D^2 values, the hundred genotypes were grouped into 9 clusters following Tocher's method. The Cluster I was poly genotypic (87 genotypes) followed by Cluster II with 10 genotypes and cluster IV with 2 genotypes and remaining clusters were monogenotypic (only 1 genotype).

In conformity to the present investigation, Dubey *et al.* (2015) found six clusters, Mishra *et al.* (2016) found eleven clusters by evaluating 50 genotypes, Mahesh *et al.* (2017) six clusters by evaluating 40 genotypes, Yadav *et al.* (2017) seven cluster by evaluating 9 advance generations, Getnet *et al.* (2019) grouped 49 genotypes into three clusters and Singh *et al.* (2020) found four clusters by evaluating 16 genotypes.

Intra and inter cluster divergence D^2 values

Cluster II showed maximum intra cluster D^2 value (2061.13) followed by cluster I (1834.39) and cluster VI (1319.41), while other clusters were mono-genotypic with no intra cluster divergence.

The highest inter cluster divergence was observed between genotypes of cluster IV and VIII (41274.40), followed by cluster V vs. VIII (40109.30), cluster I vs VIII (35937.05), cluster V vs IX (28315.96) whereas least inter cluster divergence was observed between genotypes of cluster IV vs. IV (1319.41).

Similar findings have been reported by Dubey (2015), Mishra *et al.* (2016) and Mahesh *et al.* (2017).

Percent contribution of characters towards divergence in hundred genotypes of soybean

The highest percentage contribution towards divergence was recorded by number of seeds per plant followed by plant height, number of pods per plant, harvest index, biological yield per plant, and days to flower initiation times.

In conformity to the present investigation Alpna *et al.* (2015) for plant height, 100 seed weight and days to 50% flowering, Mishra (2016) for number of pods per plant and 100 seed weight and Singh *et al.* (2020) for days to maturity.

Cluster mean values

The cluster mean values of all the twelve characters were studied in the present investigation and the values were found high in cluster IX, VI and VII.

5.7 Physiological growth parameters

Leaf Area Index (LAI)

Leaf area index (LAI) is the potential factors for determining yield under normal and water limiting condition. The leaf area of soybean is a critical variable for a yield influenced by biotic and abiotic factors.

The leaf area index recorded at 30 days, 45 days and 60 days after sowing. The genotypes possess higher values at 45 days and 60 days indicating a positive association of LAI after sowing with yield. LAI of more than 3.5 was exhibited by 23% of the genotypes at 60 days. Leaf area growth determines the light interception capacity of a crop and also has direct positive association with crop growth rate.

The results in accordance with the findings of Mottaghian *et al.* (2010). The LAI ranged from 0 to 5.5 m² / m² in soybean (Nguy Robertson 2012). The variety JS 81-335 registered greater LAI (5.9) than other varieties, (Sharma and Sharma, 1993). Leaf area index ranged from 0.54 to 3.17 (Rajput *et al.* 2004).

Leaf Area Duration (LAD)

The leaf area duration is a measure of the ability of the plant to produce and maintained leaf area and its whole opportunity for assimilation during growing season (Watson, 1947). LAD is mainly depending on the development and product of rate of initiation and size of assimilatory surface area and is closely connected with yield. The physiological processes are affected by genetic as well as environmental factors.

LAD was higher in 45-60 DAS than 30-45 DAS. Varieties, TNAU 20022 (551.31) followed by LEE 54 (375.32) and SL 682 (129.03) attained significantly maximum LAD. Welbank *et al.* (1988) reported that the ratio of grain yield to LAD increased with increase in daily radiation during grain filling. Sahoo and Guru (1998) observed the positive association of SLA, CGR, and LAD with grain yield. Chauhan *et al.* (1999) reported that the LAD and LAI measured at 30-45 days after sowing (DAS) had positive and significant association with dry accumulation at 50% flowering. These results are consistent with the study of Mottaghian *et al.* (2010). Leaf area duration indicates survival period of leaves and active period of leaf growth which is a significant factor in contributing to the photosynthetic production.

Specific leaf area

The specific leaf area represents and indicate its interrelationship between leaf area in relation to leaf dry weight.

At 30-45 DAS, significantly maximum SLA was noted in genotype DCB 137 (1565.54) followed by MACS 303 (875.85) and EC 33940 (593.46) while, least SLA value was in SQL 1 (168.84) followed by NRC 86 (166.70). Similarly, at 45-60 DAS, significantly maximum SLA was noted in genotype TNAU 20022 (2331.23) followed by LEE 54 (1246.37) and EC 389179B (510.20) while, least SLA value was found in JS 20-34 (119.35) followed by PK 1038 (112.01).

Chlorophyll content

The leaves are primary site of photosynthesis in the soybean plant and much of the variations in the photosynthesis where attributed to differences chlorophyll contents of the leaves. As it is one of the major chloroplast

components for photosynthesis, and relative chlorophyll content has a positive relationship with photosynthetic rate. The supplemental UV-B radiation adversely affected chlorophyll content and electron transport activity in PSII and consequently decreased the photosynthetic efficiency of soybean plants (Hu *et al.* 2013).

The result revealed that the genotypes EC 294003 (47.73) followed by SQL1 (46.07), JS 96-31 (44.57) and PS 1475 (42.33) had highest chlorophyll content index followed by PI 204336 (40.36) and MACS 7102 (40.03) revealing their higher photosynthetic efficiencies. While, genotypes EC 291451 (13.43) followed by PS 1467 (13.10) recorded the minimum CCI value. The Chlorophyll content and photosynthetic parameters were positively correlated with seed yield, while antioxidant capacity was negatively correlated with photosynthesis and seed yield (Betzberger *et al.* 2010). The content of total chlorophyll and apparent quantum yield (Phi) of crops increased the increasing degree of shade (Bang *et al.* 2011). Vyas and Khandwe (2014) reported that the two cultivars (JS 95-60 and JS 97-52) showed more chlorophyll content.

5.8 Biochemical estimations

5.8.1 Protein

The protein accumulation is significantly affected by cultivars, soils and agroclimatic conditions (Galova *et al.* 1999).

The results indicated that genotypes JSM 222 (41.89), trailed by JSM 245 (40.68) at standard with JS 20-34 (40.21) had the higher protein contents among the genotypes investigated. These genotypes may be utilized in a breeding programme for increasing nutritive value of soybean. Genotype EC538830 (35.92) noted lowest value of protein. Singh and Gupta (1976) reported that value of protein content in soybean seed varied from 34 per cent to 46 per cent.

