

**CHARACTERIZATION OF ADVANCED
BREEDING LINES OF SOYBEAN (*Glycine max* (L.)
Merrill) THROUGH AGRONOMIC TRAITS AND
MOLECULAR MARKERS**

Thesis

**Submitted to the Punjab Agricultural University
in partial fulfillment of requirements
for the degree of**

**MASTER OF SCIENCE
in
PLANT BREEDING AND GENETICS
(Minor Subject: Biotechnology)**

By

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CERTIFICATE I

This is to certify that the thesis entitled “**Characterization of advanced breeding lines of soybean (*Glycine max* (L.) Merrill) through agronomic traits and molecular markers**” submitted for the degree of **M.Sc.** in the subject of **Plant Breeding and Genetics** (Minor subject: **Biotechnology**) of the Punjab Agricultural University, Ludhiana, is a bonafide research work carried out by **Dibyabharati Sahu** (L-2015-A-101-M) under my supervision and that no part of this thesis has been submitted for any other degree.

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

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This is to certify that the thesis entitled “**Characterization of advanced breeding lines of soybean (*Glycine max* (L.) Merrill) through agronomic traits and molecular markers**” submitted by **Dibyabharati Sahu** (L-2015-A-101-M) to the Punjab Agricultural University, Ludhiana, in the partial fulfillment of the requirements for the degree of **M.Sc.** in the subject of **Plant Breeding and Genetics** (Minor subject: **Biotechnology**) has been approved by the Student’s Advisory Committee along with the Head of the Department after an oral examination on the same.

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ABSTRACT

The combination breeding is an important method to brought together the desirable genes from two parents into a single genotype. In the present investigation, $F_{2,7}$ lines derived from cross of SL 525 (a yellow mosaic resistant variety) and JS 335 (a widely adapted cultivar but susceptible to YMV) were evaluated with the objective to identify lines having similarity to JS 335 along with resistance to YMV. Analysis of variance revealed significant variation for all characters except seeds per pod at Ludhiana. On the basis of mean performance at Ludhiana, the line, SLJS 11-2 was superior for seed yield (37.2g), SLJS 43-7 for protein content (39.1%) and SLJS 23-2 (22.7%) for oil content whereas at Gurdaspur the line, SLJS 41-2 performed better for seed yield (37.6g), SLJS 25-1 for protein content (38.9%) and SL 525 for oil content (22.1%). Genotypic coefficient of variance, phenotypic coefficient of variance, heritability and genetic advance was moderate to high for seed yield per plant and number of pods per plant at Ludhiana and Gurdaspur. Seed yield had significant and positive correlation with plant height at 60 DAS, plant height at maturity and number of nodes per plant at both the locations i.e Ludhiana and Gurdaspur. At Ludhiana, oil content was significantly and negatively correlated with protein content (-0.21). Path analysis at Ludhiana showed that dry weight at 60 DAS (3.39) had high positive direct effect and dry weight at 45 DAS had negative direct effect (-2.65) on seed yield, however, at Gurdaspur high positive effect was observed for fresh weight 45 DAS (6.08) while fresh weight 60 DAS exerted highest negative direct effect (-5.98) on seed yield. At Ludhiana, fresh and dry weight at 45 DAS and fresh weight at 60 DAS had maximum indirect contribution on seed yield via dry weight at 60 DAS while at Gurdaspur fresh and dry weight at 30 DAS, dry weight at 45 DAS, fresh and dry weight at 60 DAS had highest indirect effect on seed yield via fresh weight at 45 DAS. Diversity analysis conducted through Mahalanobis D^2 , grouped the genotypes into 5 clusters while diversity analysed by using 16 polymorphic SSR markers, categorized lines into 3 clusters. The mean value for seed yield was high in cluster 4. Diversity analysis by both the methods revealed that more number of genotypes were grouped with JS 335 as compared to SL 525. Parental contribution of each line was estimated by analysing the behaviour of each marker towards each parent. It revealed that the lines which were present along with JS 335 had more genetic contribution of JS 335 as compared to SL 525. The lines, SLJS 41-2 (32.1g) and SLJS 43-7 (32.4g) were higher yielder than parent SL 525 (30.0g) as well as had more contribution of JS 335 and were resistant to yellow mosaic virus. In addition to diversity analysis, graphical genotyping was also done by using the polymorphic markers. The result revealed that maximum introgression occurred in linkage group 'O' as polymorphic markers like Satt 487, Satt 123 and Satt 153 were present with in this linkage group.

Keywords: Soybean, genetic variability, D^2 , SSR markers

Signature of Major Advisor

Signature of the student

ਖੋਜ ਦਾ ਸਿਰਲੇਖ	: ਐਗਰੋਨੋਮਿਕ ਲੱਛਣ ਅਤੇ ਮੋਲੀਕਿਊਲਰ ਮਾਰਕਰ ਰਾਹੀਂ ਸੋਇਆਬੀਨ ਦੀਆਂ ਅਗਰਿਮ ਬਰੀਡਿੰਗ ਲਾਇਨਾਂ ਦਾ ਚਿਤਰਾਕਨ
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CHAPTER I

INTRODUCTION

Legumes play an important role in agriculture as they are widely distributed in natural ecosystem. They are the third largest land plant family in terms of number of species after orchidaceae and asteraceae. According to Polhill *et al* (1981) legumes constitutes of 751 genera and 19,000 known species. Grain legumes contain 33 per cent of dietary protein nitrogen which is a major nutrient of human food (Vance *et al* 2000).

Soybean is an important grain legume as well as oil seed crop of the world in terms of total production and international trade. Taxonomically, soybean belongs to order Fabales, family Fabaceae, subfamily Faboidae and genus *Glycine*. Two subgenera are present under division of genus *Glycine*. One having *Glycine* which includes 16 perennial species and the other includes *Soja* (Moench) F.J. Herm with two annual species, *Glycine Soja* Siebold and Zucc (2n=40) and *G. max* (L.) Merrill (2n=40). High crossability of *Glycine max* is found with annual relatives and with most probable progenitor, *G soja* while low crossability is found with perennial species (Singh and Hymowitz 1999).

Soybean is known by many names viz. miracle bean, golden bean, wonder bean etc due to its unique chemical composition (20% oil and 40% protein). It is also rich in amino acid lysine and vitamins A, B and D. The probable origin of soybean according to Chang (1980) is the middle and lower Yellow river valley in China. It has been domesticated in China and travelled across the globe to become one of the world's important sources of edible oil and protein feed for livestock. USA, Brazil, Argentina, China and India are major soybean growing countries accounting for 88 per cent of the world's (308 MT) annual soybean production (Anonymous 2016). In India, the cultivation of soybean is concentrated in the central parts, predominantly in the states of Madhya Pradesh, Maharashtra and Rajasthan. These three states occupied about 92 per cent of total soybean area (11.07 Mha) in the country in 2015 (Anonymous 2016). Soybean is number one oilseed crop of the world as well as of India. In India, it contributed about 47 per cent and 25 per cent towards the total oilseeds and edible oil production, respectively (Anonymous 2015). However, the yield levels in India (1.0 t/ha) are less than half of the world average yield (2.6 t/ha). It can play an important role in crop diversification in Punjab. The major problems in popularization of soybean cultivation in Punjab are low returns from soybean as compared to competing paddy crop and stability of yield across environments. Thus improvement of yield and stability are very important traits both at state and national level.

Grain yield is the most important quantitative character in breeding of soybean. Traditional breeding methods like hybridization and phenotypic selection helps in achieving genetic gain in soybean (Coryell *et al* 1999). Grain yield is a complex character whose expression is influenced by environmental factors as well as genotype × environment

interactions (Soldati *et al* 1955). It is a product of many factors such as seed size (weight per 100 seed) and seed number per square meter, these traits are known as yield components (Board *et al* 1997). For successful selection procedure on higher grain yield, it is necessary to possess adequate information about the nature and magnitude of genetic variability present in the available breeding material (St. Martin 1984). Generally grain yield has low heritability and selection of genotypes based on yield alone is misleading. The knowledge of relationship among yield and component characters is required for efficient selection. The information of heritability along with genetic advance provides a clear picture of selection for a particular trait. The techniques like phenotypic coefficient of variation, genotypic coefficient of variation, heritability, genetic advance, correlation and path coefficient analysis are useful tools for determination of genetic variability and for direct and indirect selection of yield (Badkul *et al* 2014).

Genetic variability based on morphological parameters do not give clear picture of genetic variability present in the material as quantitative traits are highly influenced by environment. Hence, there is need of highly reliable and precise method for assessment of genetic variability. Assessment of genetic diversity with molecular markers overcomes these problems. They are devoid of environmental effects and provide a true representation of entire genome. Simple sequence repeat markers (SSR) are being extensively used in genome studies, marker-assisted selection and cultivar identification. They are well-known for their versatility in providing a quick assay and for their highly informative data (Cregan *et al* 1999a, Cregan *et al* 1999b).

Yellow Mosaic Virus (YMV) is a devastating disease of soybean. It occurs in more severe form in North West plain zone. Sometimes, it may cause upto 80 per cent yield loss (Nene 1972). The variety, SL 525 developed by Punjab Agricultural University is resistant to YMV and was recommended for cultivation in Punjab (Singh *et al* 2005). JS335 is a leading variety of central India which has high stability. But with due course of time the popularity of this variety decreased because of its susceptibility to YMV. Thus, need arises to incorporate the YMV resistance in the elite genotypes of soybean. For this purpose, 48 F_{2:7} lines has been selected from the cross, SL525 x JS335 with the objective of combining stability of JS335 and YMV resistance of SL525. There is a need to evaluate these lines for various agronomic traits, YMV reaction, quality traits and to assess genetic variation among these lines.

Keeping these points in view, the present study was conducted to evaluate soybean genotypes with following objectives:

1. To evaluate the lines derived from cross, SL525 x JS335 and assess genetic variation for agronomic traits and SSR based molecular markers.
2. To study the association of agronomic traits with grain yield in newly developed soybean lines

CHAPTER II

REVIEW OF LITERATURE

Genetic variability is the pre-requisite for initiating a breeding programme. The sudden appearance of yellow mosaic virus (YMV) during 2015 in central India reduced the popularity and yield of leading soybean variety, JS335. So objective is to breed a variety with improved yield and having YMV resistance as well as wider adaptability. Yield and its components are quantitative in nature, so for successful selection procedure for higher yield it is necessary to possess adequate information about nature and magnitude of genetic variability present in material. To fulfill these objectives the lines derived from cross, SL 525× JS 335 were evaluated. Correlation of yield with other agronomic traits and diversity analysis also help to know the variability present in the material. Partitioning of variance also provides information about heritability of characters. The literature pertaining to present study has been presented under following sub-headings:

2.1 Genetic variability for yield and other agronomic traits

2.2 Correlation studies

2.3 Diversity analysis

2.3 (a) Genetic diversity analysis through Mahalanobis D^2 statistics

2.3 (b) Genetic diversity analysis through molecular markers

2.1 Genetic variability for yield and other agronomic traits

The success of breeding programme depends on variability present in germplasm/ breeding material. To make selection more effective, sufficient genetic variation must be present in the material for traits of interest. The traits like pods per plant, seeds per pod, seed weight, number of nodes per plant, plant height, days to flowering and maturity are known to directly affect grain yield. Genetic variation has been reported for these characters by several workers.

Agronomic traits have been observed as the most important criteria to differentiate between soybean strains. The soybean strains differed significantly in respect of plant height, number of pods per plant, nodes per plant, seeds per pod, 100-seed weight and yield (Weatherspoon and Bentz 1934). Estimation of different components of variability helps to estimate the effect of genotype and environment on different agronomic traits. In soybean the estimates of genotypic and phenotypic variability in different environments were less consistent and the estimates of genotype with environment interaction were higher for yield than for any other important characters (Johansson *et al* 1955). In the F_2 and F_3 generations of soybean crosses, it was found that number of branches and pods were most variable while maturity showed least variability (Harway 1956). Partitioning of genetic variability and estimation of epistatic variability provides information about genetic variability of seed yield.

In soybean, the partitioning of variation was done in F_2 but the information obtained from adequate partition of genetic variability was insufficient (Hanson and Weber 1960). Extremely biased information was obtained when variability analysis and estimation of genetic parameters for yield was derived from individual plants of heterozygous population (Hinson and Hanson 1962). Under Indian condition, wide range of variability for pods per plant and plant height was observed and narrow range of variability was observed in pod length and days to maturity (Prakash *et al* 1966). High yielding soybean cultivars have higher rate of photosynthesis or net assimilation rate (Buttery and Buzzell 1972). Miku (1978) studied eleven hybrids of soybean and observed high genetic coefficient for plant height, pods per plant and yield per plant. High heritability was observed in duration of period from germination to flowering, plant height and 100-seed weight, respectively. A wide range of heritability values (36 to 96%) were obtained for protein content in soybean (Brim and Burton, 1979). In soybean, pod and seed number are the most important yield components, between these two traits, number of pods per plant contributes the highest direct effect on grain yield formation (Kadlec and Vozda 1983). Alam *et al* (1984) noticed low heritability for seed yield and 100-seed weight. High broad sense heritability for plant height and 100-seed weight in soybean genotypes and their F_2 progenies was observed by Diaz *et al* (1985). High genetic variability among 36 diverse soybean varieties for pods per plant, plant height and grain yield per plant was also estimated by Rajput *et al* (1987). As yield is an important trait, the quantitative genetic analysis and statistical techniques have been used to determine the relative importance of yield components in overall yield formation process involving genetic and environmental variables (Fehr, 1987). Pushpendra and Ram (1987) observed variation in different genetic parameters for days to flowering, days to maturity, pod length, number of branches, leaf area, pods per plant, plant height, 100- seed weight and seed yield per plant. The characters like plant height, 100-seed weight and days to flowering showed high heritability which suggested that selection for these traits would be effective. Result of such analysis significantly contributes to formulate an effective selection programme for improvement of quantity and quality of grain yield.

Resaily *et al* (1986) conducted experiment on genetic variability in soybean for yield and 12 related characters and revealed that considerable amount of genetic variability was present for plant height, seed yield and number of pods per plant. High heritability values were observed for plant height, days to flowering and days to maturity. Assessment the genetic variability of soybean germplasm was done during 1979 to 1983 by Chaudhary and Singh (1987) and this assessment revealed wide range of variability for days to flowering, days to maturity, plant height, branches per plant and seed yield per plant. The estimation of coefficient of variation i.e, GCV and PCV provides information about appropriate selection. Higher GCV as compared to PCV indicates little effect of environment in expression of

character. Selection for improvement of such character is rewarding. If PCV is higher than GCV, it indicates that the apparent variation is not only due to genotypes but also due to influence of environment. Selection for such trait is sometime misleading. An experiment was conducted by (Hossian *et al* 2003) to determine the genotype $\times$ environment interaction. Different parameters like days to flowering, 100-seed weight and seed yield were recorded and genotypes were sown across different environments to find out the stability of a variety. Parameshwar (2006) in his experiments on soybean reported high estimates of GCV and PCV for plant height while moderate values were observed for pods per plant, days to flowering, 100-seed weight, and seed yield per plant. Days to maturity, number of pods per plant, number of seeds per pod and oil percentage showed lower values of GCV and PCV. Manasa (2008) reported high values of GCV and PCV in soybean for harvest index, number of pods per plant, seed yield per plant, pod weight per plant and number of seeds per plant whereas days to flowering, days to maturity and 100-seed weight exhibited low estimates of GCV and PCV. According to Aditya *et al* (2011) seed yield per plant and number of pods per plant exhibited high estimate of PCV and GCV, whereas low magnitude of PCV was recorded for days to 50 per cent flowering. Various parameters (heritability, genetic advance, range of variability and coefficient of variation) for assessment of genetic variability for the traits which directly affect the seed yield in soybean were studied by Badkul *et al* (2014). A relative study on comparison of magnitude of PCV and GCV for different traits revealed higher PCV than that of GCV for all the characters under study. Number of branches per plant recorded the highest PCV and GCV followed by number of seeds per plant, seed yield per plant, number of pods per plant, biological yield per plant and moderate PCV and GCV were recorded for plant height, 100-seed weight, number of seeds per pod, harvest index and vegetative phase.

Heritability is a good index of transmission of characters from parents to their offspring. The estimates of heritability help the plant breeder in selection of elite genotypes from diverse genetic population. Karasu *et al* (2009) determined variance components and heritability of yield related traits in eight soybean genotypes. Moderate to low heritability estimates were observed for plant height, number of seeds per pod, 100-seed weight, number of seeds per plant, number of pods per plant and seed yield. Similarly, Recker (2010) found high heritability estimates for flowering date, maturity date, lodging and height whereas heritability estimates were medium for protein and oil content. Wiggins (2012) developed 239 F₄ derived RIL from the cross between USG 5601T $\times$ U99-310255. These lines were used as experimental material to calculate heritability of characters like seed oil, protein content and yield by parent offspring regression. The broad sense heritability observed for oil content, protein content and seed yield were 0.65, 0.78, and 0.38, respectively.

Forty five genotypes of soybean (*Glycine max* (L.) Merrill.) of diverse origin were

evaluated for variability, heritability and genetic advance. Analysis of variance revealed highly significant differences among the genotypes for the all the characters observed. High PCV with high GCV, observed for branches per plant, pods per plant, biological yield, harvest index and yield per plant indicate the presence of wider adaptability of genotypes studied for these traits. It suggested that these characters are less influenced by environment. High heritability coupled with high genetic advance was observed for days to 50 per cent flowering, plant height, branches per plant, pods per plant, pod length, seeds per pod, 100-seed weight, biological yield, harvest index and seed yield per plant. It indicated the operation of additive gene action and the ample scope for improvement in these traits through simple selection, Reni and Rao (2013). Ghodrati (2013) studied twelve soybean genotypes to analyse genotypic variation, phenotypic correlations and broad sense heritability for different agronomic and quality traits during three growing seasons. Results indicated significant differences for seed yield and quality characters which mean sufficient genetic variation for efficient selection. Ojo *et al* (2013) studied variation in 5 varieties of soybean which were collected from different countries to analyse variation in seed yield. Highly significant differences observed among genotypes for all characters like days to flowering, days to maturity, plant height, 100- seed weight and grain yield.

Malek *et al* (2014) determined genetic advance, Genetic variability, character association and genetic diversity among 27 soybean mutants and four mother parent genotypes. Analysis of variance observed significant differences among the mutants and mother parent for different morphological traits. Narrow differences between phenotypic and genotypic coefficients of variation for most of the characters indicated less environmental influence on their expression. Ali *et al* (2016) conducted an experiment to estimate genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), heritability (h^2), expected genetic advance (GA) and genetic advance as per cent of mean (GAM) for nine quantitative traits of soybean (*Glycine max* L). For all characters PCV values were higher than GCV values except for oil content. Heritability was high for oil content (99%) and low for days to pod formation (31%) where as genetic advance was low for oil content (1.78) and high for seed yield (780.80).

2.2 Correlation Studies:

Information regarding association between various attributes is necessary for conducting optimistic breeding programme and increasing efficiency of selection. The basis of phenotypic selection depends on the degree and direction of association between two characters. Correlation analysis provides information which is helpful in formulating efficient scheme of multiple trait selection as it provide means for direct and indirect selection for component characters.

Chinoy (1949) revealed the existence of close correlation between the phenomena of

growth and development. Direct correlations also exist between the length of different phases and plant characteristics like winter hardiness, drought resistance and assimilatory rate. Ecochard and Ravelomanantsoa (1982) reported that genetic correlations identified four different groups of traits comprised of seed number per pod, mean seed weight, chlorophyll content per unit leaf area and all the other characters, including seed yield and total plant weight at maturity. Among these traits, stem diameter at ground level appeared to be a good indicator of yield. Musorina (1987) observed that protein content was negatively correlated with oil content of seeds. In another study, Song *et al* (1987) observed no correlation of seed yield with protein and oil content. However, Swlan-Momorivic (1987) and Mello *et al* (2004) observed significant negative correlation between seed yield and protein content. Trypsin inhibitor content (TIC) was negatively correlated with seed weight per plant, total protein content and positively with seed oil content, Teleutsa *et al* (1989). So, it revealed that low TIC genotype could be obtained by selecting large seeded lines with high protein content. Aslam *et al* (1992) evaluated 10 soybean genotypes of diverse origin for six quantitative traits to analyse genotypic correlation and path coefficient. The result from Path coefficient analysis indicated that plant height had a very high positive direct path followed by 100-seed weight.

Lianne *et al* (2001) suggested that correlation between plant canopy reflectance and above ground biomass can possibly be used for early prediction of crop yield. Soybean grain yield was highly and positively correlated with canopy reflectance and is expressed as normalized difference vegetation index. Malik *et al* (2006) observed significant positive correlation coefficient of yield with leaf area, pods per plant, days to 50 per cent flowering, days to maturity, plant height and 100-seed weight had negative effect on yield. Results for the relationship of plant height with seed yield by Cicek *et al* (2006) showed seed yield to be strongly and positively correlated with plant height. Yadav (2007) conducted an experiment with thirty diverse genotypes of soybean and observed significant correlation of seed yield with plant height, pod length, number of pods per plant and number of seeds per plant. Yield parameters of three soybean genotypes were studied and this indicated that seed yield was significantly and positively correlated with leaf area, number of branches, total dry weight and number of leaves while it was negatively correlated with plant height (Kalyankar *et al* 2008). Based on study using eight soybean cultivars, Oz *et al* (2009) indicated that seed yield had significant and positive correlation with number of pods per plant, number of seeds per plant and number of seeds per pod. Iqbal *et al* (2010) studied variability and correlation among 9 traits in 139 genotypes of soybean. From the experiment they concluded existence of genetic variation between the observed characters. Correlation coefficient suggested that the grain yield showed positive and significant correlation with all studied traits except plant height, which showed non-significant association. Similarly, Kobraee and Shamsi (2011) reported that correlation of pod and seed number with economic yield was positive and highly

significant. There was a negative relationship between seed weight and seed number per pod. Quijano and Morandi (2011) conducted an experiment and indicated that seed number and seed size were primary components of soybean yield. Patil *et al* (2011) conducted an experiment to study correlation and path analysis in soybean. Seed yield had high positive correlation with days to 50 per cent flowering, days to maturity and plant height. Regarding path analysis all the traits showed positive direct effect on seed yield but maximum direct effect was estimated for pods per plant on seed yield. Akram *et al* (2011) concluded that number of pods per plant, number of branches per plant and plant height had significant positive correlation with seed yield as well as high direct effect on seed yield. 100- seed weight was non-significantly correlated with seed yield. Haghi *et al* (2012) reported positive and significant correlation between pod height and number of seeds per pod; pod length and pod width; seed diameter and yield; seed diameter and harvest index. Baruah *et al* (2014) studied 44 soybean genotypes including some improved varieties and breeding lines procured from various organizations. They reported that seed yield per plant had correlation with other traits like pod weight per plant and 100-seed weight among different sets of genotypes. Seed yield per plant was negatively correlated with days to maturity and days to 50% flowering. Pod weight had significant and positive correlation with pods per plant and seeds per plant. Sousa *et al* (2015b) conducted an experiment to analyse phenotypic and genotypic correlations between yield and other agronomic traits in soybean progenies derived from various crosses. The estimates for genotypic correlations were equal or greater than those for the phenotypic correlations for all the evaluated traits like number of pods, grain yield per plant, number of days for flowering, plant height at flowering, number of days for maturity, plant height at maturity, height of the first pod insertion, number of grains per pod and grain yield per plant. Akram *et al* (2016) studied 11 soybean genotype to assess genetic variability, correlation and path coefficient between yield and its components. High heritability values along with high genetic advance for plant height, yield per plant, number of pods per plant and number of seeds per plant, indicated the scope of improvement for these characters. The traits like number of branches per plant, number of pods per plant, number of seeds per plant and 100-seed weight were significantly and positively correlated with yield per plant and it showed a non-significant positive correlation with pod length.

2.3.1 Genetic diversity through Mahalanobis D^2 statistics

Multivariate technique has been proved to be the most important tool of diversity analysis. The Metroglyph analysis (Anderson, 1957) and Mahalanobis D^2 (Mahalanobis, 1936) techniques are the most useful multivariate techniques used in diversity analysis. Agarwal *et al* (2001) studied genetic diversity using Mahalanobis D^2 method in 196 soybean lines. Experiment was based on 20 agronomic traits. Germplasm lines were grouped into 11 clusters, out of which cluster 1 was largest one consisting 50% of total genotypes. Pod weight

was the single trait that contributed maximum towards genetic diversity followed by pod shattering.

Reni *et al* (2003) also conducted an experiment to study the genetic diversity of soybean genotypes that belonged to different ecogeographical regions. On the basis of Mahalanobis D^2 method, the maximum diversity was explained by days to maturity followed by number of pods per plant and days to 50 % flowering. Out of total six clusters, cluster 4 and 6 were the best for seed yield and oil content, respectively.

Bekele *et al* (2012) evaluated 49 soybean germplasm lines for genetic diversity by using Mahalanobis D^2 statistics. These lines were categorized into 16 clusters. Minimum intra cluster distance (5.53) was observed for cluster 5 indicating presence of least genetic diversity between genotypes present within the cluster. Maximum intra cluster distance (27.75) was resulted from cluster 12, exhibiting presence of more diversity between the genotypes present within this the cluster. Inter cluster distance was maximum between cluster 9 and 10 i.e 66.56. It revealed that genotypes selected from cluster 9 and 10 would be more diverse and would be useful for hybridization purpose.

Bizari *et al* (2014) conducted an experiment to analyse diversity in 50 early maturing soybean genotypes by using Mahalanobis D^2 statistics for a number of traits like days to maturity, days to flowering, Plant height at maturity, number of pods, grain yield and oil content. Genotypes were divided into five groups and the contribution of days to flowering was maximum towards diversity analysis

Sousa *et al* (2015a) conducted an experiment to assess the genetic diversity of 22 biparental crosses of soybean using Mahalanobis D^2 method. The genetic diversity was estimated based on eleven characters. Minimum distance (3.2) was observed between the cross of CR 6 and CR 16 where as maximum distance (155.5) observed from the cross between UFUS and CR 21. The traits like plant height at maturity, pods with one seed and grain yield had maximum contribution towards genetic diversity among soybean lines.

2.3.2 Genetic diversity through molecular markers

The development and utilization of molecular markers plays a major role in exploitation and identification of genetic diversity in plants. DNA based markers are now acting as a versatile tool for genetic diversity analysis and DNA fingerprinting. A molecular marker is typically a region in DNA sequence which shows polymorphism in different individuals. The abundance of molecular markers is many times higher than phenotypic markers. The advent of molecular markers is now helping researchers to know the genotype of a plant in early generations and ultimately providing information in early generation for selection of characters. There are various types of DNA markers viz. restriction fragment length polymorphism (RFLP), random amplified polymorphic DNA (RAPD), amplified fragment length polymorphism (AFLP), and simple sequence repeats (SSR). Different types

of markers have different advantages and limitations under different circumstances. So the choice of marker depends on types of study to be conducted and whether that marker would fulfill requirements like higher polymorphism, easy availability, frequent occurrence in genome, selective neutral behaviour, high reproducibility, mendelian inheritance, free of epistasis and pleiotropy etc. (Weising *et al* 1995).

Unlike morphological or protein markers, the DNA markers are not affected by environment. There are two types of DNA markers viz. hybridization based markers and PCR based markers. In the hybridization types marker system, restriction enzyme digested DNA are hybridized to a labeled probe which shares considerable homology with fragment of interest and they are identified by complementary base pairing. RFLP markers are based on hybridization based marker system. In the second approach, amplification of specific DNA sequence is done by using PCR (Polymeric chain reaction). To amplify a target sequence, specific primers are designed which flank the target region. The amplification product is visualized by gel electrophoresis techniques. The invention of PCR using thermostable DNA polymerase has changed the total scenario of molecular biology (Saiki *et al* 1988). It provides a multiple opportunity in marker research. The DNA chip (Gupta *et al* 1999) or high density oligonucleotide array and matrix assisted laser desorption ionization time of light (MALDI-TOF) mass spectrometry are recently developed techniques which helps in genotyping of biallelic loci in large number (Ross *et al* 1998). Ultra-high-throughput genotyping of either one or few individuals for hundred to thousand of markers or that of thousands of individuals for one or few markers has now become possible because of the discovery of these new methods. Diwan *et al* (1997) used fluorescent labeled allele to assess genetic variability in soybean. An average of 10.4 alleles were present per locus with an average genetic diversity of 0.80 at 20 SSR loci.

Guedira *et al* (2000) conducted an experiment to analyse diversity in North American soybean cultivars. Eighteen ancestral soybean lines were assessed for diversity analysis. These lines were divided into 11 clusters. Hudcovicova and kraic (2003) analysed SSR profile of 67 genotypes of soybean. A Total of 188 alleles were found at 18 SSR loci. Mean genetic diversity observed was 0.71 with an average of 10.4 alleles detected per locus. Wang *et al* (2006) used 129 accessions for diversity analysis. The selected accessions were analysed for phenotypic variability for 14 agronomic traits and also analysed with 60 SSR markers. Total of 732 alleles were found with an average of 12.20 alleles per locus. The Polymorphic information content (PIC) varied from 0.50 to 0.92. Genetic distance observed amongst the accessions ranged from 0.05 to 0.91 with an average of 0.23 which clearly categorized the accessions into different clusters. Priolli *et al* (2010) conducted an experiment to determine the genetic relationship in a group of 168 Brazilian soybean cultivars. 18 SSR markers were used in the study. Average number of alleles found per loci was 5.06 with mean diversity of

0.58. Tanaswata *et al* (2011) studied genetic diversity among 25 soybean genotypes. Eleven polymorphic markers were used. Total of 53 alleles were found with an average of 4.82 alleles per locus. The polymorphic information content (PIC) varied from 0.13 (Soy satt 285) to 0.88 (Soy satt 173) with an average of 0.60. Genetic similarity coefficient ranged from 0.73 to 1.00, which successfully distinguished the genotypes studied. Shadakshari *et al* (2010) conducted an experiment to assess diversity among newly introduced soybean accessions. Maximum number (4 alleles) were observed by markers, Satt 207 and Satt 135. Satt 207 had highest PIC value which indicated that it could be an effective tool to differentiate soybean accessions. Kumawat *et al* (2015) analysed 82 soybean accessions for molecular characterization by using 44 SSR markers. Forty polymorphic markers produced total of 119 alleles. No of alleles per each SSR markers varied between 2 to 4 with an average of 2.97. Bisen *et al* (2015) conducted an experiment in 38 soybean genotypes to analyse genetic diversity and varietal identification by using SSR markers. Total 51 alleles were detected with an average of 2.22 alleles per locus. Polymorphic Information Content (PIC) value varied from 0.049 to 0.526 for markers sat_243 and satt 431, respectively. Chauhan *et al* (2015) used 48 soybean varieties released from different agroclimatic zones for diversity analysis. In total, 21 SSR primers were used in the study and 84 alleles were observed. Polymorphic Information Content (PIC) value ranged from 0.781 for primer SOYHSP 173 and 0.304 for primer Satt 278. Genetic similarity coefficient range was 0.1 to 0.4 which indicated the presence of genetic diversity amongst the studied genotypes.

CHAPTER III

MATERIALS AND METHODS

The present experiment was conducted during 2016 at two locations viz. Pulses Research area of Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana and Research Station, Gurdashpur. Molecular study was done at Central Molecular Biology Laboratory and quality parameters were estimated in Quality Laboratory of Department of Plant Breeding and Genetics. The experimental material consisted of 48 derived homozygous lines of $F_{2:7}$ generation of a cross between SL525 (YMV resistant genotype) and JS335 (a leading variety of central India which is susceptible to YMV). In addition, both the parents viz. SL 525 and JS 335 and one check i.e. SL 958 were also included in the experiment. Thus, a total of 51 genotypes (Table 3.1) were evaluated in the experiment.

Table 3.1:List of genotypes used in research work

S. No.	Genotypes	S.No.	Genotypes	S.No.	Genotypes
1	SLJS 1-1	18	SLJS 14-2	35	SLJS 34-1
2	SLJS 1-2	19	SLJS 14-3	36	SLJS 37-1
3	SLJS 1-3	20	SLJS 23-2	37	SLJS 37-1-1
4	SLJS 2-1	21	SLJS 23-3	38	SLJS 41-1
5	SLJS 3-1	22	SLJS 23-4	39	SLJS 41-2
6	SLJS 3-2-1	23	SLJS 25-1	40	SLJS 43-1
7	SLJS 3-2-2	24	SLJS 25-2	41	SLJS 43-2
8	SLJS 3-3	25	SLJS 25-3	42	SLJS 43-3-1
9	SLJS 4-1	26	SLJS 25-4	43	SLJS 43-3-2
10	SLJS 4-2	27	SLJS 26-1	44	SLJS 43-4
11	SLJS 4-3	28	SLJS 26-2	45	SLJS 43-5
12	SLJS 9-1	29	SLJS 29-1	46	SLJS 43-6
13	SLJS 9-2	30	SLJS 29-2	47	SLJS 43-7
14	SLJS 9-3	31	SLJS 29-3	48	SLJS 43-8
15	SLJS 11-2	32	SLJS 29-4	49	SL 525
16	SLJS 13-1	33	SLJS 33-1	50	JS 335
17	SLJS 14-1	34	SLJS 33-2	51	SL 958

The material was sown at Ludhiana on 19th June and at Gurdaspur on 30th June. Genotypes were sown in α – Lattice design with three replications having a row length of 2 meter, two rows per entry and spacing between and within rows was 45 cm and 5 cm,

respectively at both the locations. The recommended agronomic practices were given to raise the crop. The details of the procedure and techniques used are discussed in this chapter.

3.1 Title of the experiment

CHARACTERIZATION OF ADVANCED BREEDING LINES OF SOYBEAN (*Glycine max* (L.) Merrill) THROUGH AGRONOMIC TRAITS AND MOLECULAR MARKERS

3.2 EXPERIMENT NO. 1

Assessment of genetic variability for agronomic traits and estimation of their correlation with seed yield in soybean.

Observations recorded

Observations were recorded on five plants at each of Ludhiana and Gurdaspur locations, respectively. The characters recorded are described below.

3.2.1 Plant Biomass (30 and 60 DAS) (g/plant)

Fresh plants were harvested from field and immediately weighted for fresh weight. After taking fresh weight, the samples were kept in oven at 80° C till it became completely dry and attained a constant weight. After reaching constant weight, dry weight was taken by weighing the sample.

3.2.2 Plant Height at 60 DAS and maturity (cm)

The observations on plant height were taken on five randomly taken plants per genotype with the use of scale and the mean values were calculated for obtaining height per plant in centimeter.

3.2.3 Days to flowering

The days to flowering was calculated by counting the total number of days from date of sowing to 50 per cent flowering for each genotype in each individual replication.

3.2.4 Days to maturity

The number of days to maturity was calculated by counting total number of days from date of sowing to date of attaining physiological maturity i.e the leaves and pods became yellow.

3.2.5 Number of branches per plant

The observation was recorded by counting number of branches on five randomly taken plants at Ludhiana and Gurdaspur locations. The mean was calculated to obtain number of branches per plant.

3.2.6 Number of Nodes per plant

Number of nodes were counted on five randomly taken plants at Ludhiana and Gurdaspur, respectively. Average was calculated to obtain number of nodes per plant.

3.2.7 Number of pods per plant

Total number of pods were recorded on five randomly taken plants at Ludhiana and Gurdaspur, respectively. Average values were calculated to obtain number of pods per plant.

3.2.8 Number of Seeds per pod

Ten pods were randomly picked from each of randomly taken plants. Number of seeds were counted and average values were calculated to obtain number of seeds per pod.

3.2.9 100-Seed weight (g)

Out of the total seed yield from at each location, 100 seeds were counted and the weight was recorded in grams.

3.2.10 Harvest index (%)

The observations on grain yield and biological yield were recorded and harvest index was estimated by using following formula

$$\text{Harvest index (\%)} = (\text{Grain yield} / \text{biological yield}) \times 100$$

3.2.11 Seed yield per plant (g)

Total seeds of five randomly taken plants in Ludhiana and Gurdaspur were weighted. The average value was calculated to obtain seed yield per plant.

3.2.12 Yellow mosaic virus score

Scoring of this character was done on 0-9 scale. Where, 0 indicated highly resistant genotype and 9 indicated highly susceptible one.

3.2.13 Soybean mosaic virus score

Scoring of soybean mosaic virus score was also done at 0-9 scale. Where, 0 used for highly resistant and 9 score was used for highly susceptible genotype.

3.2.14 Protein content (%)

Macro Kjeldahl method was used to determine the protein content of the selected samples (AOAC 2000). First the nitrogen content (N) was estimated and then protein content was estimated by multiplying N with a factor 6.25 (Khalil and Manan 1990).

Principle

The catalyst mixture ($\text{K}_2\text{SO}_4:\text{CuSO}_4:: 10:1$) was used in oxidising the sample with sulphuric acid to form water carbon dioxide. Nitrogen was released as ammonia exist in sulphuric acid solution as ammonium sulphate. Steam distillation of known volume of ammonium sulphate was done with NaOH. As a result ammonia was liberated which was absorbed in excess of boric acid. The amount of ammonia absorbed in boric acid was determined by titrating it with 0.01N HCl by using methyl red-bromocresol green indicator. End point was determined by change in colour from blue to pink.

Reagents

- Digestion mixture (1 part of CuSO_4 : 9 parts of K_2SO_4)
- NaOH (40%)

- Concentrated sulphuric acid
- 0.01N HCl
- 4% boric acid
- Methyl red- bromo cresol green mixed indicator (0.5g Bromo cresol green +0.1 g methyl red) volume made to 100 ml with 95% absolute alcohol

Procedure

Samples were grinded and 0.1g of weighed sample was kept in Kjeldahl digestion tubes. Pinch of digestion mixture and 10 ml of sulphuric acid was added to digestion mixture. Mixture was kept for digestion until clear solution was formed. The clear solution was taken and the volume was made to 25 ml by adding distilled water. A measured aliquot (5ml) was distilled after adding 40 % of 10 ml of sodium hydroxide solution using kjeldahl distillation unit (Kjeltec 1002 FOSS). 75-100 ml of distillate was collected and titrated with 0.01 N HCl in the presence of methyl red-bromo cresol green mixed indicator. The process of titration was continued till the colour changed to light pink to obtain the end point. Nitrogen content was determined by using the formula:

$$\% N = \frac{(X - \text{Blank}) \times 0.00014 \times 25}{\text{Wt. of sample (g)} \times 5}$$

Where X = titre value

$$\% \text{ Protein} = \% N \times 6.25$$

3.2.15 Oil content (%)

Solvent extraction method was used for oil content estimation with the help of instrument, Socsplus AS Series 4.

Principle

Solvent was heated upto its boiling point. Then condensation of vapour was done by using water cooled condenser. Solvent was dripped from the condenser into the thimble and made contact with solid sample. The process of extraction was continued till the solute got dissolved in solvent.

Procedure

The empty weight of a washed beaker was taken (W1 g). One gram sample was weighed (Wgm) and transferred to the thimble. Samples were kept in thimble holder with 100 ml petroleum ether. Beakers were placed between heater and extractor. After sealing the beaker against the Teflon ring, the POWER switch and temperature controller in the control panel was switched on. The boiling temperature was kept near the boiling point of solvent. It was ensured that no condensation was taken place during this stage, so that the time of contact between solvent and sample can be utilized fully. The boiling temperature of temperature control was set at 80°C. Start key was pressed for initiation of boiling. When level of solvent in beaker went down the thimble, at that time the valve was opened. Solvent was flown from

the thimble to remove the oil or fat sticking to the walls of thimble to beaker. Solvents were removed from the beaker. Then the beaker along with the fat was kept inside the oven for some time. Again final weight of beaker was taken (W2gms). Fat % was estimated by using the formula:

$$\% \text{ Fat} = \frac{(W2-W1)}{W} \times 100$$

3.3 STATISTICAL ANALYSIS

Statistical analysis was done separately on data for both the locations viz. Ludhiana and Gurdaspur, respectively by using the mean values. Though experiment was conducted in α – Lattice design and software suggested use of RBD for analysis. Thus data were analyzed as RBD. The ANNOVA is given below:

Table 3.2: Analysis of variance using Randomized Complete Block Design

Source of Variation	d.f	Mean squares	Expected mean squares	F-value
Replications	(r-1)	M_1	$\sigma^2 + g\sigma^2_r$	M_1/M_3
Genotypes	(g-1)	M_2	$\sigma^2 + r\sigma^2_g$	M_2/M_3
Error	(r-1)(g-1)	M_3	σ^2	
Total	(rg-1)			

Where,

r = Number of replication

g = Number of genotypes

σ^2_r = Variance due to replication

σ^2_g = Variance due to genotype

σ^2 = Error variance

For comparisons of variety means, standard error of difference for each character was estimated by using the following formula

$$SE(\text{diff.}) = \sqrt{2EMS/r}$$

Where,

EMS = Error mean square

Critical difference (CD) at 5% level of significance = SE (difference) $\times$ $t_{5\%}$ at error degree of freedom

The components of variance were calculated from the above analysis as

Genotypic variance (σ^2_g) = $(M_2 - M_3)/r$

Environmental variance (σ^2_e) = σ^2/r

Phenotypic variance (σ^2_p) = $\sigma^2_g + \sigma^2_e$

3.3.1 Genotypic coefficient of variance (GCV)

The GCV was calculated by using the following formula

$$GCV = (\sigma_g / \bar{x}) \times 100$$

Where σ_g = genotypic standard deviation

$\bar{x}$ = general mean of population

Similarly, phenotypic coefficient of variance was calculated by using the following formula

$$PCV = (\sigma_p / \bar{x}) \times 100$$

Where, σ_p = Phenotypic standard deviation

$\bar{x}$ = general mean of population

3.3.2 Heritability (h^2)

Heritability was calculated by using Lush's formula (1949).

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

3.3.3 Genetic advance (GA)

It was calculated by using formula given by Miller *et al* (1958).

$$\text{Thus, } GA = h^2 \cdot k \cdot \sigma_p$$

Where

$$h^2 = \sigma^2_g / \sigma^2_p$$

k = Selection differential, at 5% selection intensity, which is 2.06

Then GA as % of mean was calculated as

$$GA \% \text{ of mean} = (GA / \bar{x}) \times 100$$

3.3.4 Correlation coefficients

Phenotypic correlation coefficient, genotypic correlation coefficient were calculated by using method of Dewey and Lu (1959).

$$r_p X Y = \sigma_p X Y / (\sigma^2_p X \cdot \sigma^2_p Y)^{1/2}$$

Where, $r_p X Y$ = Phenotypic correlation coefficient

$\sigma^2_p X$ and $\sigma^2_p Y$ are phenotypic variance of trait X and Y and $\sigma_p X Y$ is phenotypic covariance between traits X and Y.

$$r_g X Y = \sigma_g X Y / (\sigma^2_g X \cdot \sigma^2_g Y)^{1/2}$$

Where,

$r_g X Y$ = Genotypic correlation coefficient

$\sigma^2_g X$ and $\sigma^2_g Y$ are genotypic variance of trait X and Y, respectively.

3.3.5 Path Coefficient Analysis

This was estimated by technique given by Dewey and Lu (1959). Path analysis splits the correlation coefficients into direct and indirect effects of a set of independent variables on the dependent variable.

$$ry_1 = Py_1 + Py_2.r_{12} + Py_3.r_{13} + \dots + Pyn.r_{1n}$$

$$ry_2 = Py_1.r_{12} + Py_2 + Py_3.r_{23} + \dots + Pyn.r_{2n}$$

$$ry_3 = Py_1.r_{13} + Py_2.r_{23} + Py_3 + \dots + Pyn.r_{3n}$$

$$ry_n = Py_1.r_{1n} + Py_2 + Py_3.r_{n3} + \dots + Pyn$$

Where $Py_1, Py_2, Py_3, \dots, Pyn$ are direct effect of variables 1,2,3,.....n on dependent variable 'y'.

$r_{12}, r_{13}, \dots, r_{1n}, \dots, r_{(n-1)}$ are possible correlation coefficients between all independent variables. And $ry_1, ry_2, \dots, ry_n$ are correlation coefficients of independent variables with dependent variable i.e 'y'. The unexplained variation in dependent variable are assumed due to presence of inadequate independent variables. The degree of determination was calculated as

$$\text{Residual Effect} = (1 - R^2)^{1/2}$$

Where, $R^2 = Py_1.r_1 + Py_2.r_2 + \dots + Pyn.r_n$

R^2 is the square of multiple correlation coefficient and is the amount of variation in yield that can be accounted for by the yield component traits used in this study.

3.4 EXPERIMENT NO 2: Genetic diversity in a set of soybean lines and determination of parental contribution of each line.

3.4.1 Diversity analysis through Mahalanobis D^2 statistics

3.4.2 Diversity analysis through molecular markers

Table 3.3: Forty-seven genotypes as given below were selected for diversity analyses.

S. No	Genotypes	S. No	Genotypes	S.No	Genotypes	S.No	Genotypes
1	SL 525	13	SLJS 4-3	25	SLJS 25-1	37	SLJS 37-1
2	JS 335	14	SLJS 9-1	26	SLJS 25-2	38	SLJS 37-1-1
3	SLJS 1-1	15	SLJS 9-2	27	SLJS 25-3	39	SLJS 41-1
4	SLJS 1-2	16	SLJS 9-3	28	SLJS 25-4	40	SLJS 41-2
5	SLJS 1-3	17	SLJS 11-2	29	SLJS 26-2	41	SLJS 43-1
6	SLJS 2-1	18	SLJS 13-1	30	SLJS 29-1	42	SLJS 43-2
7	SLJS 3-1	19	SLJS 14-1	31	SLJS 29-2	43	SLJS 43-3-2
8	SLJS 3-2-1	20	SLJS 14-2	32	SLJS 29-3	44	SLJS 43-5
9	SLJS 3-2-2	21	SLJS 14-3	33	SLJS 29-4	45	SLJS 43-6
10	SLJS 3-3	22	SLJS 23-2	34	SLJS 33-1	46	SLJS 43-7
11	SLJS 4-1	23	SLJS 23-3	35	SLJS 33-2	47	SLJS 43-8
12	SLJS 4-2	24	SLJS 23-4	36	SLJS 34-1		

3.4.1 Diversity analysis through Mahalanobis D^2 method

The average data of Ludhiaba and Gurdaspur locations for each character was used in Mahalanobis D^2 statistics (Mahalanobis 1936) as per method explained by Rao (1952) to

group the genotypes into different clusters. The data was analysed using the equation given below :

$$Dp2 = \sum \sum_p W_{ij} (X_{i1} - X_{i2}) (X_{j1} - X_{j2})$$

Where, W_{ij} = Variance-covariance matrix ($i, j = 1, 2, \dots, p$)

X_{i1} = Sample mean for i^{th} character for first sample

X_{i2} = Sample mean for i^{th} character for 2nd sample

In present $p = (1-20)$ were used to perform the above analysis. For conducting the D^2 analysis, the computer programme, WINDOSTAT 8.1 cluster analysis was used.

3.4.2 Genetic diversity through molecular markers

3.4.2.1 Genomic DNA extraction

Total genomic DNA was extracted from young leaves by using method of Doyle (1987).

- Fresh young leaves of young plants were collected in the morning. The collected leaves were placed in aluminium foil and placed in liquid nitrogen. Fine powder was made from the sample by grinding the leaves with liquid nitrogen in a autoclaved pistle to avoid DNase activity.
- The powdered samples were transfered immediately to a 50 ml autoclaved okridge tube containing 15 ml of pre-warmed (60°C) CTAB extraction buffer and the tubes were kept in water bath at 60°C for one hour.

Table 3.4 Composition of CTAB extraction buffer

Components	Working concentration
CTAB	1.5%
Tris HCL (pH 8.0)	100mM
NaCl	1.4M
EDTA (pH 8.0)	20mM
β-Mercaptoethanol	2%
Polyvinylpyrrolidone (PVP)	2%

- A solution of 15 ml of chloroform: isoamyl alcohol (24:1) was prepared. After incubation step the prepared solution was added to the tube till a dark green emulsion made.
- In the next step tubes were placed in rotary shaker for 45 min and centrifuged @10,000 rpm for 10 min at room temperature.
- After centrifugation the supernatant was tranfered to another clean sterile tube of 50 ml.
- After this 0.8 volume of isopropyl alcohol was added to the tubes and mixed it thoroughly for uniform mixing for precipitation of DNA.
- Then threads like DNA floated up at the top. Then the DNA was hooked by using a

pipette. The hooked DNA was transferred to a clean sterile eppendorf of 2.0 ml . It was rinsed with 70 % alcohol and centrifuged for 5 min to remove the residual salts. This step is known as washing.

- After washing the pelleted DNA was collected and the extra ethanol was dried by turning down the eppendorf on a blotting paper till it became dry.
- After drying, 500-800µl volume of 1X TE (Tris EDTA buffer -10mM Tris HCl, 1mM EDTA , pH 8.0) was added. The tubes were left in room temperature till it became completely dissolved. After complete mixing the eppendorfs were stored at 4°C.

3.4.2.2 Purification of genomic DNA

Before PCR analysis, the isolated DNA must be purified to remove impurities like polyphenols, proteins and polypeptides. Following steps were used for purification of DNA.

- The DNA samples were kept at room temperature to be thawed and equal volume of Tris saturated chloroform: phenol (1:1) was added to it.
- Then centrifugation for 5min at 12000 rpm was done. The aqueous solution was pipetted out and extraction of 2 chloroform: isoamyl alcohol were performed as before. For this, the mixture was centrifuged at 10,000 rpm for 10 min.
- The supernatant was pipette out again and chilled ethanol 2.5 times of the volume and 0.1 volume of 3M sodium acetate were added. The solution was mixed gently and the precipitated DNA was spooled out.
- The DNA samples were washed with 70% of ethanol for two times to remove extra salts then the DNA pellets were dried at room temperature.
- At last, the pellet DNA was dissolved in 1X TE buffer and 5µl of RNase treatment was given to it. It was centrifuged and incubated at 37°C in water bath for 1 hour. The DNA samples were stored at -20°C.

3.4.2.3 Determination of annealing temperature of the primers

Primers bind to the template DNA at annealing temperature. The Mazer's formula (Mazer *et al* 1991) was used to calculate melting temperature (T_m) and annealing temperature was calculated by subtracting 2°C from melting temperature.

$$T_m (^{\circ}\text{C}) = 69.3 + 0.41 (\%G+C) - (650/L)$$

Where,

T_m = Melting temperature (°C), L = Length of primer (bp)

%G+C = Per cent GC (Guanine+ Cytosine) content of primer

3.4.2.4 PCR amplification

DNA was amplified in Polymeric Chain Reaction by using SSR markers following the protocol given by Russel and Sambrook (2000). This protocol is based on heating and cooling principle. First denaturation was happened as result of heating. Then it allowed to anneal at

low temperature. This lower temperature allowed the primer to bind with the template DNA and replication took place in-vitro with the help of enzyme, Taq polymerase. The reaction was occurred in Eppendorf Mastercycler gradient by using 50ng of genomic DNA of each genotype. The final volume was made to 20µl per reaction. The stock and final concentration of different components used in PCR is given below.

Table 3.5 Stock and final concentration of different components used in PCR

Components	Stock Conc	Volume (µl)	Final Conc
Water	- - -	6.6	- - -
PCR buffer	10X*	2.0	1X
MgCl ₂	25mM	1.2	1.5mM
DNTPs	1mM	4.0	200µM
Primer Forward	5 µM	2.0	0.5 µM
Primer Reverse	5µM	2.0	0.5 µM
Taq polymerase	5U/µl	0.2	1 Unit
DNA template	25 ng/ µl	2	50ng
Total		20	

*10X PCR buffer: 10mM Tris HCl, pH 8.3, 50mM KCl, 1.5mM mgCl₂, 0.01% Gelatin

PCR amplification was done by using temperature profile given below. Total of 35 cycles of polymerisation took place for optimum yield of target amplicon.

Table 3.6 Temperature used in PCR

Step	Temperature (°C)	Time (min)	No of cycles
Initial Denaturation	94	4	1
Denaturation	94	1	35
Annealing	49-57	1	
Elongation	72	1	
Final Extension	72	10	1
Hold	4	-	-

3.4.2.5 Scoring of SSR alleles

The total number of alleles was detected in each genotype for each SSR marker. The binary matrix was prepared by using the amplified bands. The score was 1 (band present) and 0 (band absent).

3.4.2.6 Statistical Analysis

Genetic diversity was calculated by using Computer Software – DAR win (Perrier and Jacquemond-Collect 2006). The unweighted pair groups method with arithmetic mean

(UPGMA) method was adopted to generate dendrogram. Polymorphic Information Content was calculated by taking the relative frequencies of alleles into consideration. PIC values was calculated by using the formula

$$PIC = 1 - \sum x_i^2$$

Where x_i is the relative frequency of the i^{th} allele of the SSR loci

CHAPTER IV

RESULTS AND DISCUSSION

In this chapter the results of the experiment “Characterization of advanced breeding line in soybean [*Glycine max* (L.)] through agronomic traits and molecular markers” has been discussed. The population consisting of 51 genotypes were subjected to analysis of variance for seed yield and other agronomic traits. The results have been described under the following sub headings:

4.1 Analysis of variance and mean performance

4.2 Genotypic coefficient of variation (GCV), Phenotypic coefficient of variation (PCV), heritability (h^2) and genetic advance (GA)

4.3 Correlation analysis

4.4 Path coefficient analysis

4.5 Genetic diversity analysis through Mahalanobis D^2 statistics

4.6 Genetic diversity analysis through molecular markers

4.1 Analysis of variance and mean performance

The results of analysis of variance for different morphological and quality characters are presented separately for Ludhiana (Table 4.1a) and Gurdaspur (Table 4.1b) and mean values for various characters are given in 4.2. The significant values indicate the presence of high variability for different characters except for seeds per pods at Ludhiana location. The result of mean performance of different traits are described below.

4.1.1 Plant biomass (g/plant)

The observation on plant biomass were taken at both the locations viz. Ludhiana and Gurdaspur at 30, 45, 60 days after sowing. At Ludhiana, the highest biomass observed at 30 DAS was 3.3g for genotype, SLJS-3-2-1 followed by 3.2g for genotype, SLJS 23-2 and minimum value was obtained for genotype, SLJS43-3-2 i.e 1.5g. The overall range was from 1.5g to 3.3g and the overall mean was 2.1g while at Gurdaspur location, the highest biomass at 30 DAS was obtained for three genotypes, SL 958, SLJS 33-1 and SLJS 3-1 i.e 4.1g and minimum value was obtained for genotypes, SLJS37-1 i.e 1.6g. The overall mean for the character was 2.9g. In case of biomass at 45 DAS, the highest value was obtained for genotype, SLJS 3-2-2 (12.2g) and minimum was for genotype, SL 525 i.e 6.2 at Ludhiana location while the maximum value was 13.6g for genotype, SLJS 9-3 and minimum was 4.4g for genotype, SLJS 29-2 at Gurdaspur location. For biomass at 60 DAS, the variability was more at Gurdaspur location (6.9-23.9g) then Ludhiana location (10.4-22.5g). The overall mean was 13.2g for Gurdaspur and 17.7g for Ludhiana location. For Ludhiana location highest value of 22.5g was recorded for genotype, SLJS 1-2 and in case of Gurdaspur it was 23.9g for genotype, SLJS9-3.