5.8.2 Fat

The investigations revealed that the genotypes NRC 2007A (20.5) followed by TNAU 20022 and EC16213 (20.1) at standard with EC 389153, EC 325103, SQL1 and PK 701 (20.0) possessed the maximum fat contents over the remaining genotypes. EC 389179B (15.5) recorded minimum value. The oil

content of variety Belessa-95 (18.1%) was significantly ($P < 0.05$) higher than that of variety Awassa-95 (15.9%) (Pal *et al.* 2012).

5.9 Screening for Multiple Disease Resistance

Disease resistance is a major constraint in soybean production scenario. Hence, screening of disease resistance is of prime importance to achieve sufficient yield potential. YMV, CR, BP and RAB are the major diseases of central India. Therefore, all these genotypes were screened against these diseases.

Out of all the hundred genotypes of soybean under study, EC350664 was identified as absolutely resistance to both *Rhizoctonia* aerial blight and charcoal rot incidence. Hence, this genotype can be utilised as superior donor parents in future breeding programmes.

Similar results have been obtained by Mehra (2019), Amrate (2018) on several JS genotypes against CR and RAB incidences, Joshi *et al.* against *Rhizoctonia* aerial blight, Pancheshwar *et al.*, (2016) on Charcoal rot incidence.

Chapter-6



SUMMARY AND CONCLUSIONS

SUMMARY, CONCLUSIONS AND SUGGESTIONS FOR FURTHER RESEARCH WORK

6.1 Summary

Soybean is very versatile and fast emerging oil-seed crop not only in USA, Brazil, Argentina and China but also in India. Today this crop is preferred for its good quality protein and oil and other important nutrition factors. It is one of the distinctive multipurpose crops with ever increasing popularity in the present-day condition where emphasis of food security has been now dealt as nutritional security with protein rich diet. Therefore, it is the need of the hour to estimate the range of variability amongst the soybean accessions to develop varieties/genotypes with wider acceptance, distinguished morphology, yield and resistance against major biotic and abiotic stresses amongst the farming community. In view of above, to know the genetic diversity as well as relationship among soybean accessions, present study was formulated for **“Genetic Assessment and Morphological Characterization of Soybean Germplasm”** which involved the characterization of total hundred soybean accessions including four checks for phenotypic characterization. The experiment was conducted at Seed Breeding Farm, Department of Plant Breeding and Genetics, College of Agriculture, JNKVV, Jabalpur, during *Kharif*, 2019. The experimental material for the present investigation was provided by the IISR, Indore and was planted in Augmented Block Design.

Observations were recorded on five randomly selected plants from each genotype. Data were recorded on traits viz., days to flower initiation, plant height, number of primary branches per plant, number of pods per plant, number of nodes per plant, number of seeds per plant, days to maturity, 100 seed weight, harvest index and seed yield per plant. The objectives of this study were to characterize the soybean genotypes and estimate the genetic variability, heritability, genetic advance, association analysis, path coefficient analysis and to identify promising genotypes based on genetic divergence and principal component analysis for higher yield and quality related traits in soybean.

Summary:

Soybean genotypes were categorized in different groups on the basis of characters such as. hypocotyl colour, growth type, growth habit, leaf shape and size, leaf colour, flower colour, pubescence colour and presence, pod colour, seed size, seed shape, testa colour, seed coat lusture, hilum colour, funicle colour and peroxidase activity. Analysis revealed sufficient and desirable amount of variability for most of the characters which indicates that there is enough scope for selection considering these characters.

The ANOVA indicated that the mean sum of squares due to genotypes were highly significant for all the traits viz., days to flower initiation, days to maturity, plant height, number of primary branches per plant, number of pods per plant, number of nodes per plant, number of seeds per plant, biological yield per plant, 100 seed weight, harvest index and seed yield per plant. This revealed that substantial variability has been created and genetic base is broadened for most of the important characters among different genotypes.

The phenotypic coefficient of variation was higher than genotypic coefficient of variation for most of the characters. High magnitudes of PCV and GCV were observed for the traits viz. number of seeds per plant followed by seed yield per plant, number of primary branches per plant, biological yield per plant, number of pods per plant, harvest index and plant height per plant.

In the present study moderate values of PCV and GCV were recorded for number of nodes per plant and days to flower initiation. While, days to maturity showed low value of PCV and GCV.

Heritability was estimated for all the characters under study. Most of the characters expressed high estimates of broad sense heritability. The highest heritability was exhibited by biological yield per plant followed by plant height per plant, 100 seed weight, number of primary branches per plant, days to maturity, number of nodes per plant, days to flower initiation, number of pods per plant and number of seeds per plant. Medium heritability was recorded for harvest index. Low heritability was recorded for number of seed yield per plant. The highest genetic advance as percentage of mean (at 5% Selection intensity) was

recorded for number of primary branches per plant. Low genetic advance was recorded for days to maturity.

Heritability estimates along with high genetic advance as percentage of mean was observed by biological yield per plant, number of primary branches per plant, 100 seed weight, plant height per plant, number of seeds per plant, number of nodes per plant, number of pods per plant and harvest index which gives an indication that these traits might be governed by additive genes indicating that direct selection would be effective. High heritability with moderate genetic advance was recorded for days to flower initiation. High heritability with low genetic advance was recorded for days to maturity.

Correlation coefficients and path studies for yield and yield attributing traits revealed that among the eleven component characters studied, the most important traits identified among the promising genotypes of soybean are biological yield per plant, harvest index, number of nodes per plant, number of seeds per pod, days to maturity and days to flower initiation. Hence, directional selection through these traits will be very effective for improvement of seed yield.

On the basis of D^2 values, the hundred genotypes were grouped into 9 clusters following Tocher's method. The Cluster I was poly genotypic (87 genotypes) followed by Cluster II with 10 genotypes and cluster IV with 2 genotypes and remaining clusters were monogenotypic (only 1 genotype). The sufficient intra cluster distance was also observed among the genotypes of different polygenotypic clusters. These above results indicated that recently developed genotypes represent sufficient genetic diversity between clusters and within cluster. The genotypes of cluster IV and cluster I showed higher inter cluster distance with cluster VI may be crossed to broaden the genetic base of soybean. Intra cluster distance has been found as the highest of cluster II. Hence, the hybridization among the genotypes of cluster II may also result transgressive recombinants.

On the basis of principal component analysis, G 2225, UGM 75, NRC 86, GP566, TGX849D-13-4, JS 20-34, SL 752, PKS 1467 and SL (E) 1 were identified as putative genotypes and harvest index, number of pods per plant, number of seeds per plant, seed yield per plant, number of nodes per plant,

biological yield per plant, 100 seed weight and number of primary branches per plant identified as important traits. In soybean breeding programmes these genotypes and traits may be very useful in introgression to achieve improved genotypes in future.