Table : 4.1(a) Mean squares for different characters in soybean at Ludhiana location

Source of variation	df	Fresh weight at 30 DAS (g)	Dry weight at 30 DAS (g)	Fresh weight at 45 DAS (g)	Dry weight at 45DAS (g)	Fresh weight at 60 DAS (g)	Dry weight at 60 DAS (g)	Plant height at 60 DAS (cm)	Plant height at maturity (cm)	Days to flowering	Days to maturity
Replication	2	0.23	0.49	197.65	25.45	1042.81	87.46	70.60	67.36	0.47	3.58
Treatment	50	8.75**	0.49**	121.58**	7.15**	468.81**	29.09**	159.21**	320.40**	8.56**	7.13**
Error	100	0.94	0.16	41.16	2.03	158.10	7.87	21.31	27.35	0.33	0.19

Source of variation	df	Branches per plant	Nodes per plant	Pods per plant	Pods per node	Seeds per pod	100-seed weight (g)	Harvest index (%)	Seed yield per plant (g)	Protein content (%)	Oil content (%)
Replication	2	0.82	5.71	147.62	3.17	0.00	0.08	149.69	9.23	1.12	1.32
Treatment	50	3.39**	7.58**	1666.05**	6.99**	0.02	2.23**	100.14**	100.80**	2.50**	2.55**
Error	100	0.53	2.37	68.50	0.78	0.03	0.75	16.00	5.04	0.14	0.14

* Significant at 5%

** Significant at 1%

Table : 4.1 (b) Mean squares for different characters in soybean at Gurdaspur location

Source of variation	df	Fresh weight at 30 DAS (g)	Dry weight at 30 DAS (g)	Fresh weight at 45 DAS (g)	Dry weight at 45DAS (g)	Fresh weight at 60 DAS (g)	Dry weight at 60 DAS (g)	Plant height at 60 DAS (cm)	Plant height at maturity (cm)	Days to flowering	Days to maturity
Replication	2	23.99	13.69	151.99	6.75	820.13	44.73	78.89	58.68	2.12	8.01
Treatment	50	9.10**	1.42**	112.24**	9.29**	440.42**	35.53**	377.71**	355.04**	4.15**	23.45**
Error	100	2.46	0.11	9.81	1.23	35.39	4.28	47.79	20.79	0.89	0.91
		35.55	15.22	274.04	17.27	1295.94	84.54	504.39	434.51	7.16	32.37

Source of variation	df	Branches per plant	Nodes per plant	Pods per plant	Pods per node	Seeds per pod	100- seed wt (g)	Harvest index (%)	Seed yield per plant (g)	Protein content (%)	Oil content (%)
Replication	2	0.11	24.46	117.86	0.10	0.11	12.50	9.84	12.98	0.46	0.98
Treatment	50	1.00**	15.30**	319.21**	0.38**	0.03**	1.82**	30.35**	99.23**	4.26**	1.53**
Error	100	0.09	3.10	30.38	0.10	0.01	0.28	6.24	10.12	0.41	0.32
		1.20	42.86	467.45	0.58	0.15	14.60	46.43	122.33	5.13	2.83

* Significant at 5%, ** Significant at 1%

4.1.2 Plant height (cm)

Plant height is considered as an important character for estimation of variability. In this study the results for plant height was differed significantly at both the locations. The observation for this trait was recorded at 60 days after sowing and at maturity. For first observation i.e 60 DAS the plant height of 90 cm was observed as maximum at Ludhiana for genotype, SLJS 23-4 followed by genotype, SL958 (79.1 cm) and genotype, SLJS 23-3 (78.8 cm). The minimum value of 54.5 cm was obtained from genotype, SLJS-23-2. At Gurdaspur, maximum plant height was possessed by genotype, JS335 (99.0 cm) followed by SLJS-29-4 (90.7cm) and minimum height was possessed by SLJS-43-4 (46.0 cm). In case of second observation i.e plant height at maturity, mean plant height obtained was 74.0 cm and 62.8 cm for Ludhiana and Gurdaspur locations, respectively. At Ludhiana, maximum height was 107.0 cm for genotype, SLJS 23-3 followed by genotype, SLJS 23-4 (98.8 cm) and minimum plant height was observed for genotype, JS335 (39.9 cm). At Gurdaspur, maximum plant height at maturity was recorded by JS335 (107.1cm) followed by genotype, SLJS-25-2 (82.4 cm). Minimum height was obtained by genotype, SLJS 43-3-2 (41.4 cm). Ganesamoorthy and Seshasri (2002) and Gowande *et al* (2002) observed moderate variability within the soybean genotypes for plant height but Karasu *et al* (2009) and Prakash *et al* (1966) concluded high variation of plant height from their experiment.

4.1.3 Days to 50% flowering

The results for this trait differed significantly at both the locations. At Ludhiana, maximum value for this trait was obtained from genotype, SLJS 14-1 (64.3 days) followed by genotype, SLJS-41-2 (63 days). The genotype, SLJS-25-1 took minimum i.e 57 days to flower. The mean value for this character at Ludhiana was 60.5 days. At Gurdaspur, mean value for 50% flowering was 59.3 days. Maximum days to flower (61.3 days) was taken by four genotypes viz. SLJS-4-3, SLJS 29-3, SLJS 29-1 and SLJS 43-3-2. Genotype, SLJS 25-3 took minimum days (57 days) for 50% flowering. Similar results were observed for days to 50% flowering from experiment conducted by Pushpendra and Ram (1987).

4.1.4 Days to maturity

Highly significant results were obtained for this trait at both the locations. At Ludhiana, the days to maturity varied from 124.7 to 132.3 days. Maximum days to maturity were taken by genotype, SL958 (132.3 days) followed by SL525 (130.7 days). The genotype, SLJS 26-2 took minimum days i.e 124.7 days for maturity. At Gurdaspur, maximum days to maturity was obtained by genotype, SLJS-29-3 (119 days) followed by SLJS-29-4 (116 days). Minimum days to mature were taken by genotype, SLJS-9-2 (105.7 days).

4.1.5 Number of branches per plant

Significant variation among genotypes was observed at both the locations for number of branches per plant. At Ludhiana, maximum mean of three replications was observed for

Table 4.2 (a) Mean values for fresh weight and dry weight with respect to different soybean genotypes at 30 and 45 Days after sowing

Sl. No	Genotypes	Fresh weight at 30DAS (g)		Dry weight at 30 DAS (g)		Fresh weight at 45 DAS (g)		Dry weight at 45DAS (g)	
		Ludhiana	Gurdaspur	Ludhiana	Gurdaspur	Ludhiana	Gurdaspur	Ludhiana	Gurdaspur
1	SLJS 1-1	7.7	10.7	1.8	3.8	38.5	27.1	10.4	7.7
2	SLJS 1-2	8.4	8.2	1.7	2.7	40.9	22.1	12.1	7.0
3	SLJS 1-3	12.6	10.8	1.9	3.5	40.0	41.7	7.7	10.9
4	SLJS 2-1	10.5	8.0	2.1	2.3	47.4	23.3	11.7	6.8
5	SLJS 3-1	11.5	11.7	1.8	4.1	29.2	16.3	7.9	5.9
6	SLJS 3-2-1	14.6	9.7	3.3	3.0	33.0	18.7	8.6	6.0
7	SLJS 3-2-2	12.8	10.8	2.4	3.2	44.9	38.3	12.2	13.3
8	SLJS 3-3	13.1	9.1	2.7	3.5	32.2	20.3	8.0	6.3
9	SLJS 4-1	8.3	9.0	1.5	2.9	40.4	27.3	10.4	7.5
10	SLJS 4-2	11.5	8.6	1.6	2.7	40.9	21.9	10.8	6.3
11	SLJS 4-3	10.4	7.4	1.6	3.7	37.1	34.3	7.4	10.0
12	SLJS 9-1	11.1	11.4	2.2	4.0	37.2	39.1	11.0	10.1
13	SLJS 9-2	10.9	8.1	2.1	2.2	41.7	30.2	11.2	8.3
14	SLJS 9-3	13.1	6.7	2.2	3.3	34.4	43.1	9.6	13.6
15	SLJS 11-2	11.9	10.4	2.0	3.4	40.8	38.3	11.2	9.9
16	SLJS 13-1	11.6	9.1	1.9	2.1	39.9	19.8	10.3	11.4
17	SLJS 14-1	12.5	8.2	2.2	2.5	37.4	20.0	10.3	6.2
18	SLJS 14-2	12.7	9.5	2.4	2.2	40.3	27.2	9.4	7.3
19	SLJS 14-3	12.6	8.9	2.9	3.1	39.7	23.1	10.4	6.6
20	SLJS 23-2	13.9	7.4	3.1	2.7	33.5	20.8	9.1	7.5
21	SLJS 23-3	11.3	10.4	1.9	3.5	38.3	26.2	11.5	7.8
22	SLJS 23-4	12.0	12.6	2.0	3.2	41.9	34.1	8.4	9.4
23	SLJS 25-1	13.3	9.7	2.3	2.6	42.3	21.4	12.1	6.9
24	SLJS 25-2	14.7	11.1	2.4	2.5	47.0	26.1	10.8	7.8
25	SLJS 25-3	11.8	10.0	2.2	3.5	36.8	25.6	10.0	9.2
26	SLJS 25-4	11.5	9.0	1.7	2.8	23.9	23.7	10.6	7.7
27	SLJS 26-1	9.5	7.3	1.8	1.7	26.0	26.5	8.4	8.5

Contd.....

Table 4.2(a) Contd.....

Sl. No	Genotypes	Fresh weight at 30DAS (g)		Dry weight at 30 DAS (g)		Fresh weight at 45 DAS (g)		Dry weight at 45DAS (g)	
		Ludhiana	Gurdaspur	Ludhiana	Gurdaspur	Ludhiana	Gurdaspur	Ludhiana	Gurdaspur
28	SLJS 26-2	13.1	11.2	2.3	2.9	35.4	23.8	11.0	7.6
29	SLJS 29-1	10.7	9.8	2.0	3.0	31.4	21.9	8.7	5.9
30	SLJS 29-2	12.0	6.7	2.4	1.8	41.7	15.3	10.6	4.4
31	SLJS 29-3	12.2	12.1	2.3	3.6	46.0	16.9	11.8	7.2
32	SLJS 29-4	11.8	10.0	2.3	2.9	37.1	27.3	10.9	8.8
33	SLJS 33-1	12.7	11.8	1.8	4.1	32.2	31.0	8.3	7.7
34	SLJS 33-2	11.5	8.6	2.0	2.0	41.3	26.5	11.3	8.0
35	SLJS 34-1	11.7	6.5	1.9	1.8	45.9	26.6	11.4	10.3
36	SLJS 37-1	12.5	8.4	2.3	1.6	47.2	20.1	12.1	6.7
37	SLJS 37-1-1	9.2	8.9	1.8	2.8	32.2	23.9	8.4	7.8
38	SLJS 41-1	6.5	8.0	1.5	2.4	29.5	25.4	7.3	8.0
39	SLJS 41-2	8.3	12.4	1.5	3.6	31.8	24.2	10.0	8.6
40	SLJS 43-1	10.5	10.7	1.8	2.8	44.8	21.8	11.4	7.3
41	SLJS 43-2	11.6	6.8	2.0	3.2	41.2	22.2	10.1	6.7
42	SLJS 43-3-1	10.4	6.6	2.1	2.0	33.3	24.0	8.7	7.5
43	SLJS 43-3-2	10.6	6.4	1.5	2.1	44.3	25.4	11.1	8.6
44	SLJS 43-4	11.1	6.3	2.6	1.7	29.5	26.3	8.4	8.1
45	SLJS 43-5	10.5	7.6	1.5	2.2	38.8	22.7	10.9	6.4
46	SLJS 43-6	11.5	8.7	2.1	2.9	44.2	27.5	11.3	7.4
47	SLJS 43-7	13.7	10.5	1.9	3.0	38.1	24.9	8.8	8.5
48	SLJS 43-8	10.3	10.5	1.6	2.2	26.0	27.3	6.9	8.7
49	SL 525	11.3	11.3	2.0	3.6	20.6	24.3	6.2	8.1
50	JS 335	9.1	11.0	2.0	2.9	34.7	25.3	10.2	7.0
51	SL 958	11.9	10.6	2.7	4.1	29.6	26.6	8.1	9.3
	Mean	11.4	9.3	2.1	2.9	37.3	25.8	9.9	8.0
	Range	6.5-14.7	6.3-12.6	1.5-3.3	1.6-4.1	20.6-47.4	15.3-43.1	6.2-12.2	4.4-13.6
	CD (5%)	1.57	2.54	0.64	0.53	10.38	5.07	2.30	1.79

Table 4.2 (b) Mean values for fresh weight and dry weight at 60 DAS and plant height at 60 DAS and maturity with respect to soybean genotypes.

Sl. No	Genotypes	Fresh weight at 60 DAS (g)		Dry weight 60 DAS (g)		Plant height at 60 (cm)		Plant height at maturity (cm)	
		Ludhiana	Gurdaspur	Ludhiana	Gurdaspur	Ludhiana	Gurdaspur	Ludhiana	Gurdaspur
1	SLJS 1-1	69.3	43.5	19.0	11.5	61.6	79.7	67.7	64.1
2	SLJS 1-2	73.5	36.0	22.5	11.2	57.3	54.3	62.5	58.0
3	SLJS 1-3	67.4	72.4	13.5	18.2	56.7	61.7	63.3	59.0
4	SLJS 2-1	84.3	38.6	21.4	11.2	60.6	68.3	69.2	59.7
5	SLJS 3-1	46.8	20.9	14.0	8.0	57.8	71.3	80.3	66.3
6	SLJS 3-2-1	51.4	27.6	13.8	8.8	69.4	79.7	74.5	65.4
7	SLJS 3-2-2	76.9	65.7	21.9	23.3	64.1	71.0	76.0	68.0
8	SLJS 3-3	51.3	31.3	13.1	9.1	57.2	82.7	58.5	63.3
9	SLJS 4-1	72.5	45.6	19.4	12.1	65.2	67.3	77.5	53.6
10	SLJS 4-2	70.2	35.1	19.9	9.7	63.2	81.0	76.5	66.1
11	SLJS 4-3	63.8	61.2	13.3	16.2	72.9	85.7	80.7	61.0
12	SLJS 9-1	63.3	66.8	19.8	16.1	63.3	79.0	73.2	70.4
13	SLJS 9-2	72.5	52.2	20.2	14.3	59.1	57.3	70.8	53.5
14	SLJS 9-3	55.7	79.3	16.9	23.9	64.4	68.0	67.7	44.5
15	SLJS 11-2	69.6	66.2	20.4	16.3	63.5	51.7	81.5	50.8
16	SLJS 13-1	68.1	30.4	18.6	20.6	64.8	63.0	79.2	57.3
17	SLJS 14-1	62.3	31.8	18.4	9.9	73.5	57.3	83.5	48.7
18	SLJS 14-2	67.9	44.8	16.5	12.5	56.3	63.3	67.3	67.1
19	SLJS 14-3	66.8	37.2	18.0	10.0	63.3	63.7	70.3	69.5
20	SLJS 23-2	53.1	34.1	15.0	12.2	54.5	62.0	79.7	54.0
21	SLJS 23-3	65.3	41.9	21.1	12.0	78.8	66.7	107.0	72.0
22	SLJS 23-4	71.7	55.6	14.9	15.5	90.0	86.3	98.8	78.8
23	SLJS 25-1	71.2	33.1	22.0	11.2	64.0	67.7	69.8	66.1
24	SLJS 25-2	79.3	41.0	19.2	13.1	58.0	75.7	80.5	82.4
25	SLJS 25-3	61.8	41.2	17.8	14.9	64.6	83.3	79.3	68.7
26	SLJS 25-4	36.2	38.4	19.6	12.5	56.4	73.3	57.8	77.0

Contd.....

Table 4.2 (b) Contd.....

Sl. No	Genotypes	Fresh weight at 60 DAS (g)		Dry weight 60 DAS (g)		Plant height at 60 (cm)		Plant height at maturity (cm)	
		Ludhiana	Gurdaspur	Ludhiana	Gurdaspur	Ludhiana	Gurdaspur	Ludhiana	Gurdaspur
27	SLJS 26-1	42.5	45.6	15.0	15.2	55.6	60.7	59.6	65.2
28	SLJS 26-2	57.7	36.3	19.6	12.3	73.6	64.7	76.6	52.4
29	SLJS 29-1	52.0	33.9	15.4	8.8	55.0	63.0	73.3	49.2
30	SLJS 29-2	71.2	24.0	18.8	6.9	70.1	56.7	78.5	59.7
31	SLJS 29-3	79.8	21.6	21.1	10.8	68.2	56.0	76.8	65.4
32	SLJS 29-4	62.3	44.5	19.5	14.6	65.0	90.7	70.3	73.1
33	SLJS 33-1	51.7	50.2	14.8	11.1	61.3	71.0	78.7	66.5
34	SLJS 33-2	71.0	44.4	20.6	13.8	63.2	70.3	69.0	54.9
35	SLJS 34-1	80.1	46.5	21.0	18.7	60.2	65.7	64.8	66.9
36	SLJS 37-1	81.9	31.7	21.9	11.8	62.9	62.7	65.2	52.7
37	SLJS 37-1-1	55.0	38.8	15.1	12.8	70.2	49.3	73.2	57.1
38	SLJS 41-1	52.5	42.8	13.1	13.6	66.4	65.3	78.0	63.6
39	SLJS 41-2	55.2	35.9	18.5	13.5	65.7	61.3	80.7	71.0
40	SLJS 43-1	79.0	33.0	20.9	11.8	57.0	77.3	74.2	65.1
41	SLJS 43-2	70.8	37.5	18.2	10.2	68.2	63.3	86.2	66.5
42	SLJS 43-3-1	56.1	41.4	15.2	12.8	60.2	57.3	63.3	56.9
43	SLJS 43-3-2	77.9	44.3	20.6	14.9	78.0	56.3	79.2	41.4
44	SLJS 43-4	47.8	46.3	14.2	14.4	58.7	46.0	77.5	47.5
45	SLJS 43-5	67.1	37.8	20.3	10.6	67.9	47.7	71.7	58.7
46	SLJS 43-6	77.3	46.3	20.6	11.8	65.6	71.3	70.5	63.2
47	SLJS 43-7	62.5	39.3	15.6	14.0	71.7	67.3	74.8	59.6
48	SLJS 43-8	41.8	44.0	12.2	15.0	55.7	78.3	73.3	75.7
49	SL 525	29.8	37.2	10.4	12.6	70.7	70.3	73.5	65.6
50	JS 335	60.2	39.6	18.3	11.0	61.0	99.0	39.9	107.1
51	SL 958	47.3	42.6	13.5	14.4	79.1	61.7	91.5	51.1
	Mean	63.2	42.3	17.7	13.2	64.5	67.7	74.0	62.8
	Range	29.8-84.3	20.9-79.3	10.4-22.5	6.9-23.9	54.5-90	46.0-99.0	39.9-107.0	41.4-107.1
	CD (5%)	20.35	9.63	4.54	3.35	7.47	11.19	8.46	7.38

genotype, SLJS-26-1 (7.7) followed by SLJS -14-1 (7.0). Minimum mean of three replication was for genotype, SLJS -4-3 (1.5). The overall mean obtained for branches per plant was 4.9. At Gurdaspur location, maximum value for mean of three location was 4.5 branches per plant for genotype, JS335 followed by genotype, SLJS -43-6 (4.3) and minimum value of number of branches was obtained from genotype, SLJS 4-3 (1.7) with overall mean of 3.1 branches per plant. Similarly, high variation for number of branches per plant was resulted in F₂ and F₃ generation of soybean crosses (Harway, 1956)

4.1.6 Number of nodes per plant

The results for this trait were highly significant for Ludhiana and Gurdaspur. In Ludhiana location the genotype, SLJS 3-1 showed maximum value (18.1) followed by genotype, SLJS 23-4 (17.4) and SL958 (17.3) and minimum value was exhibited by genotype, SLJS 41-1 (8.9). The variability was present in the range of 8.9 to 18.1 with overall mean of 15.1. At Gurdaspur, variability for number of nodes per plant was more than Ludhiana and it was in the range of (17.7-27.3) with the overall mean of 22.6. The maximum value was 27.3 for genotype, SLJS 33-1 followed by genotype, SLJS 23-4 (26.8). Minimum value for this character was for genotype, SLJS 4-3 (17.7). Weatherspoon and Bentz (1934) and Chikale *et al* (1992) confirm the findings of present study for this character.

4.1.7 Number of pods per plant

Number of pods per plant is the main yield component and plays major role in yield determination. The estimated mean value of three replications is presented in table no 4.2 (d). At Ludhiana location, the genotype, SLJS 11-2 had maximum number of pods per plant i.e 126.8 followed by genotype, SLJS 4-1 (124.6) and SLJS 26-2 (121.1). The genotype, JS335 had minimum number of pods per plant i.e 18.6. The range of variability was 18.6 to 126.8 with mean of 78.8 at Ludhiana. At Gurdaspur location, maximum number of pods per plant was possessed by the genotype, SLJS 1-1 (111.4) followed by genotype SLJS 29-2 (86.8). The minimum number of pods per plant was observed for genotype SLJS 11-2 (48.9). The range of number of pods per plant was 48.9-111.4 with mean of 71.0. Similar findings were observed by Rajput *et al* (1987) and Jaylal (1994) in their earlier study on soybean genotype.

4.1.8 Number of pods per node

This trait was estimated on the basis of number of pods per plant and number of nodes per plant. The detailed performance of the character is presented in table 4.2 (d). At Ludhiana location, maximum value for pods per node (7.1) was observed for genotype, SLJS 11-2 followed by 3.4 for genotype, SLJS 26-2 and SLJS 9-3. Minimum number of pods per node i.e 1.2 were recorded for genotype, JS335. The values for number of pods per node varied from 1.2 to 7.1 with overall mean of 4.2. At Gurdaspur location, maximum value of pods per node i.e 4.4 was obtained in genotype, SLJS 1-1 followed by 3.9 in genotype, SLJS 43-3-2 and 3.8 in genotype, SLJS 41-2. Minimum value for this trait was obtained for

Table 4.2 (c) Mean values for Days to 50 % flowering, days to maturity, branches per plant and nodes per plant with respect to soybean genotypes

Sl. No	Genotypes	Days to flowering		Days to maturity		Branches per plant		Nodes per plant	
		Ludhiana	Gurdaspur	Ludhiana	Gurdaspur	Ludhiana	Gurdaspur	Ludhiana	Gurdaspur
1	SLJS 1-1	60.0	59.7	130.0	112.0	5.1	3.7	13.0	26.0
2	SLJS 1-2	60.3	59.0	128.3	110.3	5.0	3.4	12.5	21.3
3	SLJS 1-3	58.7	58.3	129.0	111.0	3.9	2.5	12.5	18.3
4	SLJS 2-1	58.0	59.7	129.7	110.3	4.9	2.7	14.6	20.1
5	SLJS 3-1	62.0	59.0	129.0	110.0	5.1	2.3	18.1	22.7
6	SLJS 3-2-1	62.7	58.7	130.0	107.7	4.5	3.3	17.0	22.1
7	SLJS 3-2-2	62.7	57.3	130.0	112.0	2.5	3.3	15.0	23.2
8	SLJS 3-3	60.0	60.7	126.3	107.3	5.7	2.5	15.5	20.1
9	SLJS 4-1	61.7	59.0	129.0	109.7	5.1	2.5	16.9	21.1
10	SLJS 4-2	61.0	60.0	126.7	108.0	4.0	2.1	15.6	22.1
11	SLJS 4-3	57.3	61.3	128.7	111.0	1.5	1.7	13.8	17.7
12	SLJS 9-1	58.0	59.3	128.7	106.7	5.3	3.1	14.8	24.4
13	SLJS 9-2	58.0	57.3	129.3	105.7	4.5	3.2	12.6	22.7
14	SLJS 9-3	60.3	59.3	130.0	108.0	5.8	3.4	12.5	22.6
15	SLJS 11-2	62.0	58.3	129.7	106.0	4.7	3.0	15.6	18.5
16	SLJS 13-1	62.7	59.0	129.7	107.0	4.4	3.5	16.4	23.2
17	SLJS 14-1	64.3	58.0	130.0	112.0	7.0	3.3	15.7	21.4
18	SLJS 14-2	60.7	59.0	126.7	110.7	4.6	2.8	14.6	24.8
19	SLJS 14-3	62.0	58.7	130.3	107.0	6.1	3.4	15.2	22.6
20	SLJS 23-2	58.3	58.3	129.7	111.0	5.1	3.3	15.9	22.5
21	SLJS 23-3	60.0	58.0	128.0	111.3	4.2	3.3	16.3	23.7
22	SLJS 23-4	61.3	58.3	126.3	110.0	4.7	4.2	17.4	26.8
23	SLJS 25-1	57.0	58.0	127.0	109.3	4.8	3.2	16.3	24.1
24	SLJS 25-2	59.0	58.0	128.7	108.3	3.4	3.5	15.4	24.9
25	SLJS 25-3	59.0	57.0	129.0	110.0	4.1	3.0	15.5	23.1
26	SLJS 25-4	62.7	58.7	128.7	109.7	5.7	2.4	14.4	18.1

Contd....

Table 4.2 (c) Contd.....