The leaf area index reached at 30 days, 45 days and 60 days genotypes possess higher values at 45 days and 60 days indicating a positive association of LAI after sowing with yield. LAI of more than 3.5 was exhibited by 23% of the genotypes at 60 days. LAD was higher in 45-60 DAS as compared to 30-45 DAS. Varieties, TNAU 20022 (551.31) followed by LEE- 54 (375.32) and SL 682 (129.03) attained significantly maximum LAD. At 30-45 DAS, significantly maximum SLA was noted in genotype DCB 137 (1565.54) followed by MACS 303 (875.85) and EC 33940 (593.46) while least SLA value was higher in SQL 1 (168.84) followed by NRC 86 (166.70). Similarly, at 45-60 DAS, significantly maximum SLA was noted in genotype TNAU 20022 (2331.23) followed by LEE 54 (1246.37) and EC 389179B (510.20) while least SLA value was observed in JS 20-34 (119.35) followed by PK 1038 (112.01). Genotypes; EC 294003 (47.73) followed by SQL1 (46.07), JS 96-31 (44.57) and PS 1475 (42.33) had highest chlorophyll content index followed by PI 204336 (40.36) and MACS 7102 (40.03) revealing their higher photosynthetic efficiencies. While genotype EC 291451 (13.43) followed by PS 1467 (13.10) recorded the minimum CCI value.

On the basis of biochemical estimations genotypes JSM 222 (41.89), had the higher protein content and genotype EC 538830 (35.92) noted lowest value among the genotypes investigated. Similarly, genotypes NRC 2007A (20.5) possessed the maximum fat contents over the remaining genotypes. EC 389179B (15.5) recorded minimum value.

On the basis of field screening of hundred soybean genotypes against the major diseases viz., Charcoal rot, Bacterial pustules, YMV and *Rhizoctonia* aerial blight, the genotype EC350664 was found to be absolutely resistance against both the diseases i.e. this genotype may be considered relevant for withstanding biotic stresses and further utilized for resistance breeding programme.

6.2 Conclusion

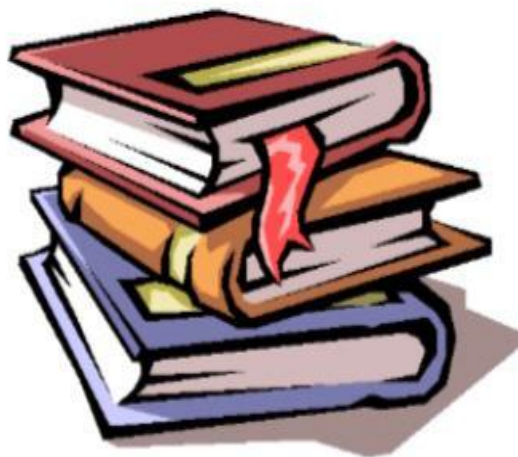
1. In the present investigation, considerable amount of genetic variability was exhibited for majority of traits among hundred genotypes which revealed that genetic base is broadened in genotypes of soybean.
2. High or moderate heritability coupled with high or moderate genetic advance was observed for all the traits under study. This indicates the preponderance of additive gene action in the inheritance of these traits.
3. On the basis of correlation and path coefficient analyses it is suggested that to improve the seed yield, due emphasis should be given on biological yield per plant, harvest index, number of nodes per plant, number of seeds per pod and days to maturity. Hence directional selection through these traits will be very effective for improvement of seed yield.
4. D² analysis exhibited sufficient genetic diversity between clusters and within cluster. This study indicated that the genotypes developed have broadened genetic base and subsequently may lead to transgressive segregants by utilizing them in breeding program me.
5. G 2225, UGM 75, NRC 86, GP 566, TGX849D-13-4, JS 20-34, SL 752, PKS 1467 and SL (E) 1 were identified as potential genotypes on the basis of principal component analysis and *per se* performance for yield and its contributing traits over different environments. Hence, these genotypes should be utilized for further breeding programme to achieve by transferring the desirable traits in future varieties of soybean with wider adaptability.
6. The leaf area index, leaf area duration and specific leaf area was found to be maximum at later stages of crop i.e. at 45-60 DAS.
7. Genotype EC 294003 (47.73) recorded highest chlorophyll content index while genotype PS 1467 (13.10) recorded the minimum CCI value.
8. JSM 222 (41.89), had the higher protein content while NRC 2007A (20.5) possessed the maximum fat contents over the remaining genotypes. Hence, these lines may be further utilized for increasing oil and protein %
9. Field screening for multiple disease resistance revealed that the genotype EC 350664 was absolutely resistance against biotic stresses

and thus, can be further utilized as superior parents/donors in future breeding programmes.

6.3 Suggestions for Further Work

1. The promising genotypes should be tested in multilocal trials for judging their adaptability and superiority across the season as well as locations.
2. The traits which were found important as evidenced from genotypic and phenotypic coefficients of variability, heritability, genetic advance, correlation coefficients, path and genetic divergence analyses should be taken care of, while planning for selection and to breed suitable cultivars of soybean.
3. Characters showing high heritability coupled with high genetic advance should be exploited to isolate potential genotypes. In future, these traits may be considered for the development of high yielding with good quality varieties.
4. The traits showing additive gene action should be exploited and their sustainability should be worked out under climatic adversity.
5. The genotypes identified on the basis of divergence, principal component and *per se* performance analyses should be utilized at large scale to exploit the heterotic effects and achieve transgressive segregates.
6. Further research with molecular characterization of identified promising soybean genotypes to provide more accurate measures of genetic diversity is also suggested.
7. The accessions may be further investigated through fine mapping to explore presence of genes resistant to biotic and abiotic stresses and also for the nutritional quality parameters for use in crop improvement programmes.

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Appendix I: Weekly meteorological parameters during Kharif season (June to October2019)