Sl. No	Genotypes	Days to flowering		Days to maturity		Branches per plant		Nodes per plant	
		Ludhiana	Gurdaspur	Ludhiana	Gurdaspur	Ludhiana	Gurdaspur	Ludhiana	Gurdaspur
27	SLJS 26-1	61.3	58.3	124.7	109.7	7.7	2.5	15.5	18.0
28	SLJS 26-2	60.0	58.7	124.7	113.0	4.9	3.2	16.1	22.7
29	SLJS 29-1	61.7	61.3	129.3	114.7	4.1	3.3	15.7	22.5
30	SLJS 29-2	62.7	60.7	127.0	112.7	5.1	3.5	16.8	24.5
31	SLJS 29-3	62.7	61.3	126.3	119.0	4.8	3.5	15.0	23.9
32	SLJS 29-4	61.3	59.0	126.7	116.0	3.8	2.5	15.2	23.5
33	SLJS 33-1	60.0	58.7	127.0	114.0	5.5	3.4	14.5	27.3
34	SLJS 33-2	58.0	57.7	129.0	115.0	3.8	3.2	12.9	22.3
35	SLJS 34-1	61.0	58.7	129.7	113.0	5.2	3.3	14.9	24.8
36	SLJS 37-1	60.0	59.3	130.0	113.0	4.2	3.7	16.4	24.2
37	SLJS 37-1-1	58.3	61.0	130.0	112.0	6.7	2.7	16.0	23.9
38	SLJS 41-1	62.7	60.0	130.0	110.3	5.3	2.5	8.9	20.9
39	SLJS 41-2	63.0	61.0	129.3	113.0	3.4	2.3	15.8	19.9
40	SLJS 43-1	61.0	60.7	129.7	112.0	5.5	3.5	13.6	26.6
41	SLJS 43-2	62.0	59.7	129.0	113.7	6.3	2.4	14.4	20.5
42	SLJS 43-3-1	60.3	60.0	129.3	112.7	4.8	2.5	14.4	23.2
43	SLJS 43-3-2	60.0	61.3	129.7	113.7	6.0	3.9	14.8	21.6
44	SLJS 43-4	60.0	60.0	129.3	112.7	5.1	2.7	15.2	22.3
45	SLJS 43-5	58.7	60.0	130.0	115.0	5.1	3.5	14.4	25.1
46	SLJS 43-6	61.0	58.7	128.7	113.0	5.7	4.3	17.1	20.3
47	SLJS 43-7	61.0	59.3	129.0	114.3	5.1	2.7	15.2	22.3
48	SLJS 43-8	60.3	58.0	130.0	110.0	5.0	2.6	14.5	22.4
49	SL 525	60.0	61.0	130.7	113.0	6.0	2.5	15.0	25.4
50	JS 335	59.3	61.0	130.3	115.0	4.6	4.5	15.3	23.5
51	SL 958	62.0	60.0	132.3	113.3	6.3	3.4	17.3	22.9
	Mean	60.5	59.3	128.8	111.3	4.9	3.1	15.1	22.6
	Range	57.0-64.3	57.0-61.3	124.7-132.3	105.7-119	1.5-7.7	1.7-4.5	8.9-18.1	17.7-27.3
	CD (5%)	0.93	1.53	0.70	1.54	1.18	0.49	2.49	2.85

Table 4.2 (d) Mean values for pods per plant, pods per node, seeds per pod and 100- seed weight with respect to soybean genotypes

Sl. No	Genotypes	Pods per plant		Pods per node		Seeds per pod		100 seed wt. (g)	
		Ludhiana	Gurdaspur	Ludhiana	Gurdaspur	Ludhiana	Gurdaspur	Ludhiana	Gurdaspur
1	SLJS 1-1	51.1	111.4	3.3	4.4	2.6	2.7	10.0	10.5
2	SLJS 1-2	69.9	72.0	5.1	3.4	2.6	2.6	7.7	10.6
3	SLJS 1-3	82.2	55.9	6.0	3.0	2.5	2.6	8.7	11.0
4	SLJS 2-1	62.6	56.2	3.4	2.8	2.6	2.6	8.7	10.9
5	SLJS 3-1	55.9	60.8	1.8	2.6	2.7	2.8	10.7	11.0
6	SLJS 3-2-1	74.1	78.5	3.1	3.6	2.6	2.8	9.3	10.7
7	SLJS 3-2-2	71.2	70.9	3.8	3.1	2.5	2.6	10.0	10.9
8	SLJS 3-3	70.1	56.4	3.5	2.8	2.6	2.7	9.3	11.1
9	SLJS 4-1	124.6	64.6	6.1	3.1	2.6	2.7	7.7	8.5
10	SLJS 4-2	65.9	63.9	3.3	2.9	2.6	2.6	8.7	9.1
11	SLJS 4-3	53.6	64.8	3.1	3.7	2.5	2.6	8.7	11.1
12	SLJS 9-1	80.5	79.4	4.5	3.3	2.7	2.7	8.0	11.9
13	SLJS 9-2	39.2	76.1	2.6	3.4	2.5	2.7	9.7	10.3
14	SLJS 9-3	86.0	68.8	6.4	3.0	2.5	2.7	9.3	12.0
15	SLJS 11-2	126.8	48.9	7.1	2.6	2.5	2.8	8.0	8.9
16	SLJS 13-1	85.5	72.9	3.9	3.2	2.6	2.8	10.0	10.8
17	SLJS 14-1	77.6	72.9	4.0	3.5	2.5	2.7	8.7	10.2
18	SLJS 14-2	90.0	76.1	5.3	3.1	2.5	2.8	7.7	10.8
19	SLJS 14-3	62.9	63.3	3.1	2.8	2.6	2.7	9.3	11.9
20	SLJS 23-2	87.3	69.0	4.4	3.1	2.5	2.8	8.7	10.0
21	SLJS 23-3	85.6	67.2	4.1	2.8	2.5	2.8	7.3	10.8
22	SLJS 23-4	105.9	82.8	4.8	3.1	2.6	2.9	8.0	12.3
23	SLJS 25-1	88.1	76.7	4.3	3.2	2.5	2.7	8.7	11.7
24	SLJS 25-2	60.1	75.9	2.8	3.1	2.6	2.7	8.0	11.6
25	SLJS 25-3	50.5	67.0	2.3	2.9	2.5	2.7	8.0	10.4
26	SLJS 25-4	98.7	58.3	6.0	3.2	2.5	2.6	8.0	11.5

Contd.....

Table 4.2 (d) Contd.....

Sl. No	Genotypes	Pods per plant		Pods per node		Seeds per pod		100 -seed wt. (g)	
		Ludhiana	Gurdaspur	Ludhiana	Gurdaspur	Ludhiana	Gurdaspur	Ludhiana	Gurdaspur
27	SLJS 26-1	54.7	60.3	2.5	3.4	2.7	2.7	8.7	10.2
28	SLJS 26-2	121.1	73.7	6.4	3.2	2.7	2.8	8.0	12.2
29	SLJS 29-1	59.2	66.5	2.8	3.0	2.5	2.8	8.7	11.5
30	SLJS 29-2	97.7	86.8	4.7	3.5	2.7	2.8	7.3	11.3
31	SLJS 29-3	57.4	72.2	2.9	3.1	2.4	2.9	7.3	11.7
32	SLJS 29-4	87.2	74.8	4.9	3.2	2.6	2.8	7.3	11.0
33	SLJS 33-1	88.2	77.1	5.4	2.8	2.4	2.8	7.3	11.8
34	SLJS 33-2	78.2	80.4	5.4	3.6	2.5	2.8	6.7	10.9
35	SLJS 34-1	84.2	76.3	4.7	3.1	2.5	2.7	8.0	10.9
36	SLJS 37-1	76.3	74.1	3.5	3.1	2.5	2.8	8.7	11.0
37	SLJS 37-1-1	88.5	56.1	4.4	2.4	2.7	2.8	10.0	11.0
38	SLJS 41-1	35.3	57.4	4.5	2.8	2.7	2.8	7.3	11.3
39	SLJS 41-2	83.9	75.7	4.2	3.8	2.6	2.9	8.7	10.2
40	SLJS 43-1	88.9	71.5	5.8	2.7	2.6	2.8	8.7	11.3
41	SLJS 43-2	96.9	57.7	5.8	2.8	2.7	2.9	8.0	11.1
42	SLJS 43-3-1	78.5	84.5	4.5	3.6	2.6	2.7	8.0	10.7
43	SLJS 43-3-2	86.3	82.9	4.9	3.9	2.6	2.6	8.3	11.3
44	SLJS 43-4	82.9	73.3	4.5	3.3	2.6	2.7	8.0	10.7
45	SLJS 43-5	103.6	80.7	6.3	3.3	2.7	2.7	8.0	10.8
46	SLJS 43-6	76.9	67.5	3.2	3.3	2.7	2.7	8.0	10.7
47	SLJS 43-7	108.3	67.6	6.1	3.0	2.7	2.7	9.3	11.7
48	SLJS 43-8	72.3	73.0	4.1	3.3	2.6	2.6	7.3	10.5
49	SL 525	94.2	73.3	3.4	2.9	2.6	2.5	8.0	12.1
50	JS 335	18.6	76.8	1.2	3.3	2.4	3.0	8.7	12.0
51	SL 958	93.9	69.5	2.5	3.0	2.6	2.7	8.0	10.6
	Mean	78.8	71.0	4.2	3.2	2.6	2.7	8.4	11.0
	Range	18.6-126.8	48.9-111.4	1.2-7.1	2.4-4.4	2.4-2.7	2.5-3	6.7-10.7	8.5-12.3
	CD (5%)	13.39	8.92	1.43	0.51	0.26	0.18	1.40	0.85

genotype SLJS 37-1-1 (2.4).

4.1.9 Number of seeds per pod

This trait was calculated based on number of seeds per plant and number of pods per plant. At Ludhiana, maximum number of seeds per pod (2.7) was possessed by genotype, SLJS 26-1 along with other 11 genotypes. Minimum value was possessed by genotype, JS335 (2.4). At Gurdaspur location, JS335 had maximum value of seeds per pod i.e 3.0 followed by four genotypes, SLJS 29-3, SLJS 23-4, SLJS 41-2, SLJS 43-2 having value of 2.9 seeds per pod. Minimum value of seeds per pod was obtained by genotype, SL525 i.e 2.5. Similar finding that seed number contributed a lot towards genetic variation was reported by Kadlec and Vozda 1983)

4.1.10 100- seed weight (g)

The results for this trait were observed to be significant at both locations. At Ludhiana, the range for the trait was 10.7g to 6.7g. The upper limit of range was possessed by genotype, SLJS 3-1 followed by genotypes, SLJS 1-1, SLJS 37-1-1, SLJS 3-2-2, SLJS 13-1 each having 100-seed weight of 10.0 g whereas lower limit was possessed by genotype, SLJS 33-2. At Gurdaspur, maximum value *vi.z* 12.3g was observed in genotype, SLJS 23-4 and 12.2g for genotype, SLJS 26-2. Minimum value was obtained for genotype, SLJS 4-1 i.e 8.5g. These findings are supported by the observation given by Diaz et al (1985) and Puspendra and Ram (1987) but it did not agree with report of Karasu (2009).

4.1.11 Harvest index (%)

This character was estimated by calculating the ratio of economic yield and biological yield. The genotypes having high harvest index were linked with high yield. This is a very important character when selection is done for yield traits. In this study, this trait was highly significant at both locations. At Ludhiana, maximum value of harvest index (46.5 %) was observed for genotype, SL525 followed by 45.2 per cent and 42.0 per cent in genotype, SL958 and SLJS 43-3-1, respectively. Minimum value of harvest index was possessed by genotype, SLJS 29-3 (22.0%). The overall mean observed for the character was 32.9 per cent. At Gurdaspur, maximum value of 39.3 per cent was obtained by genotype, SLJS 1-2 followed by 38.4 per cent and 38.2 per cent by genotypes, SLJS 2-1 and SLJS 3-1, respectively. Minimum value of 24.8 per cent was recorded by genotype, SLJS 9-3.

4.1.12 Seed yield (g/plant)

Highly significant genotypic differences were observed for this trait. At Ludhiana, maximum seed yield was obtained for genotype, SLJS 11-2 i.e 37.2g followed by genotypes SLJS 43-3-2 (36.2g), and SLJS 43-3-1 (42.0g). Lowest yield was obtained by genotype, JS335 (4.7g). The range for this character was 4.7-37.2g with the mean value of 25.0g. At Gurdaspur, maximum yield per plant (37.6g) was observed for genotype, SLJS 41-2 followed by 37.5g of genotype SLJS 23-4 and 36.3g of genotype SL958. Minimum yield was recorded

Table 4.2 (e) Mean values for harvest index, seed yield, Soybean Mosaic Virus (SMV) and Yellow Mosaic Virus (YMV) with respect to soybean genotypes

Sl. No	Genotypes	Harvest index (%)		Seed yield per plant (g)		SMV score (0-9 scale)		YMV score (0-9 scale)	
		Ludhiana	Gurdaspur	Ludhiana	Gurdaspur	Ludhiana	Gurdaspur	Ludhiana	Gurdaspur
1	SLJS 1-1	34.8	37.3	30.4	28.2	2.3	0.0	1.3	0.0
2	SLJS 1-2	23.9	39.3	21.0	24.3	2.0	0.0	1.0	0.0
3	SLJS 1-3	37.9	33.9	23.6	33.3	1.3	0.0	1.0	0.0
4	SLJS 2-1	29.2	38.4	26.0	26.8	1.3	0.0	1.0	0.0
5	SLJS 3-1	41.4	38.2	29.2	33.8	1.3	0.0	1.7	0.0
6	SLJS 3-2-1	41.5	37.7	29.3	28.3	1.7	0.0	1.7	0.0
7	SLJS 3-2-2	25.9	34.7	22.9	34.2	2.3	0.0	1.7	0.0
8	SLJS 3-3	41.4	35.1	27.7	29.3	1.3	0.0	1.3	0.0
9	SLJS 4-1	36.7	36.1	27.9	27.0	3.0	0.0	1.3	0.0
10	SLJS 4-2	24.7	36.5	18.7	25.8	2.7	0.0	1.3	0.0
11	SLJS 4-3	33.9	29.9	20.2	23.5	2.7	0.0	1.3	0.0
12	SLJS 9-1	33.8	34.5	30.1	35.7	2.3	0.0	1.3	0.0
13	SLJS 9-2	29.8	32.1	25.5	25.3	1.0	0.0	1.0	0.0
14	SLJS 9-3	33.9	24.8	25.1	20.7	1.0	0.0	1.7	0.0
15	SLJS 11-2	38.6	32.2	37.2	32.6	1.7	0.0	1.0	0.0
16	SLJS 13-1	34.3	27.9	29.0	25.2	2.7	0.0	1.7	0.0
17	SLJS 14-1	32.7	34.8	26.7	21.0	2.0	0.0	1.7	0.0
18	SLJS 14-2	32.0	28.9	22.9	31.0	1.7	0.0	1.7	0.0
19	SLJS 14-3	37.5	35.3	32.0	26.7	1.3	0.0	1.3	0.0
20	SLJS 23-2	31.2	31.7	19.8	22.3	1.0	0.0	1.7	0.0
21	SLJS 23-3	32.6	33.1	30.4	33.5	2.7	0.0	1.0	0.0
22	SLJS 23-4	40.0	35.0	29.5	37.5	2.3	0.0	1.3	0.0
23	SLJS 25-1	28.7	26.3	26.4	32.3	2.3	0.0	1.0	0.0
24	SLJS 25-2	25.8	28.8	20.0	33.0	1.7	0.0	1.7	0.0
25	SLJS 25-3	28.1	27.1	20.4	25.6	1.7	0.0	1.0	0.0
26	SLJS 25-4	31.0	33.8	26.4	28.6	1.7	0.0	1.0	0.0

Contd.....

Table 4.2 (e) Contd.....

Sl. No	Genotypes	Harvest index (%)		Seed yield per plant (g)		Smv score (0-9 scale)		Ymv score(0-9 scale)	
		Ludhiana	Gurdaspur	Ludhiana	Gurdaspur	Ludhiana	Gurdaspur	Ludhiana	Gurdaspur
27	SLJS 26-1	31.5	33.5	20.7	22.3	4.7	0.0	3.0	0.0
28	SLJS 26-2	23.5	31.2	18.0	33.5	1.3	0.0	1.7	0.0
29	SLJS 29-1	30.7	31.5	20.2	26.5	1.7	0.0	1.3	0.0
30	SLJS 29-2	34.9	31.7	30.0	22.5	2.7	0.0	1.3	0.0
31	SLJS 29-3	22.0	34.4	17.4	35.5	2.7	0.0	1.7	0.0
32	SLJS 29-4	25.6	34.0	19.3	31.0	3.0	0.0	1.0	0.0
33	SLJS 33-1	28.9	32.3	17.6	35.3	3.0	0.0	1.0	0.0
34	SLJS 33-2	25.7	34.3	21.4	26.0	1.7	0.0	1.0	0.0
35	SLJS 34-1	27.2	29.8	23.3	21.2	2.3	0.0	1.3	0.0
36	SLJS 37-1	30.3	35.2	28.5	23.8	2.0	0.0	1.7	0.0
37	SLJS 37-1-1	38.5	33.5	27.3	20.9	2.7	0.0	1.3	0.0
38	SLJS 41-1	34.6	33.9	20.6	22.2	1.3	0.0	1.0	0.0
39	SLJS 41-2	32.7	30.8	26.5	37.6	2.0	0.0	1.3	0.0
40	SLJS 43-1	28.9	29.6	25.2	32.2	3.0	0.0	1.3	0.0
41	SLJS 43-2	28.7	32.0	21.9	20.2	2.7	0.0	2.7	0.0
42	SLJS 43-3-1	42.0	35.4	33.0	21.6	1.3	0.0	1.7	0.0
43	SLJS 43-3-2	37.2	32.1	36.5	21.4	2.3	0.0	1.0	0.0
44	SLJS 43-4	34.8	29.5	22.9	18.9	3.3	0.0	1.3	0.0
45	SLJS 43-5	33.2	30.3	30.3	21.0	1.7	0.0	1.0	0.0
46	SLJS 43-6	27.7	32.5	23.6	22.5	1.0	0.0	1.3	0.0
47	SLJS 43-7	40.6	34.1	32.0	32.8	2.3	0.0	2.0	0.0
48	SLJS 43-8	32.2	33.2	17.3	33.1	2.3	0.0	1.7	0.0
49	SL 525	46.5	28.3	27.3	32.7	2.3	0.0	1.0	0.0
50	JS 335	34.7	35.8	4.7	14.6	6.0	6.0	8.7	6.0
51	SL 958	45.2	34.4	32.7	36.3	2.7	0.0	1.0	0.0
	Mean	32.9	32.9	25.0	27.7	2.2	0.1	1.5	0.1
	Range	22-46.5	24.8-39.3	4.7-37.2	14.6-37.6	1-6	0-6	1-8.7	0-6
	CD (5%)	6.47	4.04	3.63	5.15	-	-	-	-

Table 4.2 (f) Mean values for protein content and oil content with respect to soybean genotypes

Sl. No	Genotypes	Protein content (%)		Oil content (%)	
		Ludhiana	Gurdaspur	Ludhiana	Gurdaspur
1	SLJS 1-1	36.8	35.6	20.8	19.7
2	SLJS 1-2	38.1	38.0	20.7	20.0
3	SLJS 1-3	35.8	34.4	20.1	20.0
4	SLJS 2-1	35.9	35.1	20.4	18.8
5	SLJS 3-1	35.5	35.3	20.3	21.3
6	SLJS 3-2-1	36.8	35.5	20.2	21.3
7	SLJS 3-2-2	37.5	37.1	19.8	19.9
8	SLJS 3-3	37.6	38.5	20.6	20.1
9	SLJS 4-1	35.8	35.1	21.4	19.0
10	SLJS 4-2	37.6	36.3	18.8	18.9
11	SLJS 4-3	37.4	36.5	21.0	19.6
12	SLJS 9-1	36.9	35.5	20.8	20.1
13	SLJS 9-2	36.3	35.1	19.9	19.9
14	SLJS 9-3	35.0	34.2	22.1	20.2
15	SLJS 11-2	36.8	35.6	20.2	20.4
16	SLJS 13-1	36.6	35.5	19.4	20.5
17	SLJS 14-1	37.9	37.4	20.4	20.0
18	SLJS 14-2	36.6	35.7	18.8	20.6
19	SLJS 14-3	37.2	36.6	19.2	19.0
20	SLJS 23-2	38.1	37.9	21.0	20.0
21	SLJS 23-3	36.3	36.3	21.2	18.9
22	SLJS 23-4	36.2	35.1	20.5	20.0
23	SLJS 25-1	38.8	38.9	21.0	19.8
24	SLJS 25-2	36.8	35.2	19.8	19.8
25	SLJS 25-3	36.8	35.4	21.2	21.7
26	SLJS 25-4	37.5	36.9	19.3	20.0

Contd....

Table 4.2 (f) Contd.....

Sl. No	Genotypes	Protein content (%)		Oil content (%)	
		Ludhiana	Gurdaspur	Ludhiana	Gurdaspur
27	SLJS 26-1	37.1	35.7	20.1	19.7
28	SLJS 26-2	37.9	37.8	21.1	20.0
29	SLJS 29-1	37.2	35.7	21.3	20.0
30	SLJS 29-2	37.2	37.1	20.3	20.2
31	SLJS 29-3	36.6	35.9	20.3	19.8
32	SLJS 29-4	37.8	37.1	21.9	20.5
33	SLJS 33-1	36.5	36.0	21.4	20.8
34	SLJS 33-2	36.3	35.4	22.7	21.0
35	SLJS 34-1	36.6	35.8	21.8	21.0
36	SLJS 37-1	36.5	36.3	22.0	20.2
37	SLJS 37-1-1	34.9	34.9	22.1	20.6
38	SLJS 41-1	35.4	34.5	21.6	19.9
39	SLJS 41-2	37.1	37.3	21.2	20.9
40	SLJS 43-1	36.9	36.9	18.8	19.8
41	SLJS 43-2	38.0	38.1	21.1	21.2
42	SLJS 43-3-1	35.7	35.9	22.3	18.9
43	SLJS 43-3-2	35.4	35.2	20.3	19.9
44	SLJS 43-4	37.1	36.8	21.9	20.1
45	SLJS 43-5	37.1	37.2	20.5	20.4
46	SLJS 43-6	36.0	35.9	21.6	20.8
47	SLJS 43-7	39.1	38.8	20.3	19.8
48	SLJS 43-8	35.8	36.0	20.8	20.0
49	SL 525	36.9	37.3	21.0	22.1
50	JS 335	36.3	35.1	21.1	20.6
51	SL 958	37.7	38.5	20.6	21.4
	Mean	36.8	36.3	20.7	20.2
	Range	34.9-39.1	34.2-38.9	18.8-22.7	18.8-22.1
	CD (5%)	0.60	1.04	0.61	0.92

by genotype, JS335 i.e 14.6g. The trait showed wide variability (14.6-37.6g) with the mean of 27.7g at Gurdaspur. Ortiz *et al* (2000) observed lot of variability for seed yield between 19 genotypes. Other workers like Resailly *et al* (1986), Chaudhary and Singh (1987) also reported similar results for grain yield in soybean.

4.1.13 Protein content (%)

It is a quality trait. It indicates nutritive value of soybean seeds. Significant variation for this character was recorded among the genotypes. The range for this trait was (34.9-39.1%) at Ludhiana. Maximum protein content was recorded for genotype, SLJS 43-7 i.e 39.1% followed by SLJS 25-1 (38.8%) and SLJS 23-2 (38.1%). The minimum value of protein content was observed in case of genotype, SLJS 37-1-1 (34.9%). At Gurdaspur location, the maximum protein content was possessed by genotype, SLJS 25-1 i.e 38.9% followed by SLJS -43-7 i.e 38.8% and SL958 (38.5%). Minimum protein content was observed by genotype, SLJS 9-3 (34.2%). Zarkadas *et al* (1999) observed variable range of protein (33.6-42.1%) in soybean genotypes. Brim and Burton (1979) also observed this trait as a highly variable one

4.1.14 Oil content (%)

It is also an important quality trait in soybean along with protein content. Mostly soybean is used for oil extraction purpose, thus high oil content genotypes are required for oil industry. At Ludhiana, maximum oil content (22.7%) was possessed by genotype, SLJS 23-2 followed by 22.3 per cent of SLJS 43-1 and 22.1 per cent of SLJS 37-7-1. Minimum value i.e 18.8 per cent for oil content was observed for genotype, SLJS 43-3. Total 44 genotypes were having more than 20 per cent oil at Ludhiana. At Gurdaspur, maximum oil content was possessed by genotype, SL525 i.e 22.1% and minimum oil content (18.8%) by genotype, SLJS 2-1. Total 33 genotypes had more than 20 per cent oil content at Gurdaspur. The mean value was 20.7 per cent for Ludhiana and 20.2 per cent for Gurdaspur location. Clark and Synder (1989) observed significant differences of oil content in different soybean genotypes.

4.2 Genotypic Coefficient of Variance (GCV), Phenotypic Coefficient of Variance (PCV), Heritability (h^2) and Genetic Advance (GA)

The estimated values of Genotypic Coefficient of Variance (GCV), Phenotypic Coefficient of Variance (PCV), Heritability (h^2) and Genetic Advance (GA) for Ludhiana and Gurdaspur are presented in table 4.3. For most of the characters, the coefficient of phenotypic variation was more as compared to genotypic coefficient of variation which indicates the role of environment in expression of characters. At Ludhiana location, seed yield per plant exhibited highest GCV (22.57%) among total characters. The other characters which had high GCV values were pods per plant (21.56%) and pods per node (20.02%). The characters which were having moderate GCV were branches per plant (19.75%), dry weight at 30 DAS (16.16%), fresh weight at 60 DAS (16.10%) and harvest index (16.08%), dry weight at 60

Tables 4.3: Genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), heritability (h^2) and genetic advance (GA) estimated for different characters in soybean at Ludhiana and Gurdaspur.

Sl. No	Genotypes	GCV			PCV			h^2			GA			GA(%)		
		Ludhiana	Gurdaspur	Pooled	Ludhiana	Gurdaspur	Pooled	Ludhiana	Gurdaspur	Pooled	Ludhiana	Gurdaspur	Pooled	Ludhiana	Gurdaspur	Pooled
1	Fresh weight 30 DAS (g)	14.17	15.98	11.24	16.54	23.21	14.37	73.37	47.11	61.11	2.85	2.11	1.88	25.00	22.66	18.10
2	Dry weight 30 DAS (g)	16.16	23.09	14.90	24.98	25.74	18.63	41.84	80.45	63.97	0.45	1.22	0.61	21.53	42.66	24.56
3	Fresh weight 45 DAS (g)	13.88	22.62	12.55	22.10	25.66	17.30	39.44	77.69	52.62	6.70	10.61	5.92	17.96	41.07	18.76
4	Dry weight 45 DAS (g)	13.19	20.39	11.22	19.51	24.60	15.40	45.72	68.67	53.05	1.82	2.80	1.51	18.38	34.81	16.83
5	Fresh weight 60 DAS (g)	16.10	27.47	15.07	25.60	30.86	20.38	39.58	79.23	54.66	13.19	21.31	12.11	20.81	50.37	22.95
6	Dry weight 60 DAS (g)	14.99	24.50	13.49	21.80	29.10	17.97	47.32	70.90	56.34	3.77	5.60	3.23	21.25	42.50	20.86
7	Plant height 60 DAS (cm)	10.50	15.48	9.50	12.71	18.54	11.37	68.33	69.71	69.84	11.54	18.04	10.82	17.89	26.63	16.36
8	Plant height at mat. (cm)	13.36	16.82	9.25	15.11	18.32	10.59	78.13	84.27	76.35	18.00	19.96	11.39	24.32	31.80	16.66
9	Days to flowering	2.73	1.76	1.68	2.90	2.37	1.93	89.24	54.95	79.86	3.22	1.59	1.81	5.32	2.69	3.02
10	Days to maturity	1.18	2.46	1.29	1.23	2.61	1.36	92.46	89.24	89.22	3.01	5.33	3.01	2.34	4.79	2.51
11	Branches per plant	19.75	17.92	14.78	24.64	20.41	17.44	64.26	77.09	71.84	1.61	1.00	1.04	32.61	32.41	25.80
12	Nodes per plant	8.75	8.92	6.93	13.46	11.84	9.24	42.28	56.77	56.31	1.77	3.13	2.02	11.72	13.85	10.71
13	Pods per plant	21.56	13.82	13.63	22.90	15.85	14.89	88.60	76.01	83.76	44.75	17.62	22.88	41.80	24.82	25.70
14	Pods per node	20.02	9.64	13.94	23.51	13.88	16.44	72.52	48.23	71.92	2.52	0.44	1.27	45.12	13.79	24.35
15	Seeds per pod	0.00	2.50	1.11	6.10	4.75	3.77	-1.32	27.71	8.73	0.00	0.07	0.02	-0.17	2.71	0.68
16	100- seed weight (g)	8.36	6.54	5.19	13.27	8.11	7.31	39.67	64.90	50.45	0.91	1.19	0.74	10.84	10.85	7.60
17	Harvest index (%)	16.08	8.62	9.60	20.16	11.49	12.09	63.67	56.30	63.09	8.70	4.38	5.17	26.44	13.33	15.71
18	Seed yield per plant (g)	22.57	19.70	16.33	24.29	22.81	17.72	86.36	74.60	84.99	10.82	9.70	8.18	43.21	35.04	31.02
19	Protein content (%)	2.41	3.12	2.70	2.61	3.54	2.91	84.97	75.69	86.81	1.69	2.03	1.89	4.58	5.60	5.18
20	Oil content (%)	4.32	3.15	3.00	4.69	4.22	3.46	84.99	55.60	75.18	1.70	0.98	1.10	8.21	4.83	5.36

DAS (14.99%), fresh weight at 30 DAS (14.17%), fresh weight at 45 DAS (13.88%), plant height at maturity (13.36%), dry weight at 45 DAS (13.19%) and plant height at 60 DAS (10.50%). The traits which exhibited low GCV values were nodes per plant (8.75%), 100-seed weight (8.36%), oil content (4.32%), days to flowering (2.73%), protein content (2.41%), days to maturity (1.18%) and seeds per pod had zero GCV value. In case of Gurdaspur, maximum GCV was observed for fresh weight at 60 DAS (27.47%). The other character which had high GCV values were dry weight 60 DAS (24.5%), dry weight at 30 DAS (23.09%), fresh weight at 45 DAS (20.39%), seed yield per plant (19.70%). The characters which had moderate GCV estimates were branches per plant (17.92%), plant height at maturity (16.82%), fresh weight at 30 DAS (15.98%), plant height at 60 DAS (15.48%) and pods per plant (13.82%). The traits like pods per node (9.64%), nodes per plant (8.92%), harvest index (8.62%), 100- seed weight (6.54%), oil content (3.15%), protein content (3.12%), seeds per pod (2.50%), days to maturity (2.46) and days to flowering (1.76%) recorded low GCV values.

Like Genotypic coefficient of variation, PCV was also estimated for various characters. Maximum PCV at Ludhiana (25.60%) and Gurdaspur (30.86%) was obtained for fresh weight at 60 DAS. At Ludhiana, other traits which had high values of PCV were dry weight at 30 DAS (24.98%), branches per plant (24.64%), seed yield per plant (24.29%), pods per node (23.51%), pods per plant (22.90%) fresh weight at 45 DAS (22.10%), dry weight at 60 DAS (21.80%) and harvest index (20.16%). The other characters which exhibited moderate values of PCV were dry weight at 45 DAS (19.51%), fresh weight at 30 DAS (16.54%), plant height at maturity (15.11%), nodes per plant (13.46%), 100 seed weight (13.27%), plant height at 60 DAS (12.71%). The characters namely seeds per pod (6.10%), oil content (4.69%), days to flowering (2.90%), protein content (2.61%) and days to maturity (1.23%) had low PCV estimates. At Gurdaspur location, high estimates of PCV were observed for trait, fresh weight at 60 DAS (30.86%) followed by dry weight at 60 DAS (29.10%), dry weight at 30 DAS (25.74%), fresh weight at 45 DAS (25.66%), dry weight at 45 DAS (24.60%), fresh weight at 30 DAS (23.21%), seed yield per plant (22.81%), branches per plant (20.41%). Moderate values for this parameter were observed for plant height at 60 DAS (18.54%), plant height at maturity (18.32%), pods per plant (15.85%), pods per node (13.88%), nodes per plant (11.54%) and harvest index (11.49%) and low values for 100-seed weight (8.41%), seeds per pod (4.75%), oil content (4.22%), protein content (3.54%), days to maturity (2.61%) and days to flowering (2.37%).

The characters like seed yield per plant, pods per plant, pods per node, branches per plant, dry weight at 30 DAS, fresh weight at 60 DAS had high GCV as well as PCV values and the traits like nodes per plant, 100- seed weight, oil content, days to flowering, protein content, days to maturity and seeds per pod had low GCV and PCV values at both locations.

Parameswar (2006) observed high GCV and PCV values for plant height and moderate values were obtained for traits like pods per plant, days to flowering, 100-seed weight. Similar results were also obtained by Aditya *et al* (2011) for seed yield per plant and number of pods per plant.

The measure of coefficient of variation does not provide the information about heritability of characters it only estimates the extent of variability present for the trait. The information about heritability is important for selection of a character in a given environment such that the genotype can be accurately identified by its phenotypic performance. In this study at Ludhiana location, high heritability was showed by days to maturity (92.46%), days to flowering (89.24%), pods per plant (88.64%), seed yield per plant (86.36%), oil content (84.99%), protein content (84.97%), plant height at maturity (78.13%), fresh weight at 30 DAS (73.77%) and pods per node (72.52%). Moderate heritability was reported for the traits namely plant height at 60 DAS (68.33%), branches per plant (64.26%) and harvest index (63.67%) and low heritability was estimated for the characters namely dry weight at 60 DAS (47.32%), dry weight at 45 DAS (45.72%), nodes per plant (42.28%), dry weight at 30 DAS (41.84%), 100- seed weight (39.67%), fresh weight at 60 DAS (39.58%), fresh weight at 45 DAS (39.44%) and seeds per pod (1.32%). At Gurdaspur, high heritability was observed for the characters, days to maturity (89.24%), plant height at maturity (84.27%), dry weight at 30 DAS (80.45%), fresh weight at 60 DAS (79.23%), fresh weight at 45 DAS (77.69%), branches per plant (77.09%), pods per plant (76.01%), protein content (75.69%), seed yield per plant (74.60%), dry weight at 60 DAS (70.90%) while moderate heritability was observed for plant height at 60 DAS (69.71%), dry weight at 45 DAS (68.67%), 100-seed weight (64.90%), nodes per plant (56.77%), harvest index (56.30%), oil content (55.6%) and days to flowering (54.95%). For pods per node (48.23%), fresh weight at 30 DAS (47.11%) and seeds per pod (27.71%) low heritability estimate was observed.

At Ludhiana, the estimation of genetic advance was high for the characters like pods per plant (44.75%), plant height at maturity (18.00%), fresh weight at 60 DAS (13.19%), plant height at 60 DAS (11.54%) and seed yield per plant (10.82%). Moderate genetic advance (GA) was observed for harvest index (8.70%), fresh weight at 45 DAS (6.70%) where as low genetic advance i.e less than 5% was observed for dry weight at 60 DAS, days to flowering, days to maturity, fresh weight at 30 DAS, pods per node, dry weight at 45 DAS, nodes per plant, oil content, protein content, branches per plant, 100-seed weight, dry weight at 30 DAS and seeds per pod. The traits fresh weight at 60 DAS (21.31%), plant height at maturity (19.96%), plant height at 60 DAS (18.04%), pods per plant (17.62%) had high genetic advance at Gurdaspur. Moderate to low genetic advance was observed for the characters like seed yield per plant (9.70%), dry weight at 60 DAS (5.60%), days to maturity (5.33%), harvest index (4.38%), nodes per plant (3.13%), dry weight at 45 DAS (2.80%),

fresh weight at 30 DAS (2.11%), protein content (2.03%), days to flowering (1.59%), dry weight at 30 DAS (1.22%), 100-seed weight (1.19%), branches per plant (1.00%), oil content (0.98%), pods per node (0.44%) and seeds per pod (0.07%). Wiggins *et al* (2012) recorded exhibition of high broad sense heritability for oil content, protein content and seed yield upto the magnitude of 0.65, 0.78, and 0.38, respectively. High Heritability as well as high genetic advance was reported for the traits like days to 50 per cent flowering, plant height, 100-seed weight, harvest index and seed yield by Reni and Rao (2013). Recker (2010) also reported similar results regarding heritability.

At Ludhiana the traits like pods per plant, plant height at maturity, plant height at 60 DAS, seed yield per plant had high heritability as well as high genetic advance and at Gurdaspur plant height at maturity, fresh weight at 45 DAS, pods per plant, seed yield per plant exhibited high heritability along with high genetic advance.

4.3 Correlation analysis

The correlation study was conducted for all possible combination of characters for Ludhiana and Gurdaspur. The results for study are presented in table 4.4 (a & b). Study indicated that most of the characters were associated mildly to strongly with each other. The results which has been discussed below are based on phenotypic correlation coefficients.

At Ludhiana, plant height at maturity had significant positive correlation with plant height at 60 DAS (0.54). Number of branches per plant had positive correlation with days to flowering (0.18). Significant positive correlation was observed between nodes per plant and fresh weight at 30 DAS (0.27), dry weight at 30 DAS (0.24), plant height at 60 DAS (0.28) and with plant height at maturity (0.25). Number of pods per plant was positively associated with fresh weight at 30 DAS (0.25), plant height at 60 DAS (0.22), plant height at maturity (0.33) and with nodes per plant (0.21). The trait, number of pods per node showed significant association with plant height at maturity (0.17) and number of pods per plant (0.82). Number of seeds per pod was associated with number of branches per plant (0.22). 100-seed weight possessed positive correlation with days to maturity (0.18). Harvest index had positive correlation with plant height at 60 DAS (0.21), days to maturity (0.33), and number of branches per plant (0.23). The trait seed yield was positively correlated with plant height at 60 DAS (0.30), plant height at maturity (0.32), days to maturity (0.25), number of branches per plant (0.22), number of nodes per plant (0.17), number of pods per plant (0.45), number of pods per node (0.33), number of seeds per pod (0.22) and harvest index (0.55). Similar results were reported by Kobraee and Shamsi (2011) where pods per plant and seeds per pod were positively associated with seed yield and with increasing seeds per pod, the seed weight would decrease. Among quality traits, protein content was positively correlated with fresh weight at 30 DAS (0.30), dry weight at 30 DAS (0.18). Swlan-Momorivic (1987) and Mello *et al* (2004) observed increase in protein content would decrease the yield of plant but in the

Table 4.4 (a): Correlation coefficients for all possible pairs of characters at Ludhiana location

Sr. No.	Character	Fresh weight 30 DAS (g)	Dry weight 30 DAS (g)	Fresh weight 45 DAS (g)	Dry weight 45 DAS (g)	Fresh weight 60 DAS (g)	Dry weight 60 DAS (g)	Plant height 60 DAS (cm)	Plant height at maturity (cm)	Days to flowering	Days to maturity	No. of branches per plant	No. of Nodes per plant	No. of pods per plant	No. of pods per node	No. of seeds per pod	100-seed weight (g)	Harvest index (%)	Seed yield per plant (g)	Protein content (%)	Oil content (%)
1.	Fresh weight 30 DAS (g)	-	0.60**	0.16*	0.12*	0.05	0.04	0.03	0.10	-0.03	-0.14	-0.07	0.27**	0.25**	0.10	-0.12	0.07	-0.06	0.06	0.30**	-0.16*
2.	Dry weight 30 DAS (g)	0.77	-	0.07	0.06	0.03	-0.07	0.00	-0.01	0.03	0.02	0.06	0.24**	0.01	-0.11	0.03	0.02	0.09	0.05	0.18*	-0.05
3.	Fresh weight 45 DAS (g)	0.24	0.02	-	0.73**	0.97**	0.72**	0.10	0.04	-0.08	-0.03	-0.18*	0.01	0.11	0.07	-0.03	-0.05	-0.47**	0.07	0.00	-0.12
4.	Dry weight 45 DAS (g)	0.04	-0.06	0.76	-	0.69**	0.99**	0.00	-0.03	-0.02	-0.07	-0.10	0.01	0.14	0.11	-0.10	-0.05	-0.68**	0.03	0.14	-0.08
5.	Fresh weight 60 DAS (g)	0.08	-0.14	1.00	0.81	-	0.69**	0.09	0.03	-0.07	-0.07	-0.18	-0.01	0.07	0.05	-0.01	-0.05	-0.44**	0.06	-0.04	-0.10
6.	Dry weight 60 DAS (g)	-0.06	-0.19	0.75	0.99	0.81	-	0.00	-0.03	-0.02	-0.07	-0.11	-0.01	0.14	0.13	-0.01	-0.05	-0.69**	0.02	0.11	-0.07
7.	Plant height 60 DAS (cm)	0.07	-0.10	0.12	-0.04	0.11	-0.03	-	0.54**	0.12	-0.01	-0.05	0.28**	0.22**	0.04	0.10	-0.07	0.21**	0.30**	0.00	0.07
8.	Plant height at maturity (cm)	0.18	0.01	0.13	-0.09	0.11	-0.09	0.60	-	0.17*	0.00	-0.07	0.25**	0.33**	0.17*	0.06	-0.12	0.06	0.32**	0.04	-0.02
9.	Days to flowering	-0.02	0.03	-0.18	-0.03	-0.18	-0.04	0.17	0.22	-	0.03	0.18**	0.14	0.12	0.04	0.06	0.01	0.08	0.12	0.07	0.23**
10.	Days to maturity	-0.19	-0.01	-0.12	-0.15	-0.09	-0.14	0.00	0.01	0.30	-	0.04	-0.12	-0.20**	-0.11	0.01	0.18*	0.33**	0.25**	-0.20**	0.09
11.	No. of branches per plant	-0.11	-0.01	-0.44	-0.21	-0.42	-0.20	-0.03	-0.10	0.25	0.03	-	0.09	0.11	0.05	0.22**	0.01	0.23**	0.22**	-0.05	0.01
12.	No. of Nodes per plant	0.50	0.39	0.01	0.10	-0.06	0.05	0.30	0.35	0.26	0.16	0.04	-	0.21**	-0.36**	0.02	0.07	0.15	0.17*	0.13	-0.05
13.	No. of pods per plant	0.30	-0.08	0.17	0.18	0.13	0.19	0.26	0.38	0.14	0.23	0.10	0.32	-	0.82**	0.11	-0.16*	0.02	0.45**	0.15	0.01
14.	No. of pods per node	0.11	-0.26	0.15	0.11	0.14	0.15	0.12	0.24	0.05	-0.16	0.11	-0.12	0.89	-	0.09	-0.20*	-0.05	0.33**	0.05	0.06
15.	No. of seeds per pod	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-	0.05	0.15	0.22**	-0.04	-0.04
16.	100 seed weight (g)	0.10	0.26	0.01	-0.11	-0.02	-0.15	-0.17	-0.18	0.02	0.32	-0.03	0.27	-0.26	0.39	0.00	-	0.19*	0.15	0.02	-0.21
17.	Harvest index (%)	-0.01	0.11	-0.47	-0.60	-0.50	-0.61	0.32	0.11	0.12	0.43	0.33	0.25	0.04	-0.06	0.00	0.40	-	0.55**	-0.18*	-0.00
18.	Seed yield per plant	0.09	0.03	0.09	0.06	0.08	0.05	0.37	0.35	0.17	0.27	0.23	0.27	0.48	0.38	0.00	0.30	0.60	-	-0.05	-0.11
19.	Protein content (%)	0.35	0.40	0.00	0.21	-0.03	0.15	0.02	0.04	0.10	-0.24	-0.07	0.22	0.18	0.09	0.00	-0.06	-0.21	-0.06	-	-0.21**
20.	Oil content (%)	-0.24	-0.08	-0.19	-0.14	-0.16	-0.12	0.14	-0.03	-0.28	0.12	-0.02	-0.09	0.00	0.06	0.00	-0.36	0.01	-0.13	-0.26	-

Note: Above diagonal= phenotypic correlation coefficient, Below diagonal= Genotypic correlation coefficient

Table 4.4 (b): Correlation coefficients for all possible pair of characters at Gurdaspur location

Sr. No.	Character	Fresh weight 30 DAS (g)	Dry weight 30 DAS (g)	Fresh weight 45 DAS (g)	Dry weight 45 DAS (g)	Fresh weight 60 DAS (g)	Dry weight 60 DAS (g)	Plant height 60 DAS (cm)	Plant height at maturity (cm)	Days to flowering	Days to maturity	No. of branches per plant	No. of Nodes per plant	No. of pods per plant	No. of pods per node	No. of seeds per pod	100 - seed weight (g)	Harvest index (%)	Seed yield per plant (g)	Protein content (%)	Oil content (%)
1.	Fresh weight 30 DAS (g)	-	0.52**	0.17*	0.11	0.02	-0.01	0.29**	0.39**	-0.04	0.06	0.10	0.17*	0.07	-0.07	0.17*	0.16*	0.07	0.76**	-0.03	0.15*
2.	Dry weight 30 DAS (g)	0.75	-	0.25**	0.15*	0.16*	-0.01	0.31**	0.18*	0.07	-0.01	-0.07	0.04	-0.09	-0.16*	-0.03	0.11	0.07	0.49**	0.03	0.20**
3.	Fresh weight 45 DAS (g)	0.10	0.31	-	0.72**	0.98**	0.68**	0.13	-0.01	-0.18*	-0.23**	-0.03	-0.16*	-0.07	0.04	-0.17*	0.05	-0.13	0.19*	-0.30**	-0.03
4.	Dry weight 45 DAS (g)	0.06	0.20	0.82	-	0.71**	0.97**	0.06	-0.05	-0.13	-0.14	-0.02	-0.12	-0.07	0.02	-0.14	0.05	-0.26**	0.15*	-0.19*	0.04
5.	Fresh weight 60 DAS (g)	-0.02	0.22	0.99	0.82	-	0.69**	0.09	-0.07	-0.17*	-0.25**	-0.05	-0.19*	-0.08	0.06	-0.20**	0.02	-0.15*	0.07	-0.30**	-0.06
6.	Dry weight 60 DAS (g)	-0.04	0.07	0.77	0.98	0.78	-	0.00	-0.09	-0.16*	-0.15*	-0.01	-0.13	-0.06	0.04	-0.15*	0.03	-0.28**	0.04	-0.20**	0.01
7.	Plant height 60 DAS (cm)	0.49	0.37	0.14	0.09	0.08	0.01	-	0.57**	-0.03	-0.10	0.02	0.11	0.11	0.04	-0.01	0.20**	0.10	0.18*	-0.10	0.07
8.	Plant height at maturity (cm)	0.54	0.18	-0.02	-0.09	-0.09	-0.13	0.73	-	-0.02	0.01	0.07	0.16*	0.06	-0.06	0.12	0.25**	0.11	0.18*	-0.07	0.07
9.	Days to flowering	-0.13	0.10	-0.34	-0.35	-0.33	-0.37	-0.10	-0.11	-	0.32**	-0.08	-0.00	0.01	0.03	0.07	0.20**	0.02	-0.10	0.05	-0.01
10.	Days to maturity	0.06	-0.02	-0.26	-0.20	-0.26	-0.20	-0.09	-0.01	0.45	-	0.14	0.17*	0.23**	0.12	0.24**	0.19*	0.01	-0.06	0.17*	0.14
11.	No. of branches per plant	0.15	-0.11	-0.00	-0.01	-0.02	-0.02	-0.02	0.11	-0.12	0.17	-	0.44**	0.44**	0.11	0.27**	0.24**	-0.01	-0.08	-0.09	0.03
12.	No. of Nodes per plant	0.43	0.01	-0.11	0.06	-0.16	-0.06	0.13	0.22	0.01	0.28	0.55	-	0.53**	-0.24**	0.19*	0.25**	-0.11	0.15*	-0.04	0.06
13.	No. of pods per plant	0.07	-0.14	-0.09	-0.07	-0.09	-0.04	0.13	0.08	0.05	0.28	0.51	0.70	-	0.67**	0.20**	0.14	0.01	0.02	0.01	0.00
14.	No. of pods per node	-0.29	-0.21	-0.03	-0.04	-0.01	-0.01	-0.06	-0.07	0.10	0.17	0.21	0.10	0.77	-	0.06	-0.03	0.10	-0.12	0.05	-0.05
15.	No. of seeds per pod	0.26	0.03	-0.34	-0.27	-0.37	-0.27	-0.08	0.26	0.35	0.49	0.53	0.52	0.15	-0.29	-	0.05	0.06	-0.02	-0.05	0.15*
16.	100 seed weight (g)	0.30	0.17	0.01	0.04	0.02	0.01	0.24	0.30	0.21	0.28	0.34	0.48	0.21	-0.12	0.26	-	-0.14	0.11	0.10	0.09
17.	Harvest index (%)	0.17	0.14	-0.22	-0.43	-0.24	-0.46	0.14	0.13	0.01	0.03	-0.04	-0.23	-0.07	0.07	-0.01	-0.28	-	0.03	0.00	-0.19
18.	Seed yield per plant	0.88	0.61	0.19	0.18	0.08	0.07	0.20	0.19	-0.25	-0.06	-0.10	0.24	0.01	-0.21	-0.03	0.17	0.06	-	0.11	0.05
19.	Protein content (%)	0.01	0.11	-0.41	-0.29	-0.41	-0.33	-0.10	-0.06	0.08	0.24	0.14	0.01	0.00	-0.01	-0.18	0.01	-0.09	0.18	-	0.06
20.	Oil content (%)	0.23	0.25	-0.07	0.11	-0.10	0.07	0.07	0.07	0.002	0.25	0.09	0.23	0.07	-0.10	0.24	0.19	-0.34	0.05	0.07	-

present investigation no correlation was observed between protein content and seed yield. Oil content was positively correlated with days to flowering (0.23) in present study but as reported by Swathi (2009), oil content was negatively associated with days to flowering. Oil content was negatively correlated with seed yield per plant. Song *et al* (1987) reported no association of seed yield with protein and oil content.

Significant negative correlation in case of number of branches per plant with fresh weight at 45 DAS (-0.18) and fresh weight at 60 DAS (-0.18) was observed. Number of pods per plant showed significant negative correlation with days to maturity (-0.20). Number of pods per node had highly significant negative correlation with number of nodes per plant. The trait, 100-seed weight was negatively correlated with number of pods per node (-0.20). Harvest index was negatively correlated with characters like fresh weight at 45 DAS (-0.47), dry weight at 45 DAS (-0.68), fresh weight at 60 DAS (-0.44) and dry weight at 60 DAS (-0.69). Protein content had negative association with days to maturity (-0.20) and with harvest index (-0.18). Oil content was negatively correlated with fresh weight at 30 DAS (-0.16), 100 seed weight (-0.21) and protein content (-0.21).

Correlation analysis at Gurdspur showed that plant height at 60 DAS was positively associated with fresh weight at 30 DAS (0.29), dry weight at 30 DAS (0.31) whereas plant height at maturity was associated with fresh weight at 30 DAS (0.39), dry weight at 30 DAS (0.18) and plant height at 60 days (0.57). Number of nodes per plant was positively correlated with fresh weight at 30 DAS (0.17), plant height at maturity (0.16), days to maturity (0.17), and number of branches per plant (0.44). Positive association was observed for number of pods per plant with days to maturity (0.23), with number of branches per plant (0.44) and with number of nodes per plant (0.53). Number of pods per node was positively associated with number of pods per plant (0.67). Baruah *et al* (2014) observed that pod weight was positively correlated with number of pods per plant and seeds per plant. Number of seeds per pod had significant positive correlation with fresh weight at 30 DAS (0.17), days to maturity (0.24), number of branches per plant (0.27) and nodes per plant (0.19). The trait, 100-seed weight was correlated with fresh weight at 30 DAS (0.16), plant height at maturity (0.25), days to maturity (0.19), number of branches per plant (0.24), number of nodes per plant (0.25). Seed yield had positive association with fresh weight at 30 DAS (0.76), dry weight at 30 DAS (0.49), fresh weight at 45 DAS (0.19), plant height at 60 DAS (0.18) and plant height at maturity (0.18). Seed yield was positively associated with pods per plant, days to flowering, days to maturity, plant height and 100-seed weight as reported by Malik *et al* (2006). Protein content was positively correlated with days to maturity (0.17) and oil content was positively correlated with dry weight at 30 DAS (0.20).

Days to flowering was negatively correlated with fresh weight at 45 DAS (-0.18), with fresh weight at 60 DAS (-0.17) and dry weight at 60 DAS (-0.16). The trait, days to

maturity was negatively correlated with fresh weight at 45 DAS (-0.23), fresh weight at 60 DAS (-0.15). Number of nodes per plant had negative association with fresh weight at 45 DAS (-0.16) and fresh weight at 60 DAS (-0.19). Number of pods per node had negative association with dry weight at 30 DAS (-0.16), nodes per plant (-0.24). Number of seeds per pod was negatively correlated fresh weight at 45 DAS (-0.17), fresh weight at 60 DAS (-0.20). Harvest index had negative association with dry weight at 45 DAS (-0.26), with dry weight at 60 DAS (-0.28). Protein content was negatively correlated with fresh weight at 45 DAS (-0.30), dry weight at 45 DAS (-0.19) and fresh weight at 60 DAS (-0.30). In literature negative correlation was observed between seed yield and protein content by Swlan-Momorivic (1987) and Mello (2004). Protein content was negatively correlated with oil content in investigation conducted by Wang and Yu (1988)

4.4 Path analysis

The results from phenotypic path coefficient of Ludhiana revealed that among all the characters under study, 13 traits exhibited direct positive effects and 6 traits showed direct negative effect on seed yield. Dry weight at 60 DAS had maximum positive direct effect (3.392), followed by harvest index (1.069), dry weight at 30 DAS (0.335), plant height at maturity (0.272), number of pods per plant (0.198). Dry weight at 45 DAS had maximum negative direct effect (-2.656) followed by plant height at 60 DAS (-0.113), fresh weight at 60 DAS (-0.074), number of nodes per plant (-0.062), oil content (-0.021). Low negative direct effect was observed for the trait days to maturity (-0.013) which showed indirect effect on seed yield through harvest index (0.358) followed by dry weight at 60 DAS (0.247), dry weight at 45 DAS (0.188). Oil content also had low negative direct effect on seed yield but had high indirect effect via dry weight at 45 DAS (0.232). The trait number of nodes per plant also had low negative direct effect (-0.062) but it had high indirect effect via harvest index (0.165) and dry weight at 30 DAS (0.086). The trait, harvest index which expressed low positive direct effect (0.001) also had high indirect effect on seed yield via dry weight at 45 DAS (1.821) and dry weight at 30 DAS (0.032). Days to flowering also exhibited low direct effect (0.002) towards seed yield but it had moderate indirect effect via harvest index (0.089), dry weight at 45 DAS (0.063). Contradictory result was observed by Karnwal and Singh (2009). Some traits had high direct effect like plant height at maturity (0.272) and also had moderate indirect effect via dry weight at 45 DAS (0.087) and harvest index (0.074). The trait seeds per pod had high direct effect (0.090) also had indirect effect via dry weight at 45 DAS (0.274) and harvest index (0.169).