Month	SW	T max.	Tmin.	Sun Shine hrs.	Rainfall (mm)	RH Mor	RH Eve	Wind Speed	Vapur Presure (MM)		Evapo (mm)	Rainy days
									Morning	Evening		
July	27	29.9	23.1	1.3	178.8	94	87	5.9	22.5	24.5	2.9	3
	28	31.4	25.0	2.6	59.8	82	64	6.9	22.3	22.8	5.0	1
	29	34.9	25.0	8.7	24.4	82	59	4.8	22.8	23.7	5.3	2
	30	32.3	24.0	3.5	48.0	88	74	4.0	22.9	24.6	3.7	3
	31	29.6	23.9	1.5	47.6	93	81	5.1	23.6	24.5	2.5	4
August	32	29.9	23.5	2.7	210.0	92	81	3.3	23.0	23.8	2.8	4
	33	28.6	22.9	2.9	302.1	91	83	3.2	22.4	22.9	1.9	4
	34	29.2	22.5	1.4	212.9	97	83	2.1	23.0	23.6	4.9	7
	35	30.9	23.4	3.3	57.2	93	75	0.7	23.5	24.5	3.2	4
September	36	31.6	23.4	3.8	185.0	94	79	1.8	23.9	25.0	4.9	5
	37	28.5	23.4	1.2	101.4	93	83	1.9	22.9	23.7	2.5	5
	38	31.7	22.7	4.5	53.1	91	78	1.1	22.7	22.5	3.5	3
	39	29.5	22.1	2.5	77.6	93	78	1.6	21.4	21.7	2.7	4
October	40	30.1	21.0	7.2	14.3	90	66	1.1	20.6	20.2	3.0	2
	41	30.3	18.0	8.4	0.0	91	56	0.6	17.7	17.9	3.3	0
	42	29.2	18.7	5.6	2.2	93	63	0.6	17.9	17.4	2.3	0
	43	27.1	19.1	0.9	1.0	92	60	2.0	17.5	16.2	1.8	0
	44	30.3	17.7	5.3	0.0	92	52	1.1	17.3	16.5	2.3	0

Appendix II: Categorization of soybean genotype based on morphological characters

S NO	Genotype	HC	PGT	PGH	LS	LSZ	LC	FC	P: POH	PC	POD CL	SSZ	SS	TC	SCL	HC	FC	PA
1	K-53	9	2	2	3	2	2	2	1	2	2	2	2	1	2	5	2	3
2	EC 109540	9	2	2	2	2	2	2	1	2	2	1	2	3	2	3	1	2
3	UGM 75	9	2	2	3	2	2	2	1	2	2	2	3	3	2	5	1	4
4	MACS 303	9	2	2	2	2	2	2	1	2	3	2	3	1	2	4	1	2
5	TNAU 20022	9	2	2	2	2	2	2	1	2	3	2	2	4	2	5	1	0
6	EC 528640	9	2	2	2	2	2	2	1	2	1	2	2	2	2	3	1	2
7	EC-389153	9	2	2	3	1	2	2	1	2	3	2	1	1	3	3	1	3
8	UPSL 152	1	2	2	2	2	2	1	1	1	3	2	2	1	3	4	1	2
9	JS 20-34	9	2	2	2	2	1	2	1	2	2	1	4	1	1	1	1	0
10	JS 97-52	1	2	2	2	1	3	1	1	2	2	2	3	1	2	5	1	4
11	NRC 2007A	1	2	2	2	2	1	1	1	1	2	2	2	1	3	5	1	5
12	NRC 80-1	1	2	2	2	2	2	1	1	2	3	2	1	1	2	3	1	4
13	JS 20-01	9	2	2	2	1	3	2	1	2	2	2	4	1	2	4	1	3
14	EC 396065	9	2	2	2	1	2	2	1	2	3	2	4	1	2	1	1	2
15	DCB 137	1	2	2	2	2	3	1	1	1	1	1	1	1	2	3	1	1
16	EC 457214	9	2	2	2	2	2	2	1	2	3	1	1	1	3	5	1	1
17	DE 201	9	2	2	2	2	1	2	1	2	2	2	2	4	1	5	2	0
18	EC 457336	1	2	2	2	1	3	1	1	2	2	3	4	5	1	3	2	0
19	AGS 12	9	2	2	3	2	3	2	2	3	3	2	2	1	2	3	1	2
20	F4P20	1	2	2	3	2	2	1	1	1	1	2	2	1	2	5	1	1
21	EC 103336	9	2	2	2	2	3	2	1	2	2	2	4	1	1	1	1	2
22	NRC 86	9	2	2	2	2	3	2	1	2	1	2	1	1	2	3	1	4
23	EC 106998	9	2	2	2	2	1	2	1	2	1	2	2	1	2	3	1	1
24	SL 752	9	2	2	3	2	1	2	2	3	3	1	2	1	1	5	1	2
25	SQL 37	9	2	2	2	2	2	2	1	1	2	2	4	1	1	1	1	3

26	WT 88	1	2	2	3	3	2	1	2	3	2	2	4	1	2	5	1	2
27	EC 538830	1	2	2	3	2	3	1	1	2	1	1	2	1	2	5	2	1
28	NRC 2006M	1	2	2	2	2	2	1	1	2	2	2	1	1	2	3	1	0
29	EC16213	9	2	2	2	1	2	2	1	2	2	2	2	1	1	5	1	2
30	JS 20-52	1	2	2	2	1	2	1	1	2	2	2	1	1	2	5	1	3
31	PS 1475	1	2	2	2	2	2	1	1	2	3	2	3	1	1	5	2	4
32	EC 389179B	1	2	2	2	2	1	1	1	1	2	2	2	1	3	4	1	1
33	JSM 227	9	2	2	3	2	2	2	2	2	1	2	3	1	2	3	1	0
34	SL 2951	9	2	2	2	1	1	2	1	2	2	1	4	1	2	3	1	2
35	EC 389099	9	2	2	2	1	1	2	1	2	1	2	3	1	1	1	1	1
36	JS 20-69	1	2	2	2	1	2	1	1	1	2	1	2	1	2	5	2	1
37	JSM 195	1	2	2	2	2	3	1	1	1	2	2	1	1	2	3	1	2
38	EC 291397	9	2	2	2	1	2	2	1	2	2	2	3	1	2	1	1	2
39	PS 1336	1	2	2	2	2	2	1	1	2	3	2	2	1	2	3	1	3
40	EC 294003	9	2	2	2	2	2	2	1	2	2	2	4	4	2	5	2	0
41	EC 291451	9	2	2	2	2	2	2	1	2	1	2	3	1	1	1	2	1
42	EC 24091	9	2	2	2	3	3	2	1	2	2	2	4	1	1	1	1	1
43	RSC 14	1	2	2	2	2	3	1	1	2	2	2	2	1	2	3	1	2
44	EC 325103	9	2	2	3	3	3	2	1	2	3	2	2	1	2	3	1	3
45	JSM 285	9	2	2	3	2	3	2	2	1	1	2	2	1	1	5	1	1
46	EC 33872B	9	2	2	2	2	2	2	1	2	2	2	2	1	2	5	1	4
47	SQL 1	9	2	2	2	2	2	2	1	2	2	1	3	1	1	5	2	1
48	JSM 232	1	2	2	3	3	3	1	2	1	3	2	2	1	2	3	1	1
49	JSM 222	9	2	2	2	3	3	2	1	1	3	1	1	1	2	3	1	2
50	JSM 245	1	2	2	3	3	3	1	2	3	3	2	2	1	2	3	1	1
51	PS 1467	1	2	2	3	2	3	1	2	3	3	2	2	1	2	5	1	0
52	SL (E)1	9	2	2	2	3	3	2	1	2	1	3	2	1	2	3	1	3
53	PK 701	9	2	2	3	2	2	2	2	2	3	2	2	1	2	3	1	2