Table 4.5 (a): Path analysis for seed yield based on phenotypic correlations among different traits of soybean genotypes at Ludhiana

Sr. No.	Character	Fresh weight 30 DAS (g)	Dry weight 30 DAS (g)	Fresh weight 45 DAS (g)	Dry weight 45 DAS (g)	Fresh weight 60 DAS (g)	Dry weight 60 DAS (g)	Plant height 60 DAS (cm)	Plant height at maturity (cm)	Days to flowering	Days to maturity	No. of branches per plant	No. of Nodes per plant	No. of pods per plant	No. of pods per node	No. of seeds per pod	100-seed weight (g)	Harvest index (%)	Protein content (%)	Oil content (%)
1.	Fresh weight 30 DAS (g)	0.037	0.214	0.017	-0.338	-0.004	-0.147	-0.003	0.027	-0.001	0.001	-0.003	-0.017	0.051	0.005	-0.011	0.004	-0.069	-0.001	0.003
2.	Dry weight 30 DAS (g)	0.020	0.335	0.008	-0.174	-0.002	-0.237	-0.001	-0.001	0.001	-0.001	0.003	-0.015	0.002	-0.005	0.003	0.001	0.098	0.001	0.001
3.	Fresh weight 45 DAS (g)	0.006	0.026	0.106	-1.945	-0.072	2.445	-0.011	0.013	-0.001	0.001	-0.009	-0.001	0.022	0.003	-0.003	-0.003	-0.504	0.001	0.003
4.	Dry weight 45 DAS (g)	0.004	0.023	0.078	-2.656	-0.051	3.361	-0.0002	-0.009	-0.001	0.001	-0.005	-0.001	0.028	0.005	-0.009	-0.003	-0.733	0.001	0.002
5.	Fresh weight 60 DAS (g)	0.002	0.011	0.104	-1.853	-0.074	2.349	-0.010	0.009	-0.001	0.001	-0.009	0.001	0.015	-0.002	-0.001	-0.003	-0.476	-0.001	0.002
6.	Dry weight 60 DAS (g)	0.001	-0.024	0.076	-2.631	-0.051	3.392	-0.001	-0.008	-0.001	0.001	-0.005	0.001	0.028	0.006	-0.009	-0.003	-0.747	0.001	0.001
7.	Plant height 60 DAS (cm)	0.001	0.002	0.011	-0.003	-0.007	0.002	-0.113	0.146	0.001	0.001	0.002	-0.017	0.044	0.022	0.009	-0.004	0.230	0.001	-0.001
8.	Plant height at maturity (cm)	0.003	-0.002	0.005	0.087	-0.002	-0.109	-0.061	0.272	0.001	-0.001	-0.003	0.015	0.066	0.008	0.006	-0.007	0.074	0.001	0.001
9.	Days to flowering	-0.001	0.013	-0.009	0.063	0.005	-0.099	-0.014	0.048	0.002	-0.001	0.009	-0.009	0.025	0.002	0.006	0.001	0.089	0.001	0.005
10.	Days to maturity	-0.005	0.007	-0.003	0.188	0.001	0.247	0.001	0.001	0.001	-0.013	0.002	0.007	-0.041	-0.006	0.001	0.010	0.358	-0.001	-0.002
11.	No. of branches per plant	-0.002	0.022	-0.019	0.281	0.013	-0.386	-0.006	-0.020	0.001	-0.001	0.049	-0.006	0.022	0.003	0.020	0.001	0.249	-0.001	-0.001
12.	No. of Nodes per plant	0.010	0.086	0.001	-0.041	0.0009	-0.067	-0.03	-0.06	0.001	0.001	0.004	-0.062	0.043	0.018	0.002	0.004	0.165	0.001	0.001
13.	No. of pods per plant	0.009	0.004	0.011	-0.380	-0.005	0.485	0.025	0.091	0.001	0.002	0.005	-0.13	0.198	0.042	0.010	-0.009	0.029	0.001	-0.001
14.	No. of pods per node	0.004	-0.040	0.007	-0.30	-0.004	0.453	-0.004	0.047	0.001	0.001	0.002	0.022	0.163	0.051	0.008	-0.011	-0.003	0.001	-0.001
15.	No. of seeds per pod	-0.004	0.012	-0.003	0.274	0.001	-0.360	-0.012	0.018	0.001	-0.001	0.011	-0.001	0.023	0.004	0.090	0.003	0.169	-0.001	0.001
16.	100 seed weight (g)	0.002	0.010	-0.005	0.142	0.003	-0.197	0.008	-0.032	0.001	-0.002	0.001	-0.004	-0.033	-0.10	0.005	0.058	0.208	0.001	0.005
17.	harvest index (%)	-0.002	0.032	-0.050	1.821	0.033	-2.370	-0.024	0.018	0.001	-0.004	0.011	-0.009	0.005	-0.003	0.014	0.011	1.069	-0.001	0.001
18.	protein content (%)	0.011	0.065	0.001	-0.379	0.003	0.391	-0.001	0.013	0.002	0.002	-0.002	-0.008	0.030	0.002	-0.003	0.001	-0.193	0.001	0.005
19.	Oil content	-0.006	-0.01	-0.013	0.232	0.007	-0.265	-0.008	-0.007	-0.001	-0.001	0.001	0.003	0.003	0.003	-0.003	-0.012	-0.003	-0.001	-0.021

Table 4.5 (b): Path analysis for seed yield based on phenotypic correlations among different traits of soybean genotypes at Gurdaspur

Sr. No.	Character	Fresh weight 30 DAS (g)	Dry weight 30 DAS (g)	Fresh weight 45 DAS (g)	Dry weight 45 DAS (g)	Fresh weight 60 DAS (g)	Dry weight 60 DAS (g)	Plant height 60 DAS (cm)	Plant height at maturity (cm)	Days to flowering	Days to maturity	No. of branches per plant	No. of Nodes per plant	No. of pods per plant	No. of pods per node	No. of seeds per pod	100-seed weight (g)	Harvest index (%)	Protein content (%)	Oil content (%)
1.	Fresh weight 30 DAS (g)	-0.167	0.107	1.046	-0.078	-0.051	-0.014	-0.001	-0.055	0.008	-0.005	-0.018	-0.043	0.038	0.038	-0.010	0.009	0.001	-0.004	-0.019
2.	Dry weight 30 DAS (g)	-0.087	0.207	1.522	-0.112	-1.003	-0.011	-0.001	-0.025	-0.004	0.001	0.014	-0.012	-0.052	0.075	0.002	0.006	0.001	0.005	-0.025
3.	Fresh weight 45 DAS (g)	-0.28	0.051	6.080	-0.509	-5.900	0.520	-0.001	0.001	0.009	0.018	0.006	0.040	-0.038	-0.021	0.009	0.003	0.001	0.47	0.004
4.	Dry weight 45 DAS (g)	0.018	0.033	4.384	-0.706	-4.269	0.741	-0.004	0.007	-0.007	0.011	0.005	0.030	-0.037	-0.012	0.008	0.003	0.001	-0.030	-0.006
5.	Fresh weight 60 DAS (g)	-0.001	0.034	5.998	-0.504	-5.981	0.530	-0.001	0.010	0.009	0.020	0.009	0.048	-0.045	-0.027	0.011	0.001	0.001	-0.047	0.008
6.	Dry weight 60 DAS (g)	0.003	-0.003	4.169	-0.690	-4.184	0.758	0.001	0.013	0.008	0.012	0.003	0.032	-0.032	-0.021	0.008	-0.001	0.001	-0.033	-0.002
7.	Plant height 60 DAS (cm)	-0.048	0.065	0.833	-0.048	-0.543	0.005	-0.005	0.080	0.001	0.008	-0.005	-0.028	0.063	-0.020	0.004	0.011	0.001	-0.016	-0.008
8.	Plant height at maturity (cm)	-0.066	0.037	-0.038	0.039	0.431	-0.073	-0.003	-0.140	0.001	-0.001	-0.014	-0.041	0.032	0.030	-0.006	0.049	0.001	-0.011	-0.009
9.	Days to flowering	-0.008	0.016	-1.113	0.096	1.063	-0.125	0.001	0.004	-0.065	-0.025	0.016	-0.001	0.006	-0.016	-0.004	0.012	0.012	0.009	0.001
10.	Days to maturity	-0.011	-0.003	-1.440	0.105	1.504	-0.116	0.001	-0.001	-0.017	0.079	-0.027	-0.044	0.122	-0.057	-0.013	0.011	0.001	0.028	-0.018
11.	No. of branches per plant	-0.016	-0.015	-0.202	0.021	0.300	-0.013	-0.001	-0.011	0.004	-0.001	-0.187	-0.110	0.235	-0.053	-0.015	0.014	0.001	-0.014	-0.003
12.	No. of Nodes per plant	-0.029	0.010	-0.974	0.086	1.146	-0.098	-0.001	-0.023	-0.001	-0.014	-0.082	-0.250	0.284	0.108	-0.011	0.014	0.001	-0.006	-0.008
13.	No. of pods per plant	-0.012	-0.020	-0.443	0.050	0.515	-0.047	-0.006	-0.008	-0.001	-0.018	-0.083	-0.134	0.529	-0.304	-0.011	0.008	0.001	0.001	-0.001
14.	No. of pods per node	0.013	-0.034	0.292	-0.018	-0.369	0.036	-0.002	0.009	-0.001	-0.010	-0.022	0.060	0.360	0.448	-0.003	-0.001	0.001	0.009	0.007
15.	No. of seeds per pod	0.029	-0.007	-1.036	0.103	1.211	-0.117	0.001	-0.017	-0.003	-0.019	-0.051	-0.049	0.106	-0.029	-0.056	0.003	0.001	-0.009	-0.019
16.	100 seed weight (g)	0.027	0.023	0.311	-0.036	-0.154	0.023	-0.001	-0.035	-0.011	-0.015	-0.045	-0.062	0.075	0.013	-0.003	0.058	0.001	0.016	-0.011
17.	harvest index (%)	-0.012	0.015	-0.834	0.186	0.909	-0.213	-0.001	-0.015	-0.001	-0.001	0.003	0.028	0.009	-0.047	-0.003	-0.008/	-0.002	0.002	0.023
18.	protein content (%)	0.005	0.006	-1.833	0.137	1.800	-0.158	0.001	-0.010	-0.003	-0.014	0.017	0.010	0.005	-0.025	0.003	0.005	0.001	0.157	-0.008
19.	Oil content (%)	-0.026	0.043	-0.242	-0.035	0.400	0.012	-0.001	-0.010	0.001	-0.011	0.005	-0.017	0.001	0.026	-0.068	0.005	0.001	0.010	-0.088

At Gurdaspur, out of 19 characters studied, 11 characters exhibited negative direct effects and eight characters showed positive direct effect on seed yield. The traits which exhibited high direct positive effect towards seed yield were fresh weight at 60 DAS (5.981) followed by dry weight at 45 DAS (0.706), pods per plant (0.529) and pods per node (0.448). Similar finding was observed by Patil et al (2011) that pods per plant had direct effect towards seed yield. Negative direct effects were observed for fresh weight at 60 DAS (-5.981), dry weight at 45 DAS (-0.706), nodes per plant (-0.250) and branches per plant (-0.187). Low positive direct effect was observed for 100- seed weight (0.058) but it had indirect effect for seed yield via fresh weight at 45 DAS (0.311) and pods per plant (0.075). The trait, days to maturity also had low direct effect i.e (0.079) towards seed yield but had indirect effect via fresh weight at 60 DAS (1.504) and dry weight at 45 DAS (0.105). Low negative direct effect was observed for harvest index (-0.001) but showed high indirect effect on seed yield via fresh weight at 60 DAS (0.909) and dry weight at 45 DAS (0.186). Low negative direct effect was observed for plant height at 60 DAS (-0.005) but its indirect effect via fresh weight at 45 DAS (0.833) and plant height at maturity (0.080) were high. The trait, dry weight at 60 DAS had high direct effect (0.758) as well as high indirect effect via fresh weight at 45 DAS (4.169). Similarly protein content which had high direct effect on seed yield i.e (0.157) as well as high indirect effect via fresh weight at 60 DAS (0.800) and dry weight at 45 DAS (0.137). Akram *et al* (2011) found direct positive effect of number of pods per plant, number of branches per plant and plant height on seed yield. Present results are also supported by the findings of Oz *et al* (2009).

4.5 Genetic diversity through Mahalanobis D² statistics

Genetic diversity among 51 lines of *Glycine max* (L.) Merrill was carried out on the basis of 20 characters namely fresh weight at 30 DAS, dry weight at 30 DAS, fresh weight at 45 DAS, dry weight at 45 DAS, fresh weight at 60 DAS, dry weight at 60 DAS, plant height at 60 DAS and maturity, days to flowering, days to maturity, number of branches of plant, number of nodes per plant, number of pods per plant, number of pods per node, number of seeds per pod, 100- seed weight, harvest index, seed yield per plant, protein content and oil content to generate Euclidian distance graph (Fig 4.1) based on D² statistics. The results obtained from this analysis are discussed in the following sub sections.

4.5.1 Distribution of different genotypes into different clusters

The soybean lines were distributed into five clusters depending on the similarities and differences among the genotypes. The detail of clustering is given in table 4.6. Cluster 1 comprised of 16 genotypes which was highest among all clusters and cluster 2 consisted of 9 genotypes including parent SL 525, cluster 3 consisted of 15 genotypes including the parent, JS 335. Cluster 4 and 5 consisted of 5 and 6 genotypes, respectively. The genotypes within the cluster indicated less diversity among the genotypes and the genotypes between the

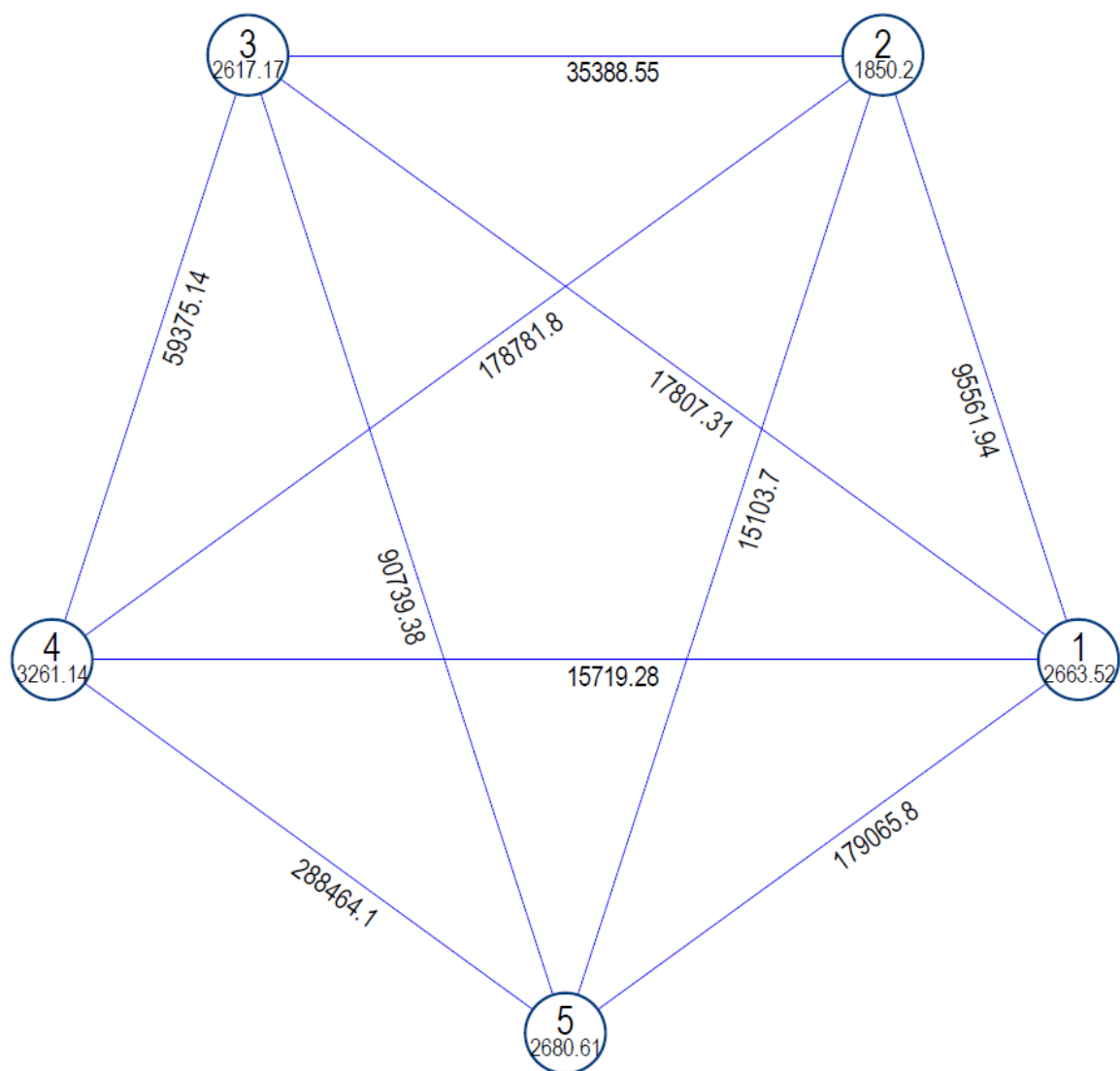


Fig. 4.1 Average intra and inter cluster distance based on morphological traits of 51 soybean genotypes

clusters were more diversified. In this study more number of genotypes were grouped with parent, JS 335 as compared to parent, SL 525. Shinde *et al* (2013) used 40 genotypes of soybean to estimate diversity by using Mahalanobis D^2 statistics and these genotypes were grouped into 12 clusters with D^2 value ranging 27.14 to 36.16. A total of 20 genotypes were present in cluster 1 followed by 2 genotypes in each cluster 2 and 4, respectively. The presence of different genotypes in different clusters indicated the presence of diversity among the lines studied.

Table 4.6 Clustering pattern observed by Mahalanobis D^2 analysis

Cluster	Frequency	Genotypes
1	16	SLJS 4-2,SLJS 25-1,SLJS 3-2-1, SLJS 26-1, SLJS 43-3-2,SLJS 3-3, SLJS 25-2, SLJS 13-1, SLJS 3-2-2,SLJS 9-2, SLJS 14-3, SLJS 43-2, SLJS 25-4, SLJS 37-1, SLJS 1-2, SL958
2	9	SLJS 3-1, SLJS 14-2, SLJS 23-2, SLJS 29-1, SLJS 43-1, SL 525, SLJS 37-1-1, SLJS 23-3, SLJS 26-2
3	15	SLJS 29-3, SLJS 43-8, SLJS 9-3, SLJS 25-3, SLJS 11-2, SLJS 33-1,SLJS 9-1,SLJS 1-1, SLJS 2-1, JS 335, SLJS 1-3, SLJS 43-4, SLJS 29-4, SLJS 43-5, SLJS 43-7
4	5	SLJS 29-2, SLJS 4-3, SLJS 33-2, SLJS 14-1, SLJS 4-1
5	6	SLJS 23-4, SLJS 34-1, SLJS 43-3-1, SLJS 41-1, SLJS 41-2, SLJS 43-6

4.5.2 Identification of desirable lines

The desirable lines could be obtained on the basis of intra and inter cluster distance and mean performance of characters. The clusters which were separated by maximum inter cluster distance were desirable and the selection of genotypes depends on mean performance of genotypes within the cluster. So for this purpose intra and inter cluster distance were important and given in following the table.

Table : 4.7 Mahalanobis D^2 cluster distance matrix

Cluster	1	2	3	4	5
1	2663.52	95561.94	17807.31	15719.28	179065.8
2		1850.2	35388.55	178781.8	15103.7
3			2617.17	59375.14	90739.38
4				3261.14	288464.1
5					2680.61

The maximum inter cluster distance (288464.1) was observed between clusters 4 and 5 and the minimum inter cluster distance (15103.7) was observed between the clusters 2 and 5 which indicated that the genotypes between the clusters were more diverse. Maximum intra

cluster distance i.e 3261 was recorded for cluster 4 where as minimum intra cluster distance (1850.2) was observed for cluster 2. The intermediate intra- cluster distance between maximum and minimum values were cluster 3 (2617.17), cluster 1 (2663.52) and cluster 5 (2680.61). The more the intra cluster distance present, the more diverse the genotypes were present within that cluster.

The cluster mean value for 20 morphological characters (Table 4.8) indicated considerable differences for all characters between the clusters. No difference in mean cluster value was observed for fresh weight at 30 DAS, dry weight at 30 DAS, plant height at 60 DAS, number of nodes per plant, number of pods per node, seeds per pod, 100- seed weight, harvest index, protein content and oil content. The minimum mean value for fresh weight at 45 DAS and dry weight at 45 DAS were observed in cluster 1 where as high mean values were observed for the traits, seed yield per plant, plant height at maturity and fresh weight at 60 DAS in cluster 1. Seed yield and plant height at maturity had minimum mean value in cluster 5. Fresh weight at 45 DAS and branches per plant had high mean value in cluster 2.

So on the basis of mean value of different clusters, genotypes can be selected from specific cluster. Genotypes for seed yield may be selected from cluster (1, 4), for pods per plant (1 and 5), for branches per plant (2 and 5). The selected genotypes may be used in hybridization programme and will be helpful for identification of transgressive segregants.

4.6 Genetic diversity analysis through molecular markers

4.6.1 Cluster analysis based on SSR data

Clustering was done using the symmetric matrix of DICE coefficients based on unweighted paired group method of arithmetic average (UPGMA) using Darwin 5.0 (Perrier *et al* 2006). The results of cluster analysis are represented in figure 4.3. Total 108 SSR markers were used, out of which 16 were polymorphic. Total 48 genotypes were grouped into 3 major clusters. Cluster A consisted of 26 genotypes including parent, JS 335 and cluster B consisted of 12 genotypes including parent, SL 525 and cluster C of 9 genotypes. Cluster A was divided into two sub groups viz. A1 and A2. A1 comprised of 20 genotypes (SLJS 43-5, SLJS 43-2, SLJS 43-3-2, SLJS3-3, SLJS 33-1, SLJS 29-4, SLJS 37-1, **JS335**, SLJS 14-2, SLJS 14-1, SLJS 14-3, SLJS 43-7, SLJS 43-6, SLJS 13-1, SLJS 41-2, SLJS 41-1, SLJS 29-3, SLJS 25-4, SLJS 25-3, SLJS 43-1) and A2 had 6 genotypes , (SLJS 33-2, SLJS 1-3, SLJS 34-1, SLJS 1-2, SLJS 37-1-1, SLJS 1-1). Cluster B consisted of genotypes, SLJS 29-1, SLJS 3-1, SLJS 26-2, SLJS 23-4, **SL525**, SLJS 4-3, SLJS 4-2, SLJS 4-1, SLJS 3-2-2, SLJS 3-2-1, SLJS 25-1, SLJS 2-1 and the genotypes, SLJS 9-3, SLJS 9-2, SLJS 9-1, SLJS 11-2, SLJS 43-8, SLJS 29-2, SLJS 25-2, SLJS 23-3, SLJS 23-2 were included in cluster C.

Based on the similarities and dissimilarities the genotypes were grouped into 3 clusters by using DARwin 5.0. The parental contribution of each line was also calculated by using the behaviour of each marker towards each parent. The genotypes in which contribution

Table: 4.8 Mean D² values of different clusters for agronomic traits of soybean

Character/	Fresh weight 30 at DAS (g)	Dry weight at 30 DAS (g)	Fresh weight at 45 DAS (g)	Dry weight at 45 DAS (g)	Fresh weight at 60 DAS (g)	Dry weight at 60 DAS (g)	Plant height at 60 DAS (cm)	Plant height at maturity (cm)	Days to flowering	Days to maturity
1	10.7	2.59	28.85	8.45	46.8	14.34	66.14	70.21	4.15	19.13
2	10.08	2.47	35.72	9.84	61.33	17.14	65.44	66.09	3.96	18.49
3	10.05	2.40	30.99	8.69	52.16	14.98	66.08	68.32	4.02	18.99
4	10.73	2.81	26.02	8.31	41.01	13.85	69.47	71.62	4.23	19.42
5	10.46	2.29	38.83	10.54	67.20	18.61	64.86	64.59	3.76	17.93

Character/	No. of branches per plant	No. of Nodes per plant	No. of pods per plant	No. of pods per node	No. of seeds per pod	100- seed weight (g)	Harvest index (%)	Seed yield per plant (g)	Protein content (%)	Oil content (%)
1	86.51	9.78	26.56	2.69	4.88	59.99	119.83	33.47	36.65	20.27
2	91.06	9.83	25.94	2.69	5.49	59.87	119.89	32.65	36.53	20.44
3	93.57	9.6	26.48	2.69	5.47	59.99	120.57	32.97	36.69	20.55
4	79.49	9.63	25.43	2.71	4.53	60.37	121.10	34.37	36.45	20.49
5	89.41	9.72	27.08	2.62	5.49	59.22	118.75	30.60	36.18	20.34

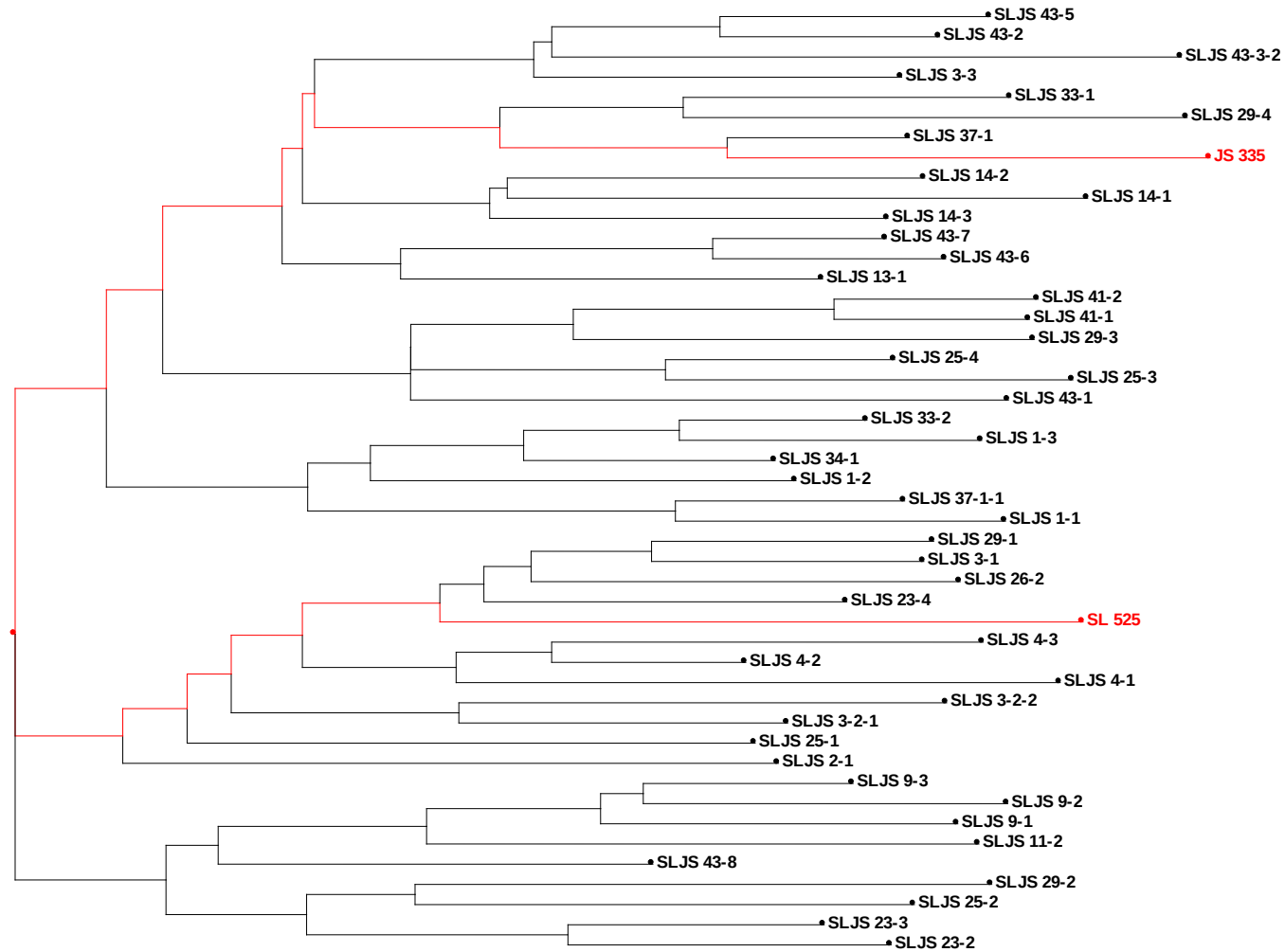


Fig. 4.2 Dendrogram obtained by SSR marker analysis using DARwin 5.

Table 4.9 Mean performance of soybean genotypes present in different clusters for different observed traits

Sl. No	Genotypes	Fw30	dw30	fw45	dw45	fw60	dw60	pl ht 60	ht mat	flring	maturity	branches	nodes	pods/pl	pds/node	seeds/pd	100sdwt	HI	sd yld	SMV	YMV	Protein	Oil
1	SLJS 1-1	9.2	2.8	32.8	9.0	56.4	15.3	70.6	65.9	59.8	121.0	4.4	19.5	96.2	5.4	2.7	10.2	36.1	29.3	1.2	0.7	36.2	20.2
2	SLJS 1-2	8.3	2.2	31.5	9.6	54.7	16.9	55.8	60.3	59.7	119.3	4.2	16.9	86.0	5.8	2.6	9.1	31.6	22.7	1.0	0.5	38.1	20.3
3	SLJS 1-3	11.7	2.7	40.9	9.3	69.9	15.9	59.2	61.2	58.5	120.0	3.2	15.4	84.1	6.0	2.6	9.8	35.9	28.4	0.7	0.5	35.1	20.1
4	SLJS 3-3	11.1	3.1	26.3	7.1	41.3	11.1	70.0	60.9	60.3	116.8	4.1	17.8	78.3	4.7	2.7	10.2	38.3	28.5	0.7	0.7	38.0	20.4
5	SLJS 13-1	10.4	2.0	29.8	10.8	49.3	19.6	63.9	68.3	60.8	118.3	4.0	19.8	94.2	5.0	2.7	10.4	31.1	27.1	1.3	0.8	36.0	19.9
6	SLJS 14-1	10.3	2.4	28.7	8.3	47.1	14.2	65.4	66.1	61.2	121.0	5.2	18.5	90.3	5.2	2.6	9.5	33.8	23.8	1.0	0.8	37.6	20.2
7	SLJS 14-2	11.1	2.3	33.8	8.4	56.3	14.5	59.8	67.2	59.8	118.7	3.7	19.7	98.0	5.7	2.7	9.2	30.5	27.0	0.8	0.8	36.1	19.7
8	SLJS 14-3	10.8	3.0	31.4	8.5	52.0	14.0	63.5	69.9	60.3	118.7	4.8	18.9	78.1	4.5	2.6	10.6	36.4	29.3	0.7	0.7	36.9	19.1
9	SLJS 25-3	10.9	2.9	31.2	9.6	51.5	16.4	74.0	74.0	58.0	119.5	3.6	19.3	73.7	4.1	2.6	9.2	27.6	23.0	0.8	0.5	36.1	21.5
10	SLJS 25-4	10.3	2.2	23.8	9.2	37.3	16.0	64.9	67.4	60.7	119.2	4.0	16.2	93.5	6.1	2.6	9.8	32.4	27.5	0.8	0.5	37.2	19.7
11	SLJS 29-3	12.1	3.0	31.4	9.5	50.7	16.0	62.1	71.1	62.0	122.7	4.1	19.5	79.8	4.5	2.7	9.5	28.2	26.4	1.3	0.8	36.2	20.1
12	SLJS 29-4	10.9	2.6	32.2	9.9	53.4	17.0	77.8	71.7	60.2	121.3	3.1	19.4	96.0	5.5	2.7	9.2	29.8	25.2	1.5	0.5	37.4	21.2
13	SLJS 33-1	12.2	3.0	31.6	8.0	51.0	13.0	66.2	72.6	59.3	120.5	4.5	20.9	97.7	5.6	2.6	9.6	30.6	26.5	1.5	0.5	36.2	21.1
14	SLJS 33-2	10.0	2.0	33.9	9.6	57.7	17.2	66.8	62.0	57.8	122.0	3.5	17.6	94.3	6.0	2.7	8.8	30.0	23.7	0.8	0.5	35.8	21.9
15	SLJS 34-1	9.1	1.9	36.2	10.9	63.3	19.8	62.9	65.9	59.8	121.3	4.3	19.9	95.3	5.4	2.6	9.5	28.5	22.3	1.2	0.7	36.2	21.4
16	SLJS 37-1	10.5	2.0	33.7	9.4	56.8	16.8	62.8	58.9	59.7	121.5	4.0	20.3	90.2	4.8	2.6	9.9	32.8	26.1	1.0	0.8	36.4	21.1
17	SLJS 37-1-1	9.1	2.3	28.0	8.1	46.9	14.0	59.8	65.1	59.7	121.0	4.7	20.0	87.3	4.9	2.8	10.5	36.0	24.1	1.3	0.7	34.9	21.4
18	SLJS 41-1	7.3	2.0	27.5	7.7	47.7	13.4	65.9	70.8	61.3	120.2	3.9	14.9	61.4	5.1	2.8	9.3	34.3	21.4	0.7	0.5	35.0	20.7
19	SLJS 41-2	10.4	2.6	28.0	9.3	45.6	16.0	63.5	75.9	62.0	121.2	2.9	17.9	94.8	5.5	2.8	9.5	31.8	32.1	1.0	0.7	37.2	21.0
20	SLJS 43-1	10.6	2.3	33.3	9.4	56.0	16.4	67.2	69.6	60.8	120.8	4.5	20.1	95.2	5.7	2.7	10.0	29.3	28.7	1.5	0.7	36.9	19.3
21	SLJS 43-2	9.2	2.6	31.7	8.4	54.2	14.2	65.8	76.3	60.8	121.3	4.4	17.5	92.3	5.8	2.8	9.5	30.3	21.1	1.3	1.3	38.1	21.1
22	SLJS 43-3-2	8.5	1.8	34.8	9.8	61.1	17.8	67.2	60.3	60.7	121.7	5.0	18.2	99.6	5.9	2.6	9.8	34.7	28.9	1.2	0.5	35.3	20.1
23	SLJS 43-5	9.1	1.9	30.8	8.7	52.5	15.5	57.8	65.2	59.3	122.5	4.3	19.8	107.2	6.3	2.7	9.4	31.8	25.7	0.8	0.5	37.2	20.5
24	SLJS 43-6	10.1	2.5	35.9	9.3	61.8	16.2	68.5	66.9	59.8	120.8	5.0	18.7	87.2	4.8	2.7	9.4	30.1	23.1	0.5	0.7	35.9	21.2
25	SLJS 43-7	12.1	2.5	31.5	8.7	50.9	14.8	69.5	67.2	60.2	121.7	3.9	18.8	103.0	6.1	2.7	10.5	37.4	32.4	1.2	1.0	39.0	20.0
26	JS 335	10.1	2.4	30.0	8.6	49.9	14.7	80.0	73.5	60.2	122.7	4.6	19.4	47.7	2.3	2.7	10.3	35.2	9.7	6.0	7.3	35.7	20.8
Mean of genotypes grouped with JS 335		10.2	2.4	31.6	9.0	52.9	15.6	65.8	67.5	60.1	120.6	4.1	18.6	88.5	5.2	2.7	9.7	32.5	25.5	1.2	0.9	36.6	20.5

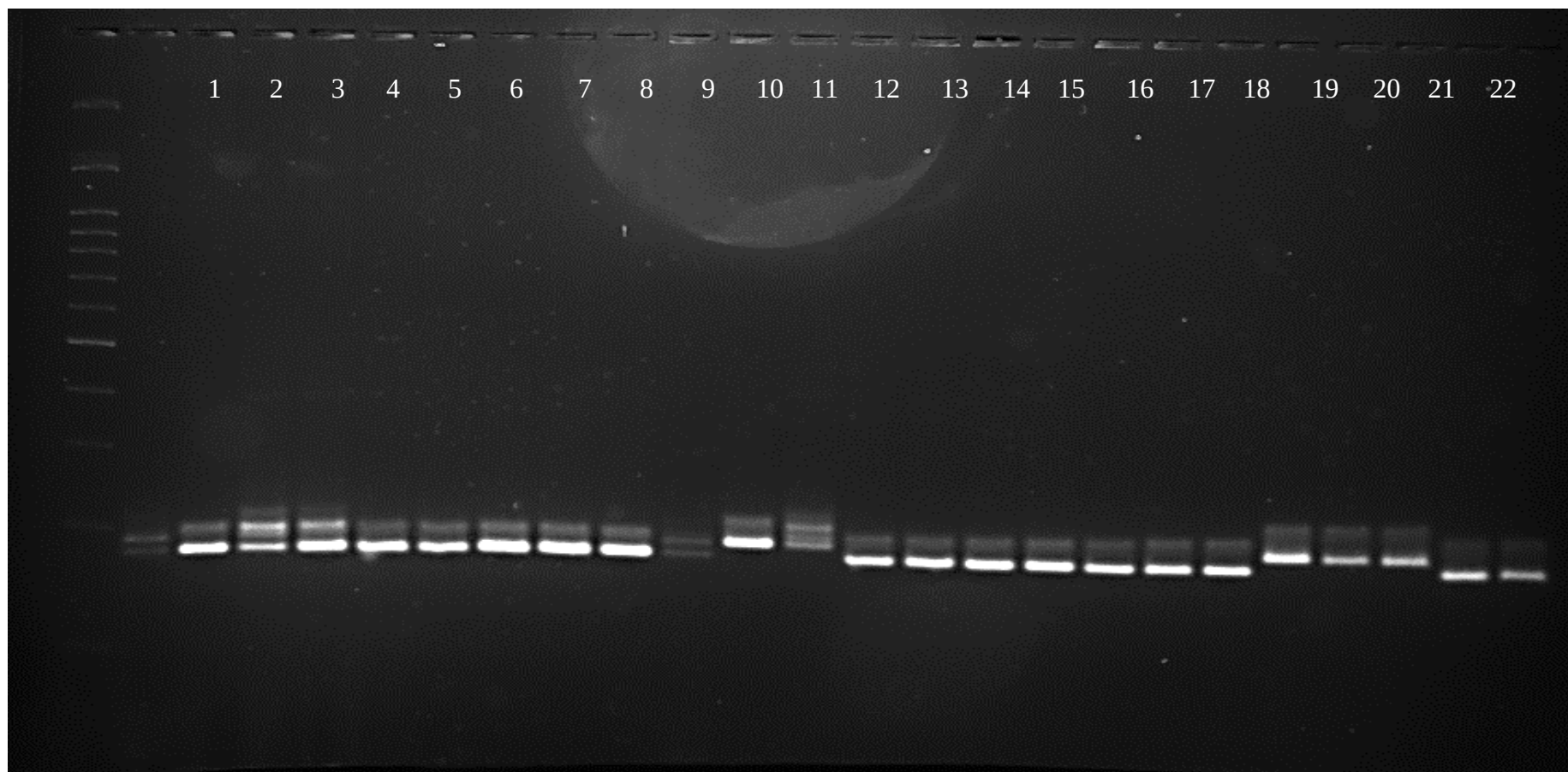
Contd.....

Table 4.9 Contd....

Sl. No	Genotypes	Fw30	dw30	fw45	dw45	fw60	dw60	pl ht 60	ht mat	flring	maturity	branches	nodes	pods/pl	pds/node	seeds/pd	100sdwt	HI	sd yld	SMV	YMV	Protein	Oil
1	SLJS 2-1	9.3	2.2	35.4	9.2	61.5	16.3	64.5	64.4	58.8	120.0	3.8	17.3	74.4	4.6	2.6	9.8	33.8	26.4	0.7	0.5	35.5	19.6
2	SLJS 3-1	11.6	3.0	22.7	6.9	33.8	11.0	64.6	73.3	60.5	119.5	3.7	20.4	73.3	3.7	2.7	10.8	39.8	31.5	0.7	0.8	35.4	20.8
3	SLJS 3-2-1	12.2	3.2	25.9	7.3	39.5	11.3	74.6	70.0	60.7	118.8	3.9	19.5	91.3	4.9	2.7	10.0	39.6	28.8	0.8	0.8	36.2	20.7
4	SLJS 3-2-2	11.8	2.8	41.6	12.7	71.3	22.6	67.6	72.0	60.0	121.0	2.9	19.1	86.0	4.9	2.6	10.5	30.3	28.6	1.2	0.8	37.3	19.9
5	SLJS 4-1	8.7	2.2	33.9	9.0	59.1	15.7	66.3	65.6	60.3	119.3	3.8	19.0	109.6	6.1	2.7	8.1	36.4	27.4	1.5	0.7	35.5	20.2
6	SLJS 4-2	10.1	2.2	31.4	8.5	52.7	14.8	72.1	71.3	60.5	117.3	3.1	18.8	79.9	4.6	2.6	8.9	30.6	22.2	1.3	0.7	37.0	18.9
7	SLJS 4-3	8.9	2.7	35.7	8.7	62.5	14.7	79.3	70.9	59.3	119.8	1.6	15.7	74.2	4.9	2.5	9.9	31.9	21.9	1.3	0.7	36.9	20.3
8	SLJS 23-4	12.3	2.6	38.0	8.9	63.6	15.2	88.2	88.8	59.8	118.2	4.5	22.1	109.4	5.5	2.7	10.1	37.5	33.5	1.2	0.7	35.6	20.2
9	SLJS 25-1	11.5	2.4	31.9	9.5	52.1	16.6	65.9	68.0	57.5	118.2	4.0	20.2	97.4	5.2	2.6	10.2	27.5	29.4	1.2	0.5	38.8	20.4
10	SLJS 26-2	12.1	2.6	29.6	9.3	47.0	16.0	69.2	64.5	59.3	118.8	4.1	19.4	112.4	6.3	2.7	10.1	27.4	25.8	0.7	0.8	37.9	20.6
11	SLJS 29-1	10.3	2.5	26.6	7.3	43.0	12.1	59.0	61.3	61.5	122.0	3.7	19.1	77.9	4.4	2.6	10.1	31.1	23.4	0.8	0.7	36.5	20.6
12	SL 525	11.3	2.8	22.4	7.2	33.5	11.5	70.5	69.5	60.5	121.8	4.2	20.2	83.7	4.7	2.6	10.1	37.4	30.0	1.2	0.5	37.1	21.5
Mean of genotypes grouped with SL 525		10.8	2.6	31.2	8.7	51.6	14.8	70.1	70.0	59.9	119.6	3.6	19.3	89.1	5.0	2.6	9.9	33.6	27.4	1.0	0.7	36.6	20.3
1	SLJS 9-1	11.3	3.1	38.2	10.5	65.0	18.0	71.2	71.8	58.7	117.7	4.2	19.6	95.0	5.4	2.7	10.0	34.2	32.9	1.2	0.7	36.2	20.4
2	SLJS 9-2	9.5	2.2	35.9	9.7	62.4	17.3	58.2	62.1	57.7	117.5	3.8	17.7	72.7	4.5	2.6	10.0	31.0	25.4	0.5	0.5	35.7	19.9
3	SLJS 9-3	9.9	2.8	38.7	11.6	67.5	20.4	66.2	56.1	59.8	119.0	4.6	17.5	92.4	6.2	2.6	10.7	29.4	22.9	0.5	0.8	34.6	21.2
4	SLJS 11-2	11.2	2.7	39.6	10.5	67.9	18.3	57.6	66.2	60.2	117.8	3.9	17.1	102.9	6.4	2.7	8.5	35.4	34.9	0.8	0.5	36.2	20.3
5	SLJS 23-2	10.7	2.9	27.1	8.3	43.6	13.6	58.3	66.9	58.3	120.3	4.2	19.2	93.1	5.3	2.6	9.4	31.5	21.0	0.5	0.8	38.0	20.5
6	SLJS 23-3	10.9	2.7	32.2	9.6	53.6	16.6	72.7	89.5	59.0	119.7	3.8	20.0	91.4	5.0	2.7	9.1	32.9	32.0	1.3	0.5	36.3	20.1
7	SLJS 25-2	12.9	2.5	36.6	9.3	60.2	16.1	66.8	81.5	58.5	118.5	3.5	20.2	83.0	4.5	2.6	9.8	27.3	26.5	0.8	0.8	36.0	19.8
8	SLJS 29-2	9.3	2.1	28.5	7.5	47.6	12.8	63.4	69.1	61.7	119.8	4.3	20.6	107.3	5.6	2.8	9.3	33.3	26.2	1.3	0.7	37.2	20.2
9	SLJS 43-8	10.4	1.9	26.7	7.8	42.9	13.6	67.0	74.5	59.2	120.0	3.8	18.5	87.6	5.2	2.6	8.9	32.7	25.2	1.2	0.8	35.9	20.4
Mean of genotypes grouped with no parents		10.66	2.54	33.72	9.43	56.74	16.29	64.60	70.84	59.22	118.93	4.01	18.91	91.70	5.32	2.65	9.50	31.94	27.45	0.91	0.69	36.24	20.30

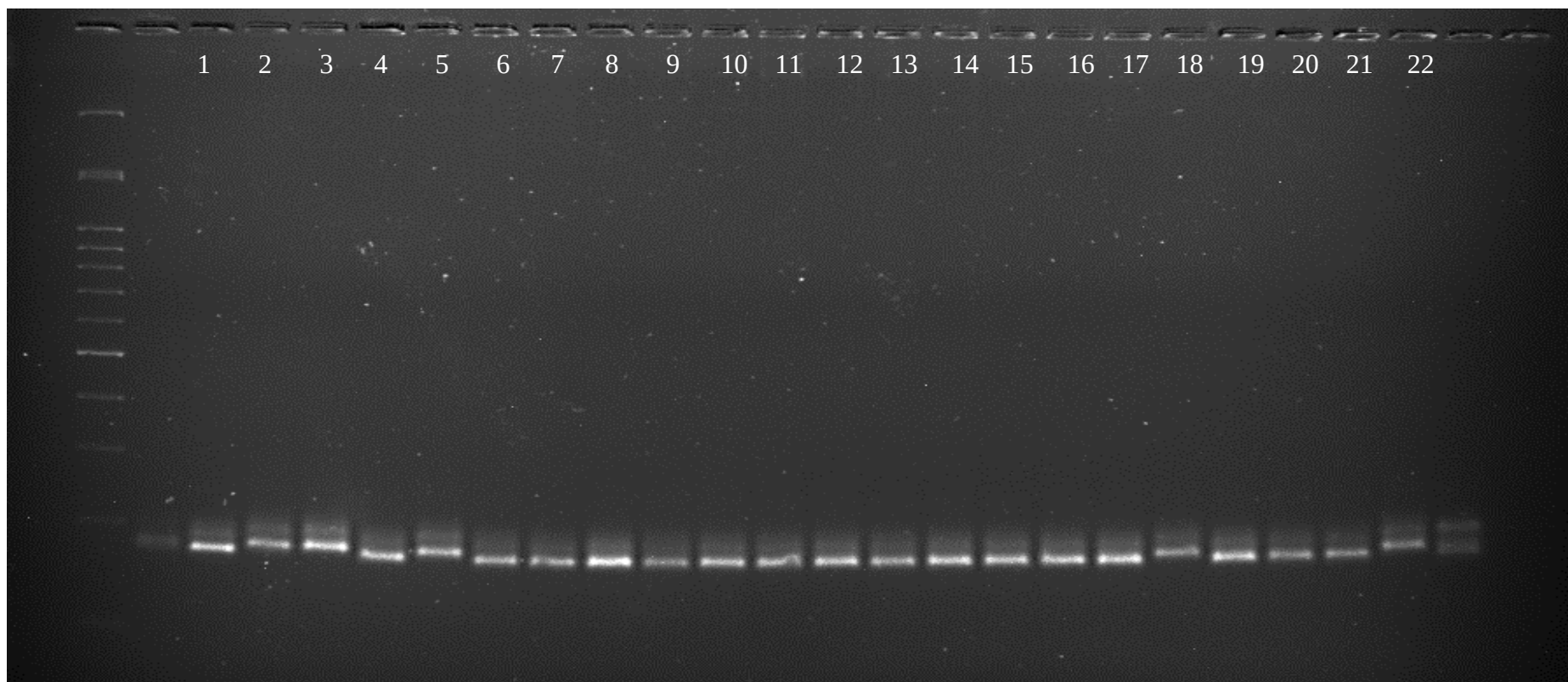
Table 4.10 Per cent contribution of parents to each line

S No	Individuals	Contribution of total markers towards JS335	Contribution of total markers towards SL525	Total No of markers	(%) contribution of JS335	(%) Contribution of SL525
1	SLJS 1-1	9	7	16	56.25	43.75
2	SLJS 1-2	7	9	16	43.75	56.25
3	SLJS 1-3	11	5	16	68.75	31.25
4	SLJS 2-1	8	8	16	50.00	50.00
5	SLJS 3-1	6	12	18	33.33	66.66
6	SLJS 3-2-1	4	12	16	25.00	75.00
7	SLJS 3-2-2	5	11	16	31.25	68.75
8	SLJS 3-3	10	6	16	62.5	37.5
9	SLJS 4-1	9	8	17	52.94	47.05
10	SLJS 4-2	6	10	16	37.52	62.54
11	SLJS 4-3	5	11	16	31.25	68.75
12	SLJS 9-1	4	13	17	23.52	76.47
13	SLJS 9-2	5	10	15	33.33	66.66
14	SLJS 9-3	4	14	18	22.22	77.77
15	SLJS 11-2	7	12	19	36.84	63.15
16	SLJS 13-1	9	8	17	52.94	47.05
17	SLJS 14-1	8	9	17	47.05	52.94
18	SLJS 14-2	6	10	16	37.50	62.50
19	SLJS 14-3	9	7	16	56.25	43.75
20	SLJS 23-2	9	7	16	56.25	43.75
21	SLJS 23-3	6	10	16	37.50	62.50
22	SLJS 23-4	5	11	16	31.25	68.75
23	SLJS 25-1	7	9	16	43.75	56.25
24	SLJS 25-2	9	7	16	56.25	43.75
25	SLJS 25-3	11	7	18	61.11	38.88
26	SLJS 25-4	10	6	16	62.50	37.50
27	SLJS 26-2	8	9	17	47.05	52.94
28	SLJS 29-1	13	3	16	81.25	18.75
29	SLJS 29-2	8	7	15	53.33	46.66
30	SLJS 29-3	9	7	16	56.25	43.75
31	SLJS 29-4	12	4	16	75.00	25.00
32	SLJS 33-1	13	2	15	86.66	13.34
33	SLJS 33-2	10	5	15	66.66	33.33
34	SLJS 34-1	11	5	16	68.75	31.25
35	SLJS 37-1	11	4	15	73.33	26.66
36	SLJS 37-1-1	9	7	16	56.25	43.75
37	SLJS 41-1	10	5	15	66.66	33.33
38	SLJS 41-2	10	6	16	62.50	37.50
39	SLJS 43-1	7	11	18	38.88	61.11
40	SLJS 43-2	8	8	16	50.00	50.00
41	SLJS 43-3-2	8	10	18	44.44	55.55
42	SLJS 43-5	11	7	18	61.11	38.88
43	SLJS 43-6	8	8	16	50.00	50.00
44	SLJS 43-7	9	8	17	52.94	47.05
45	SLJS 43-8	7	10	17	41.17	58.82



Genotypes marked by order (1-22): SL 525, JS 335, SLJS 1-1, SLJS 1-2, SLJS 1-3, SLJS 2-1, SLJS 3-1, SLJS 3-2-1, SLJS 3-2-2, SLJS 3-3, SLJS 4-1, SLJS 4-2, SLJS 4-3, SLJS 9-1, SLJS 9-2, SLJS 9-3, SLJS 11-2, SLJS 13-1, SLJS 14-1, SLJS 14-2, SLJS 14-3, SLJS 23-2

Fig. 4.4 Amplification of genomic DNA of different F₇ derived lines of soybean with primer Satt 153



Genotypes marked by order (1-22): SL 525, JS 335, SLJS 1-1, SLJS 1-2, SLJS 1-3, SLJS 2-1, SLJS 3-1, SLJS 3-2-1, SLJS 3-2-2, SLJS 3-3, SLJS 4-1, SLJS 4-2, SLJS 4-3, SLJS 9-1, SLJS 9-2, SLJS 9-3, SLJS 11-2, SLJS 13-1, SLJS 14-1, SLJS 14-2, SLJS 14-3, SLJS 23-2

Fig. 4.5 Amplification of genomic DNA of different F₇ derived lines of soybean with primer Satt 487

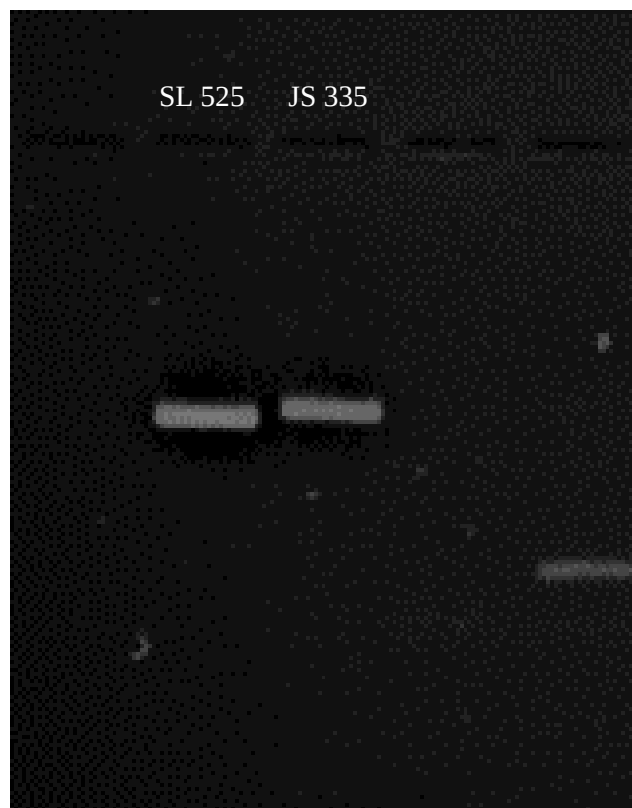


Fig. 4.6 Parental polymorphism with SSR marker Satt 478

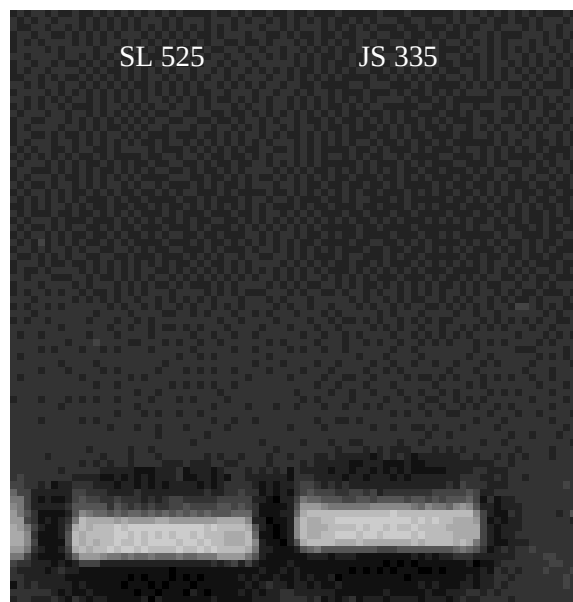


Fig. 4.7 Parental polymorphism with SSR marker Satt 153

of JS 335 was high, were grouped with JS 335 and the genotypes in which contribution of SL 525 was more, were grouped with SL 525 and the lines which had almost equal contribution of both the parents, were grouped in third category. Qin *et al* (2014) conducted an experiment to study the contribution of parental lines (Hobbit and Zao5241) on the sibling lines Jiduo 17 and Jinf58. They found large segment of linkage group C1 and J were passed from maternal line Hobbit and the segment from linkage group A1 was passed down from parental line Zao 5241. In present study, more number of genotypes had high contribution of JS 335. The mean data for different agronomic traits were also classified on the basis of genotypes present in each cluster with the objective to find out the lines which were agronomically superior, having high yield and resistance to YMV along with high contribution of parent, JS 335. The line, SLJS 41-2 was resistant to YMV and also had high yield (32.1g/plant). The contribution of JS 335 towards SLJS 41-2 was 62.5%.