54	PK 1038	9	2	2	2	2	1	2	1	2	2	2	4	1	3	3	1	5
55	RKS 54	1	2	2	2	2	3	1	1	1	1	1	2	1	1	5	1	4
56	EC 33940	9	2	2	2	2	2	2	1	2	2	2	2	1	1	3	1	2
57	G2225	9	2	2	2	2	3	2	1	2	1	1	2	1	2	3	1	3
58	JS 20-29	1	2	2	2	2	3	1	1	1	2	2	2	2	3	3	1	5
59	G4P15	9	2	2	2	2	3	2	2	3	2	2	2	1	1	3	1	2
60	GP 465	1	2	2	2	3	3	1	1	2	3	2	2	1	3	3	1	3
61	TGX 849-D-13-4	9	2	2	2	2	2	2	1	2	2	2	2	4	3	5	2	0
62	MACS 171	1	2	2	2	2	2	1	1	1	3	2	1	1	2	3	1	2
63	JS 20-98	1	2	2	2	2	3	1	1	2	1	2	1	1	1	5	1	3
64	TG X 849-813	9	2	2	2	2	3	2	1	2	1	2	2	1	3	3	1	0
65	KB-17	9	2	2	2	2	1	2	1	2	2	2	3	1	2	3	1	1
66	KDS 256	1	2	2	2	2	3	1	1	1	1	2	4	1	2	5	1	3
67	LEE-54	9	2	2	2	2	2	2	1	2	2	2	4	1	1	3	1	2
68	JS 96-31	1	2	2	2	2	3	1	1	2	2	3	3	1	2	3	1	3
69	TNAU 20024	9	2	2	3	2	3	2	2	2	3	2	2	1	2	3	1	4
70	PK 258	9	2	2	3	2	3	2	2	3	2	2	1	1	2	3	1	2
71	EC 468597	9	2	2	3	2	2	2	2	3	3	2	2	1	2	5	1	1
72	EC 572160	9	2	2	2	1	2	2	1	2	2	2	3	1	3	3	1	3
73	NRC 37	9	2	2	2	2	2	2	1	2	2	2	4	1	1	1	1	3
74	EC 391181	9	2	2	2	2	2	2	1	2	1	2	4	1	1	1	1	1
75	VGM 70	9	2	2	2	1	3	2	1	1	2	2	1	1	2	3	1	3
76	VLS 75	9	2	2	2	2	2	2	1	1	1	2	3	1	1	1	1	4
77	EC 391316	9	2	2	2	2	2	2	1	2	2	2	3	1	1	1	1	5
78	SL 682	9	2	2	2	2	3	2	1	1	3	1	1	1	3	3	1	4
79	PI 204336	9	2	2	2	2	3	2	1	2	2	2	2	1	2	4	1	0
80	UGM 70	9	2	2	2	2	3	2	1	1	2	3	3	1	1	3	1	1
81	LEE 96	9	2	2	2	2	1	2	1	2	1	2	3	1	2	1	1	1

82	TG X 1488-9-1D	9	2	2	2	3	2	2	1	1	2	2	2	1	2	3	1	5
83	GP566	1	2	2	2	2	2	1	1	1	2	2	2	1	2	3	1	3
84	PS1421	9	2	2	2	2	1	2	1	2	2	2	4	1	2	1	1	1
85	VLS 11	9	2	2	2	2	2	2	1	2	1	2	2	1	2	3	1	3
86	UPSM 77	1	2	2	2	3	3	1	1	2	2	2	2	1	2	3	1	0
87	EC 350664	9	2	2	2	2	3	2	1	2	2	2	2	1	2	4	1	2
88	EC 377883B	9	2	2	2	2	2	2	1	2	1	3	3	1	3	4	1	1
89	JS 20-34	1	2	2	3	1	1	1	2	3	3	2	2	1	2	5	1	5
90	GC 84051-32-1	9	2	2	2	2	2	2	1	1	1	2	4	1	1	1	1	1
91	JS 20-50	1	2	2	3	2	1	1	2	2	2	2	3	1	3	3	1	1
92	MACS-7102	9	2	2	3	2	2	2	2	3	3	2	1	1	2	3	1	2
93	20-40B(Z-9)	1	2	2	3	3	1	1	1	2	2	2	2	1	3	5	1	5
94	20-148 (Z-15)	1	2	2	2	2	1	1	1	2	2	2	3	1	3	5	1	4
95	23-10B(Z-17)	1	2	2	2	2	2	1	1	2	2	2	3	1	2	5	1	5
96	23-11A(Z-18)	1	2	2	2	2	2	1	1	2	2	2	2	5	3	5	1	5
97	JS 20-34	1	1	1	3	2	2	1	2	2	2	2	1	1	1	5	1	5
98	JS 335	9	2	2	3	2	3	2	2	3	1	2	2	1	1	3	1	3
99	JS 20-98	1	2	2	2	2	2	1	1	2	2	2	2	1	1	5	1	2
100	NRC 86	9	2	2	2	2	3	2	1	2	3	3	4	1	3	4	1	3

Here:

HC= Hypocotyl colour

PGT= Plant Growth type

PGH= Plant Growth habit

LS = Leaf shape

LSZ = Leaf size of lateral leaflet

LC= Leaf intensity of green colour

FC= Flower colour

P: POH= Pod: presence of hairs

PC= Pod: colour of hairs

POD CL= Pod: intensity of brown colour

SSZ= Ripe seed: seed size

SS= Ripe seed: seed shape

TC= Ripe seed: ground colour of testa

SCL= Ripe seed: seed coat lusture

HC= Ripe seed: hilum colour

FC= Ripe seed: colour of hilum funicle

PA= Ripe seed: colouration due to
peroxidase activity

Appendix III: Mean performance of soybean genotypes for yield and its component characters

S. No.	Genotype	dfi	dm	Ph	nbp	nnp	npp	nsp	100sw	by	hi	SY/P
1	K-53	45.0	104.0	77.0	2.9	14.0	43.0	32.0	6.3	22.3	12.99	2.9
2	EC 109540	46.0	99.0	66.3	2.6	13.7	38.0	34.6	5.2	20.2	13.37	2.7
3	UGM 75	47.0	112.0	87.7	5.6	15.3	41.0	63.0	7.9	54.6	10.62	5.8
4	MACS 303	44.0	98.0	76.6	2.6	14.7	54.6	81.0	4.6	24.6	18.70	4.6
5	TNAU 20022	48.0	102.0	108.3	3.6	14.7	47.6	43.6	5.3	23.2	13.79	3.2
6	EC 528640	44.0	102.0	77.0	2.2	14.0	53.3	59.0	9.6	23.9	27.20	6.5
7	EC-389153	61.0	105.0	88.6	4.9	16.3	74.3	141.6	5.3	41.3	20.34	8.4
8	UPSL 152	61.0	113.0	88.6	3.2	16.3	65.0	112.0	9.3	54.7	20.48	11.2
9	JS 20-34	35.0	104.0	57.0	1.6	9.3	45.3	40.6	7.0	23.6	15.67	3.7
10	JS 97-52	46.0	103.0	57.3	3.89	12.3	45.0	77.3	7.8	28.6	24.13	6.9
11	NRC 2007A	46.0	110.0	81.6	2.3	17.6	73.0	110.3	10.0	37.6	31.38	11.8
12	NRC 80-1	45.0	100.0	80.7	2.2	16.0	59.3	61.3	7.9	28.9	19.72	5.7
13	JS 20-01	46.0	100.0	77.0	1.9	13.6	53.3	93.0	11.3	29.4	38.44	11.3
14	EC 396065	46.0	99.0	74.6	1.6	14.0	52.3	53.6	6.4	30.3	14.19	4.3
15	DCB 137	38.0	104.0	66.3	3.6	13.3	60.3	101.0	6.5	30.3	24.42	7.4
16	EC 457214	44.0	99.0	74.3	2.6	14.7	68.3	73.0	5.1	25.2	18.25	4.6
17	DE 201	37.0	101.0	82.0	2.9	13.0	67.3	55.0	6.2	24.8	17.34	4.3
18	EC 457336	38.0	102.0	79.6	3.6	12.3	48.0	52.3	12.3	26.2	27.48	7.2
19	AGS 12	49.0	104.0	75.6	3.9	14.0	37.6	78.0	7.9	28.6	24.48	7
20	F4P20	44.0	104.0	82.3	2.2	13.0	41.0	74.6	7.0	23.1	26.41	6.1
21	EC 103336	37.0	100.0	80.0	2.6	15.6	38.6	41.7	5.8	22.1	14.93	3.3
22	NRC 86	43.0	102.0	70.6	3.2	13.6	46.3	92.0	9.4	27.3	34.80	9.5
23	EC 106998	44.0	101.0	78.6	3.9	14.3	36.6	36.6	5.2	23.6	11.86	2.8
24	SL 752	46.0	104.0	100.3	3.6	13.6	43.7	52.6	6.9	25.7	17.51	4.5

25	SQL 37	36.0	112.0	78.3	2.9	14.3	46.3	80.0	8.1	25.9	28.19	7.3
26	WT 88	43.0	112.0	54.0	4.2	12.6	60.6	65.3	8.7	52.1	12.48	6.5
27	EC 538830	43.0	101.0	84.3	2.9	13.6	44.3	57.0	6.5	21.6	21.30	4.6
28	NRC 2006M	46.0	113.0	71.6	4.2	11.6	58.0	92.0	12.8	50.2	24.90	12.5
29	EC16213	47.0	91.0	51.3	1.9	10.6	44.0	47.0	9.1	17.4	29.31	5.1
30	JS 20-52	43.0	103.0	61.0	1.3	13.3	40.3	26.3	8.6	27.6	11.23	3.1
31	PS 1475	37.0	104.0	58.3	1.9	10.6	50.0	35.6	8.3	17.3	21.97	3.8
32	EC 389179B	47.0	93.0	57.6	2.9	12.0	65.0	47.6	8.1	24.7	19.03	4.7
33	JSM 227	44.0	103.0	68.3	2.9	15.0	68.3	95.3	10.1	41.9	24.82	10.4
34	SL 2951	45.0	102.0	54.0	1.6	12.0	35.6	19.6	5.6	21.3	8.92	1.9
35	EC 389099	46.0	99.0	52.6	1.6	11.6	69.6	24.6	5.3	22.8	9.65	2.2
36	JS 20-69	44.0	102.0	56.3	1.9	11.3	39.6	92.0	3.4	16.6	24.70	4.1
37	JSM 195	34.0	99.0	51.3	2.2	11.7	72.0	60.3	8.2	18.7	31.02	5.8
38	EC 291397	35.0	102.0	48.6	1.3	12.0	72.7	27.0	9.6	16.8	20.24	3.4
39	PS 1336	43.0	98.0	58.6	1.6	15.7	32.3	49.0	6.2	18.1	21.55	3.9
40	EC 294003	44.0	103.0	63.7	3.6	13.0	61.0	42.3	5.7	20.3	16.26	3.3
41	EC 291451	43.0	102.0	78.6	1.9	14.7	35.6	25.6	7.2	27.6	9.78	2.7
42	EC 24091	43.0	101.0	83.3	3.2	14.3	45.6	54.7	6.1	23.6	17.80	4.2
43	RSC 14	46.0	104.0	76.0	4.2	15.6	76.0	56.3	9.4	33.6	18.15	6.1
44	EC 325103	44.0	93.0	80.7	1.9	13.3	48.6	67.6	7.0	26.4	21.21	5.6
45	JSM 285	42.0	97.0	84.3	2.6	16.0	49.3	104.6	9.9	22.1	50.68	11.2
46	EC 33872B	37.0	101.0	74.7	3.6	14.6	30.6	65.6	11.2	20.6	39.32	8.1
47	SQL 1	41.0	104.0	73.6	3.3	11.0	36.6	41.6	5.8	21.5	15.35	3.3
48	JSM 232	37.0	104.0	79.6	5.9	15.6	72.3	125.0	8.9	38.8	30.93	12
49	JSM 222	42.0	104.0	79.6	3.9	21.0	84.6	125.3	5.8	41.4	19.81	8.2
50	JSM 245	42.0	110.0	95.7	3.6	13.6	67.6	109.3	7.5	27.5	32.73	9
51	PS 1467	47.0	112.0	68.7	3.2	17.3	59.0	83.6	10.3	37.2	25.27	9.4
52	SL (E)1	47.0	110.0	87.6	3.6	15.0	64.6	80.6	11.2	44.7	21.92	9.8