Graphical genotyping was also done by using polymorphic marker data. The total number of markers used for the experiment was described in detail in table (4.11). The introgression in each linkage group has diagrammatically represented in fig (4.3). On the basis of 16 polymorphic markers, maximum introgression was done in linkage group O. The polymorphic markers Satt 487, satt123, Satt 153 were present in linkage group O. The amplification result of Satt 153 and Satt 487 has represented in fig 4.4 and 4.5.

Table 4.11 List of SSR Primers

Linkage group	SSR locus	No. of alleles	Upper primer sequence (5'→3')	Lower primer sequence (5'→3')	PIC value
A1	Satt684	1	GGGCTTCATTTTAGATGGAGTC	TGGAGCTCATATTCGTCACAAAG	-
	Sat_267	1	GCGATTGGATGATGGATTTATGAGTT	GCGCCCAACAAGGTGAGAAATCAAGA	-
	Satt211	1	GAAAAAGCCCACATCCAA	CATGGGCATGCAGTAACA	-
	Sat_217	1	GCGAAAAATTGTCAATGATATGATCAGTAAG	GCGGTCTAGATGAAAAATGCTTTGTAA	-
A2	Satt390	1	AGTGGCTGATAAAAAAATACTCA	ATAATCGCGGCACAATAATTC	-
	Satt315	1	GCGCGACAACCTCTAATGAAAATCT	GCGGAGTTTGATTTTTTCAAAAGT	-
	Satt341	1	GCGGAGCTTACCAACATAAAAAAACT	GCGGTCCAACATTGAGGCAAGAATAC	-
	Satt089	1	AAAAATTAACGGTTGAGAAT	TTAAGGAAATAAAAGAAGAAAAG	-
	Satt525	1	GCGCATAGCTTTCAGAGAAGTTT	CATTCACCAATCCTCATTAGA	-
	Satt378	5	TACAATGACGAGAGGAGAAGAGAC	TGAAACCACAAACAACAAC	0.31
B1	Satt426	1	GCGCCCATTATTATTTTCCTTGAATTGT	GCGAATGCCTAATGTGATGATAAAAAAATA	-
	Satt251	1	CCTCCACCCCCTTCCCACCCAAAA	GGTGATATCGCGCTAAAATTA	-
	Satt197	1	CACTGCTTTTTCCCCTCTCT	AAGATACCCCCAACATTATTTGTAA	-
	Satt519	1	GGATTTCAAAGAATGAACACAGA	CCGCAAGGTTACGAACTGCTCGAA	-
	Satt484	1	GCGTTTAATAAAACTAATTTAATTGTACT	GCGTTCCTTTCTCTCCTTTCTTTCTT	-
	AQ851479	1	GCGCTGCAAAAATTAGTT	GCGTTCAGGACCCAATA	-
B2	Satt577	1	CAAGCTTAAGTCTTGGTCTTCTCT	GGCCTGACCCAAAATAAGGGAAGTG	-
	Sct_034	3	AATTCTCACTCTCACAACTTC	CCATGGAATAGTTGGGT	-
	Satt066	5	GGGAAGCTTAATAATGAAAATGACAC	TTGATCACTTCTGTAACATTC	0.53
	Satt560	1	GCGATCGTGCAAGAAAATA	GCGGTGGACTTCGCCTCAAATAAT	-
C1	Satt565	1	GCGCCCGGAACCTTGTAATAACCTAAT	GCGCTCTCTTATGATGTTTATAATAA	-
	Sat_367	1	GCGTTTCTGTCCAAAATTTATGATATTAGTT	GCGGAACGCCCCATTTTACCTTATCATCCTT	-
	Satt646	1	GCGGGGTATGAATTAATTAATGTAGAAT	GCGCCTTCAAAAATAATGACATATCAT	-
	Satt476	1	TTTGCTGATTAAAAAACAAAACTG	TTGTTAGAATGGGGACTACTTCACTA	-
	AI794821	3	GCGTTCGGCTCAAATAATAT	GCGAAAACTAGGAGAGAATGAA	0.35

Contd.....

Table 4.11 Contd.....

Linkage group	SSR locus	No. of alleles	Upper primer sequence (5'→3')	Lower primer sequence (5→3')	PIC value
C2	Satt281	1	AAGCTCCACATGCAGTTCAAAAC	TGCATGGCACGAGAAAGAAGTA	-
	Satt305	1	TTCCCAACAACAGACAACAC	TTAATTCTCCTTTATCATCATCAC	-
	Satt322	1	GGGACCCATCATTAAGAA	GTTTTGCCGGACACCACA	-
	Sat_076	1	GCGTAATTAACACCAATATATGACATG	GCGGGGTAAAAATTCAAAATGT	-
	Satt357	1	CCTGAGCAATTCATACTCC	TAACCGATCCGATCCTTGACA	-
D1a	Satt221	1	GCGATTGTACCACTAAAAACCATAG	GCGGCAAACCATTATCTTCATT	-
	Satt077	2	GATCTAAAGTCTGATATTTTTAACTA	AAAAGGAGAAGGAATGC	-
	Satt129	1	TTCAGTACAAGTCGGGTGAATAATAATA	TCACATGTTCCGGACTTAAGGTAT	-
D1b	BE021153	2	GCGAAACTGCTTGTATTTTA	GCGCTCCAATTGAAAGTG	0.74
	AI856415	1	GCGAAGTCAGTAAAAACATTGGATA	GCGGGCGTGAATAAGAGAAGAA	-
	Satt542	3	CACCAGCACAGAACAATCATT	CACGGTCTAACCTTTCCTTCTA	0.44
	Satt266	1	GCGAAACTCTACGGGTCAGTAGTTAT	GCGTAAGATGGCCTAGAAAGAGGATG	-
	Satt005	1	TATCCTAGAGAAGAATAAAAAA	GTCGATTAGGCTTGAAATA	-
	Satt041	1	TGTTGTGTGGCTTTATTATT	TTAAGGTGGGATATGGTC	-
	Sat_139	1	CATGTTGAATCACTAATTC AATTT	GGGTCGTTCTGCTACAGGCATGAAG	-
	Sat_069	1	CGACCAGCTGAAGAAA	CTGAATACCCATCATTACTTAA	-
	Satt328	1	TGACCACCATGAGTTCATT	GGGGGTGGCTTTTAGATTC	-
	Satt135	1	CACGGATTTTAAATCATTATTACAT	TTCCAATACCTCCCAACTAAC	-
D2	Satt372	1	CAGAAAAGGAATAATAACAACATCAC	GCGAAAACATAATTCACACAAAAGACAG	-
	Satt002	1	TGTGGGTAAAATAGATAAAAAT	TCATTTTGAATCGTTGAA	-
	Satt582	1	CCGGTGATACTCCATACCAATAAC	CAACGCCGATTTTCTATTTGTCTG	-
	Satt447	1	CGAAACTACGGTTGATTAT	TCCAAACACTGTCCTTCTT	-
	Satt543	1	GCGGATCTAAGGATAATTCATTAA	GGGAGCGGATCATTCGGTGAAA	-
	Satt186	3	GGGAAGTTATAAGCAGAT	GGGAATCCATTCTGATGAGT	0.41
	Satt720	1	GCGCATATACGAAACATATTGTCAAGTTACA	GCGTCATGAGTGGTTTGTCTATACTTCTAT	-
	Satt230	1	CCGTCACCGTTAATAAAAATAGCAT	CTCCCCCAAATTTAACCTTAAAGA	-
	Satt268	1	TCAGGGGTGGACCTATATAAAATA	CAGTGGTGGCAGATGTAGAA	-

Contd.....

Table 4.11 Contd.....

Linkage group	SSR locus	No. of alleles	Upper primer sequence (5'→3')	Lower primer sequence (5'→3')	PIC value
F	Satt586	1	GCGGCCTCCAAACTCCAAGTAT	GCGCCCAAATGATTAATCACTCA	-
	Satt145	1	AGCATATGGGATACAAGTGATTAG	CGGTGTTGGTGTGGTATGT	-
	Satt160	1	TCCCACACAGTTTTTCATATAATATA	CATCAAAAGTTTATAACGTGTAGAT	-
	Satt425	1	GCGCAATTAAGATCCACTAAGTGATT	GCGGCTTTTCACTCTTCTTTTATTATT	-
	Satt595	1	GATGGGAAGCAAACAAGAAG	AACCCCTCCCCTAAAT	-
	SOYHSP176	1	TTTTTGTTTAAGTTACTGTACTGT	GCTAGTCTTCTACAACCTTCTA	-
	Satt334	1	GCGTTAAGAATGCATTTATGTTTAGTC	GCGAGTTTTTGTTGGATTGAGTTG	-
	Satt072	1	GGAAAGAATCAGCAAAAT	CCCCACATAAATAATAAA	-
	Satt554	1	GCGATATGCTTTGTAGAAAATTA	GCGCAAGCCCAAATATTACAAATT	-
	Satt656	3	GCGTACTAAAAATGGCAATTATTTGTTG	GCGTGTTTCAGTATTTGGATAATAGAAT	0.22
	Satt688	1	ATGCCTCCAAAGAGAAAT	CTGCCCATGACCATCT	-
	Sct_187	1	CATGCTCCCATTCTCT	AACATTGGCTTTTTACTTAG	-
H	Sat_127	1	GGGGTTTTGTGTCTAGTCTA	GGGATTAATAAATAACAATACT	-
	Scrt009	1	TGGTAAAGGAGGAAGT	AGAATGTGCTGATGACA	-
	Satt541	1	GCGAATCCATCACACATAAA	GCGGTACTCCCTCCAGAAAATAACC	-
	Satt293	3	GCGCAGAAGGTTTGCATAAAAAGAAT	GCGGGCTAAAAAGTTGATGTAATGTG	0.40
	Satt127	1	CGCTTGTGAACCCTGCTAAA	CCATCCTCTGAAACCGTTATCT	-
I	Satt354	1	GCGAAAATGGACACCAAAAGTAGTTA	GCGATGCACATCAATTAGAATATACAA	-
	Satt650	1	CAGTTGGCTGGTCAAATC	TCTGGGTACTTTTTATTGTCA	-
	Satt671	1	GCGTAAATCCAAAAGTAGAATAAAATAA	GCGAGAAATGAGATAAGTGGTGATA	-
	Satt292	4	GCGGAATTAGAACTCCAGTAAAGA	GCGAGGCCAACATTGAAAAGT	0.53
	Satt623	1	GCGGTGCAATGATTTTAATGATATGAT	GCGCGTGTAAGGTTATAACGTGTAA	-
	Sct_189	1	CTTTTCCTGGCAATGAT	AAAATCGCAAAACCTTAGT	-
	AW310961	1	GCGCAACTTTTTAGTAAATATTGCATAA	GCGCATAACATCTTTTGGGATTTCT	-
J	Satt674	1	GCGAATCCTCTAGCTTACCAAAGAA	GCGATTAGCCATCAAAACCTAT	-
	Satt529	1	GCGCATTAAGGCATAAAAAAGGATA	GCACAATGACAATCACATACA	-
	Satt431	5	GCGTGGCACCCTTGATAAATAA	GCGCACGAAAGTTTTTCTGTAAACA	0.30

Contd.....

Table 4.11 Contd.....

Linkage group	SSR locus	No. of alleles	Upper primer sequence (5'→3')	Lower primer sequence (5'→3')	PIC value
K	Satt715	1	GCGAAAAAATTTCAATTTCTTGTTTATGTGA	GCGGGCTTATTTTTTAATAACAAGTTAGATTC	-
	Satt055	1	AGTTAAGGAAGAATTTATTGTTAT	AACATTTTATTTGAGTATTTAGAAT	-
	Satt178	1	GGGAAAATTCTTTTCATATAGATG	GGGGTTGAGATATTTTGTTTCATAC	-
	Satt326	1	AGATTCTCCTTTGCTTCTTAGT	GTTAGTTCACCTTCCAGTATTTGA	-
	Sat_167	1	AAGGCACTCTTCCATCAATACAA	TTGAGCCGAAAGTTCAATTCTA	-
	Satt196	1	TTGGGAAATAGTGATTGAGGTAAAA	AAATCCCCATTGAATGAGAATAAG	-
L	Satt182	1	GGTCCACATGAAATGAAGGT	TCTCAGCCTGCAAAGAAAA	-
	Satt238	1	GCGCCATTTTAATGATTTATTTA	GCGGAAAGAAGAGGAAGAAAG	-
	Satt284	1	TGGGCTAGGAGTGACCAC	GGTCACCACTCACCATCA	-
	Satt156	1	CGCACCCCTCATCTATGTA	CCAATAATCCCAGGGACTTACTT	-
	Satt166	1	TTGCACAGTTGATTTTTGTTT	GCATCGAATTTCTGGATTTAC	-
	Sat_099	1	GCGAAAATGGCAGAGATAA	AATGCTAAAAGAGGAATGAAATAA	-
	Satt006	1	CAATGTGATTAGTTTTGGAAA	GGGTTAATGTTGTTTTTTATA	-
	Satt590	1	GCGCGCATTTTTTAAGTTAATGTTCT	GCGCGAGTTAGCGAATTATTTGTC	-
M	Satt150	1	AAGCTTGAGGTTATTCGAAAATGAC	TGCCATCAGGTTGTGTAAGTGT	-
	BE823543	1	GCGAAATGCCGAAAGAG	GCGGGGATAAGAAAAACAAT	-
	Satt551	3	GAATATCACGCGAGAATTTTAC	TATATGCGAACCCTCTTACAAT	0.37
	Satt336	1	AATTGGAGTGGGTCACAC	TTCCCGGAAAGAAAGAAA	-
	Sct_195	1	GCGCTATGCAAGGTCTAACTACA	GCGAAACCGTCACACAGTCTCTG	-
N	Satt387	1	GCGTTACGTTTCACTATTTATTTAACAT	GCGGCAGGCTAGCTACATCAAGAG	-
	Satt234	1	TGAGAGCAGGACATTTTTT	TCTGCGAGTGTTTTCTG	-
	Satt022	2	GGGGGATCTGATTGTATTTTACCT	CGGGTTTCAAAAAACCATCCTTAC	0.49
	Satt487	2	ATCACGGACCAGTTCATTTGA	TGAACCGCGTATTCTTTTAATCT	0.51
	Satt345	1	CCCCTATTTCAAGAGAATAAGGAA	CCATGCTCTACATCTTCATCATC	-
O	Satt123	2	TTCAACCATTCAAACATG	AATTGAAAAGATGTGAAACAT	0.34
	Satt592	1	GCGAAGATTGGTCTTTTATGTCAAATG	GCGGAGGAATACAAGTCTCTATTCAA	-
	Satt153	3	GGGTTATATCAGTTTTTCTTTTGT	CCATCCTCGTTAGCATCTAT	0.57
	Scaa001	1	AGAATTAGAAAACCATAAATCTG	TATGGCGGGAGTTGA	-

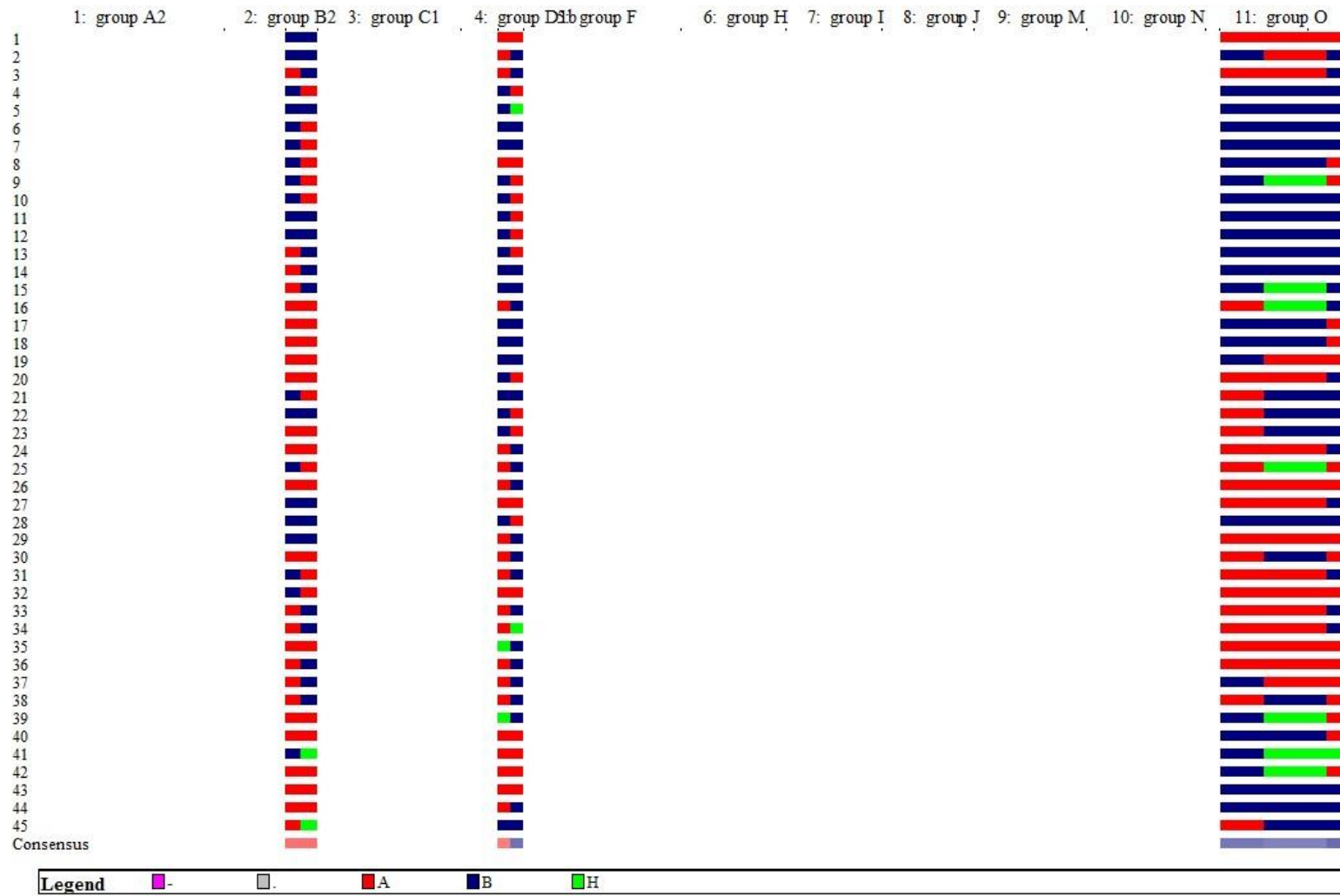


Fig. 4.3 Graphical genotyping by using SSR primers

CHAPTER V

SUMMARY

Genetic variability in the breeding material plays crucial role in crop improvement programme. Therefore, the assessment of genetic diversity is an integral part of any breeding programme. To fulfill this need, the present study entitled “CHARACTERIZATION OF ADVANCED BREEDING LINES OF SOYBEAN (*Glycine max* (L.) Merrill) THROUGH AGRONOMIC TRAITS AND MOLECULAR MARKERS” was carried out during *khariif*, 2015 with the objective of assessing variability and association of characters in F_{2:7} lines derived from the cross of SL 525 (a yellow mosaic resistant genotype) and JS 335 (a very high yielding and stable genotype but susceptible to Yellow Mosaic Virus).

The study consisted of two experiments viz experiment 1 and experiment 2. Total of 48 derived lines from above mentioned cross, two parents (SL 525 and JS 335) and a check (SL 958) were used in the study. Experimental material was sown in three replication, three rows per genotype with row length of 3m at Ludhiana and Gurdaspur locations. Data were analysed using RBD design. Observations were taken for different traits like biomass at (30, 45 and 60 DAS), plant height at 60 days and maturity, days to flowering and maturity, number of nodes per plant, number of branches per plant, seeds per pod, pods per plant, pods per node, soyabean mosaic virus and yellow mosaic virus score, 100- seed weight, seed yield per plant, harvest index, protein content and oil content.

Analysis of variance was performed and genotypic coefficient of variation, phenotypic coefficient of variation, heritability, genetic advance, correlation and path coefficient were done. Significant variation was observed among lines for all traits except for seeds per pod at Ludhiana. Mean performance of different characters at Ludhiana revealed that plant biomass at 30 DAS observed to have maximum mean value (3.3g) for genotype, SLJS 3-2-1 and minimum value (1.5g) for genotype, SLJS 43-3-2. For biomass at 45 and at 60 DAS, highest mean values of 12.9g and 22.5g were obtained by genotypes, SLJS 3-2-2 and SLJS-1-2, respectively, whereas lowest mean value (6.2g) and (10.4g) was observed for genotype, SL 525. Maximum plant height at 60 DAS and maturity and was observed for genotype, SLJS 23-4 (90.0cm) and SLJS 23-3 (107.0cm), respectively. Minimum plant height at 60 DAS and maturity was possessed by genotypes, SLJS 23-2 and JS 335. Highest mean value (64.3days) and lowest value (57.0days) were observed by genotype, SLJS 14-1 and SLJS 25-1 for days to flowering. Days to maturity estimated to be maximum (132.3 days) and minimum (124.7 days) was for genotypes, SL 958 and SLJS 26-2, respectively. The traits, number of branches per plant and nodes per plant were maximum for genotype, SLJS 26-1 and SLJS 3-1, respectively and minimum for genotype, SLJS 4-3 and SLJS 41-1, respectively. Pods per plant had highest mean value (126.8) for SLJS 11-2 and lowest mean

value (18.6) for JS 335. 100-seed weight was observed to be maximum (10.7g) for genotype, SLJS 3-1 and minimum (6.7g) for genotype, SLJS 33-2. Highest harvest index (46.5%) was estimated for SL 525 and lowest harvest index (22.0%) for SLJS 29-3. Genotype, SLJS 11-2 possessed high seed yield per plant (37.2g) and JS 335 possessed low seed yield (4.7g). Regarding quality traits, highest protein (39.1%) and oil content (22.7%) was observed for SLJS 43-7 and SLJS 23-2, respectively. The genotypes, SLJS 37-1-1 and SLJS 43-1 were observed for low protein and oil content.

At Gurdaspur, Plant biomass at 30 DAS was highest for genotypes, SL 958 and lowest for genotype, SLJS 37-1. Biomass at 45 and 60 DAS observed to have maximum and minimum mean values for genotype, SLJS 9-3 and SLJS 29-2, respectively. For plant height at 60 DAS, Genotype JS 335 possessed maximum mean value (99.0cm) and genotype, SLJS 43-4 had minimum value (46.0cm) of plant height at 60 DAS. At maturity, maximum plant height (107.1cm) was for genotype, JS 335 and minimum plant height (41.4cm) for genotype, SLJS 43-3-2. The genotype, SLJS 4-3 and SLJS 29-3 took maximum days to flower (61.3) and genotype, SLJS 25-3 took minimum days (57.0) to flower. Maximum number of days to maturity (119.0 days) was taken by genotype, SLJS 29-3 and minimum days to maturity (105.7days) was taken by genotype, SLJS 9-2. The genotype, JS 335 and SLJS 4-3 possessed high mean value (4.5) and low mean value (1.7) for number of branches per plant. Number of nodes per plant was maximum (27.3) for genotype, SLJS 33-1 and minimum (17.7) for SLJS 4-3. Maximum value of seeds per pod (2.7) was observed for genotype, JS 335 and minimum value (2.5) for SL 525. The genotype, SLJS 23-4 showed high 100-seed weight (12.3g) and genotype SLJS 4-1 observed to have low 100-seed weight (8.5g). High harvest index (39.3%) was produced by genotype, SLJS 1-2 and low harvest index, 24.8 per cent was observed for genotype, SLJS 9-3. Maximum value of seed yield (37.6g) was recorded for genotype, SLJS 41-2 and minimum value (14.6g) for genotype, JS 335. Maximum protein (38.9%) and oil content (22.1%), values were exhibited by genotypes, SLJS 25-1 and SL 525, respectively. Genotype, SLJS 9-3 had minimum protein content (34.2%) and genotype, SLJS 2-1 had minimum oil content (18.8%).

For all characters, phenotypic coefficient of variance (PCV) was more than genotypic coefficient of variance (GCV) at both the locations i.e Ludhiana and Gurdaspur. Maximum GCV and PCV values were obtained for traits like dry weight at 30, 45 and 60 DAS, branches per plant, pods per plant, seed yield per plant. High heritability and genetic advance was observed for number of pods per plant and seed yield per plant and at both locations. For the traits viz seed yield per plant and pods per plant, GCV, PCV, heritability and genetic advance was high at both locations. Correlation analysis at Ludhiana revealed that grain yield was significantly and positively correlated with plant height at 60 days after sowing, plant height at maturity, days to maturity, number of branches per plant, number of nodes per plant,

number of pods per plant, pods per node and seeds per pod. Regarding quality traits oil content was negatively correlated with fresh weight at 30 days and protein content but positively associated with days to flowering. Number of Pods per plant exhibited positive correlation with plant height at 60 DAS, plant height at maturity, number of nodes per plant and fresh weight at 30 DAS and negatively associated with days to maturity. At Gurdaspur, seed yield had significant and positive correlation with fresh and dry weight at 30 and 45 DAS, plant height at 60 DAS and maturity and number of nodes per plant. Oil content exhibited non significant correlation other traits but it was positively correlated with fresh and dry weight at 30 DAS and number of seeds per pod. Number of pods per plant showed positive correlation with days to maturity and number of branches per plant. Path coefficient analysis revealed that maximum positive direct effect was observed for harvest index, dry weight at 60 DAS in case of Ludhiana. Days to flowering and protein content had low direct effect but it had high indirect effect on yield through harvest index and dry weight at 60 DAS, respectively. High negative direct effect was observed for dry weight at 45 DAS. At Gurdaspur, fresh weight at 45 DAS had high direct effect on seed yield. Seed weight had low direct effect but showed high indirect effect (0.311) on seed yield via fresh weight at 45 DAS. High negative direct effect (-5.981), on seed yield was observed for fresh weight at 60 DAS

Diversity analysis was done by using Mahalanobis method and also through SSR markers. Diversity analysis based on Mahalanobis D^2 statistics divided the genotypes into 5 clusters. Maximum inter cluster distance (288464.1) was obtained between cluster 4 and 5 and minimum intercluster distance (15103.7), between cluster 2 and 5. On the basis of morphological data, total of 5 clusters were formed. The genotype, JS 335 was put in cluster 3 along with other 14 genotypes where as SL525 was present in cluster 2 along with other 9 genotypes. Out of 108 SSR markers used, 17 markers were polymorphic and were used for further analysis. Diversity analysis based on marker data categorized the genotypes into 3 clusters. In first cluster, JS 335 was present along with 26 genotypes and SL525 was present in cluster 2 along with other 11 genotypes. Maximum number of genotypes were grouped with JS 335. Parental contribution of each line was calculated on the basis of behaviour of markers towards the parents. The dendrogram figure was compared with parental contribution value. The genotypes in which contribution of JS 335 was high were grouped with JS 335. The genotypes in which contribution of SL 525 was more were grouped with SL 525. The genotypes having equal contribution of SL 525 as well as JS 335 were grouped in third cluster. Comparison of mean seed yield for different clusters revealed that the two genotypes i.e. SLJS 41-2 (32.1g/ plant) and SLJS 43-7 (32.4 g/plant) had 62.5 and 52.94 per cent contribution, from JS 335 and were better yielder than SL 525 (30.0 g/plant), were also resistant to yellow mosaic virus. Thus these two lines should be further evaluated over locations to check their adaptability and yield potential.

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