53	PK 701	46.0	102.0	96.7	2.2	13.3	50.6	61.3	8.8	30.3	20.46	6.2
54	PK 1038	58.0	102.0	115.7	4.9	15.6	95.0	127.3	7.1	20.9	47.37	9.9
55	RKS 54	46.0	103.0	77.3	4.3	11.6	82.6	151.3	5.5	33.8	27.22	9.2
56	EC 33940	46.0	101.0	65.6	2.6	12.3	47.0	19.3	6.4	27.7	7.58	2.1
57	G2225	66.0	117.0	95.7	3.6	18.0	114.7	223.0	7.5	28.2	62.06	17.5
58	JS 20-29	36.0	109.0	76.0	2.3	11.6	49.6	30.0	8.9	15.9	22.01	3.5
59	G4P15	36.0	105.0	69.0	2.9	14.0	65.3	52.6	8.7	21.8	24.77	5.4
60	GP 465	38.0	112.0	74.0	1.9	16.0	53.0	95.6	10.5	43.3	24.94	10.8
61	TGX 849-D-13-4	64.0	118.0	95.3	3.6	19.3	99.0	182.3	6.4	32.9	37.99	12.5
62	MACS 171	45.0	100.0	68.3	1.6	15.3	47.3	65.6	8.3	21.0	29.96	6.3
63	JS 20-98	38.0	103.0	82.0	2.6	16.0	45.0	90.0	11.1	29.7	36.36	10.8
64	TG X 849-813	44.0	104.0	82.3	2.9	15.0	53.3	41.3	9.4	27.7	16.97	4.7
65	KB-17	43.0	104.0	94.0	2.9	14.6	44.0	48.6	9.7	24.8	22.18	5.5
66	KDS 256	44.0	104.0	83.6	2.3	13.3	63.0	55.7	6.5	19.3	23.32	4.5
67	LEE-54	45.0	99.0	68.3	2.6	16.0	47.6	88.3	7.1	23.0	30.87	7.1
68	JS 96-31	36.0	101.0	77.3	1.9	10.0	34.0	68.3	9.2	22.5	31.56	7.1
69	TNAU 20024	44.0	109.0	146.0	4.6	19.6	90.6	106.0	8.9	24.3	42.39	10.3
70	PK 258	44.0	102.0	102.6	4.3	17.3	78.0	80.6	6.7	27.8	22.66	6.3
71	EC 468597	43.0	103.0	80.3	1.9	14.0	40.0	62.3	5.8	25.7	17.51	4.5
72	EC 572160	43.0	100.0	79.6	2.3	15.6	36.6	27.0	9.6	15.7	21.66	3.4
73	NRC 37	44.0	112.0	57.0	3.2	15.3	33.0	39.3	9.1	25.5	17.25	4.4
74	EC 391181	46.0	101.0	83.0	2.6	14.6	49.6	62.0	9.5	23.6	28.39	6.7
75	VGM 70	48.0	103.0	95.6	4.2	15.0	53.3	83.3	9.7	28.4	31.34	8.9
76	VLS 75	45.0	110.0	58.0	3.2	13.0	49.3	67.3	10.9	36.6	22.13	8.1
77	EC 391316	45.0	99.0	65.3	1.8	15.0	32.3	54.0	5.6	16.4	23.78	3.9
78	SL 682	44.0	109.0	116.6	2.9	12.7	62.6	103.7	8.3	18.1	51.93	9.4
79	PI 204336	42.0	103.0	67.3	3.3	15.0	53.3	71.0	8.4	23.9	28.45	6.8
80	UGM 70	60.0	101.0	83.0	3.2	14.6	63.6	39.6	11.7	21.8	24.77	5.4

81	LEE 96	43.0	98.0	74.0	1.6	12.3	53.3	48.6	4.7	17.3	18.50	3.2
82	TG X 1488-9-1D	43.0	103.0	68.6	2.9	12.6	49.0	58.3	7.5	27.3	19.05	5.2
83	GP566	49.0	101.0	136.6	2.6	11.6	29.6	53.7	5.2	17.0	21.76	3.7
84	PS1421	47.0	98.0	69.0	0.9	14.0	43.3	31.6	7.4	16.7	19.16	3.2
85	VLS 11	46.0	102.0	73.0	3.2	13.3	41.0	71.7	6.6	21.9	25.57	5.6
86	UPSM 77	67.0	118.0	88.3	3.2	15.3	37.0	39.0	5.9	17.0	18.82	3.2
87	EC 350664	46.0	104.0	63.3	3.6	12.0	62.3	64.3	10.9	24.8	31.45	7.8
88	EC 377883B	45.0	112.0	77.0	2.6	15.0	37.0	71.6	15.2	42.5	27.29	11.6
89	JS 20-34	33.0	101.0	42.3	1.3	8.3	50.0	47.3	7.5	15.9	27.67	4.4
90	GC 84051-32-1	43.0	102.0	58.3	1.6	14.0	37.6	56.0	2.2	16.8	13.10	2.2
91	JS 20-50	43.0	109.0	69.6	3.9	11.0	42.0	22.6	6.3	24.3	9.47	2.3
92	MACS-7102	43.0	101.0	70.0	3.3	12.3	40.3	61.6	10.6	34.3	21.28	7.3
93	20-40B(Z-9)	34.0	109.0	65.3	3.6	10.7	37.0	30.3	8.1	15.2	21.71	3.3
94	20-148 (Z-15)	43.0	102.0	59.3	1.6	11.0	46.3	16.0	7.9	17.3	12.14	2.1
95	23-10B(Z-17)	34.0	112.0	66.6	2.6	14.7	49.3	60.0	9.3	28.6	22.38	6.4
96	23-11A(Z-18)	44.0	101.0	57.0	3.6	11.0	40.0	36.0	6.8	15.1	21.85	3.3
97	JS 20-34	28.0	88.5	32.9	0.0	10.1	18.8	46.6	7.5	16.0	63.34	4.5
98	JS 335	35.3	98.0	63.8	2.1	11.8	35.7	97.6	9.2	17.7	66.32	10.0
99	JS 20-98	38.5	98.3	60.2	0.5	11.8	23.8	62.2	7.5	16.0	73.30	5.7
100	NRC 86	55.0	99.3	75.7	2.2	16.2	78.0	187.3	11.7	20.2	79.93	23.0

Here:

Dfi= Days to flowering

Nbp= number of primary brancher per plant

Npp= number of pods per plant

100sw= hundred seed weight (g)

Dm= Days to maturity

Nnp= number of nodes per plant

Nsp = number of seeds per plant

By= Biological yield per plant

Ph= plant height (cm)

Hi= harvest index

Syp= seed yield per plant

Appendix IV: Scoring of disease in soybean genotypes

S. NO	Name of germplasm lines	YMV	Severity grade	BP	Rating	CR	Rating	RAB	Rating
1	K-53	R	1	MR	3	MR	3	MS	5
2	EC-389153	R	1	MS	5	AR	0	MR	3
3	UPSL 152	HR	0	AR	0	AR	0	HR	1
4	EC 389179B	MS	3	HR	1	S	7	MR	3
5	UPSM 77	MS	3	AR	0	MR	3	MR	3
6	EC 391181	S	4	AR	0	AR	0	MR	3
7	VGM 70	MR	2	AR	0	MR	3	MS	5
8	VLS 75	S	4	MR	3	MR	3	MR	3
9	EC 391316	MS	3	AR	0	MR	3	MS	5
10	JS 97-52	R	1	MS	5	MR	3	MR	3
11	NRC 2007A	S	4	AR	0	MR	3	MR	3
12	NRC 80-1	MS	3	AR	0	MR	3	MR	3
13	JS 20-01	MR	2	S	7	S	7	MS	5
14	EC 396065	R	1	HR	1	MS	5	MS	5
15	DCB 137	HR	0	MS	5	AR	0	HR	1
16	EC 457214	R	1	AR	0	MS	5	MS	5
17	DE 201	HR	0	MR	3	HS	9	MS	5
18	EC 457336	HR	0	HR	1	HS	9	MR	3
19	AGS 12	MR	2	HR	1	AR	0	HR	1
20	F4P20	MR	2	HR	1	MR	3	HR	1
21	EC 103336	HR	0	AR	0	MS	5	S	7
22	NRC 86	MR	2	MR	3	MR	3	MS	5
23	EC 106998	HR	0	MR	3	MS	5	MS	5
24	SL 752	MR	2	HR	1	AR	0	MR	3
25	EC 109540	MR	2	HR	1	AR	0	MS	5
26	UGM 75	R	1	AR	0	AR	0	MR	3
27	MACS 303	MS	3	AR	0	AR	0	HR	1
28	NRC 2006M	MR	2	MS	5	AR	0	MR	3
29	EC16213	MR	2	MR	3	AR	0	MS	5
30	JS 20-52	MR	2	HR	1	S	7	MS	5
31	PS 1475	MR	2	MR	3	AR	0	MR	3
32	NRC 37	MS	3	MS	5	MR	3	MS	5
33	MACS 171	R	1	AR	0	HS	9	MR	3
34	SL 2951	MS	3	AR	0	HS	9	MS	5
35	EC 389099	HR	0	MS	5	AR	0	MS	5
36	JS 20-69	HR	0	AR	0	MR	3	MS	5
37	JSM 195	R	1	AR	0	MS	5	MR	3
38	EC 291397	HR	0	AR	0	MR	3	MS	5
39	PS 1336	HR	0	AR	0	MS	5	MR	3
40	EC 294003	HR	0	AR	0	MR	3	MR	3

41	EC 291451	HR	0	AR	0	MS	5	MR	3
42	EC 24091	HR	0	AR	0	MR	3	MR	3
43	RSC 14	MR	2	AR	0	MS	5	MR	3
44	EC 325103	HR	0	MR	3	AR	0	MR	3
45	JSM 285	R	1	AR	0	AR	0	HR	1
46	EC 33872B	HR	0	MR	3	MS	5	MS	5
47	SQL 1	R	1	AR	0	AR	0	MS	5
48	JSM 232	HR	0	AR	0	AR	0	HR	1
49	JSM 222	MR	2	MR	3	AR	0	MR	3
50	JSM 245	MR	2	MR	3	AR	0	MS	5
51	JS 20-34	MR	2	MR	3	AR	0	MR	3
52	SL (E)1	MS	3	HR	1	AR	0	MS	5
53	PK 701	HR	0	AR	0	AR	0	MS	5
54	PK 1038	MS	3	MR	3	AR	0	MR	3
55	RKS 54	MS	3	HR	1	AR	0	HR	1
56	EC 33940	HR	0	AR	0	AR	0	MS	5
57	G2225	R	1	AR	0	AR	0	HR	1
58	JS 20-29	HR	0	AR	0	S	7	MS	5
59	G4P15	HR	0	MR	3	AR	0	MR	3
60	GP 465	HR	0	MR	3	S	7	MR	3
61	TGX 849-D-13-4	HR	0	AR	0	AR	0	MR	3
62	JSM 227	MR	2	AR	0	AR	0	MR	3
63	JS 20-98	R	1	AR	0	AR	0	MR	3
64	TG X 849-813	R	1	AR	0	AR	0	MR	3
65	KB-17	R	1	AR	0	MR	3	MS	5
66	KDS 256	HR	0	MS	5	AR	0	MR	3
67	LEE-54	R	1	AR	0	MR	3	MR	3
68	JS 96-31	R	1	AR	0	MR	3	MR	3
69	TNAU 20024	R	1	AR	0	MR	3	MR	3
70	SQL 37	MR	2	AR	0	AR	0	MS	5
71	WT 88	MR	2	AR	0	AR	0	MS	5
72	TNAU 20022	S	4	HR	1	MR	3	MR	3
73	EC 528640	HR	0	MR	3	MR	3	MS	5
74	EC 538830	MR	2	AR	0	MR	3	MR	3
75	PK 258	MS	3	MR	3	AR	0	MR	3
76	EC 468597	R	1	AR	0	MR	3	MR	3
77	EC 572160	MR	2	MS	5	S	7	MR	3
78	SL 682	MS	3	AR	0	MS	5	MR	3
79	PI 204336	MS	3	AR	0	AR	0	MR	3
80	UGM 70	S	4	AR	0	AR	0	MR	3
81	LEE 96	S	4	AR	0	HS	9	MR	3
82	TG X 1488-9-1D	MS	3	MR	3	MR	3	MR	3

83	GP566	MS	3	MS	5	MR	3	MS	5
84	PS1421	HR	0	MR	3	HS	9	MR	3
85	VLS 11	HR	0	MR	3	AR	0	MR	3
86	PS 1467	MR	2	MS	5	AR	0	HR	1
87	EC 350664	HR	0	AR	0	AR	0	HR	1
88	EC 377883B	HR	0	AR	0	AR	0	MS	5
89	JS 20-34	MR	2	MR	3	AR	0	MR	3
90	GC 84051-32-1	HR	0	MS	5	S	7	MS	5
91	JS 20-50	R	1	AR	0	MS	5	MS	5
92	MACS-7102	MR	2	MR	3	MS	5	MR	3
93	20-40B(Z-9)	HR	0	AR	0	MR	3	S	7
94	20-148 (Z-15)	HR	0	AR	0	MS	5	S	7
95	23-10B(Z-17)	HR	0	AR	0	AR	0	S	7
96	23-11A(Z-18)	R	1	AR	0	MR	3	MS	5
97	JS 20-34 (C)	MR	2	AR	0	AR	0	MR	3
98	JS 335 (C)	MS	3	AR	0	MR	3	MS	5
99	JS 20-98 (C)	HR	0	AR	0	AR	0	MR	3
100	NRC86 (C)	MR	2	MR	3	MR	3	MR	3

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