

EARLY GENERATION SELECTION BASED ON GENETIC PARAMETERS AND MOLECULAR DIVERSITY IN PARENTAL LINES OF SOYBEAN [*Glycine max* (L.) Merrill]

Thesis

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By

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*Pantnagar
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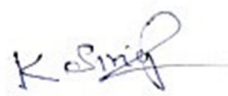
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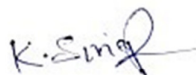
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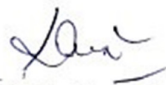
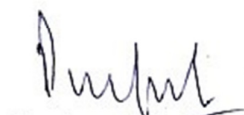

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We, the undersigned members of the Advisory Committee of **Ms. Meenakshi Bisht, Id. No. 42515**, a candidate for the degree of **Doctor of Philosophy** with major in **Genetics and Plant Breeding** and minor in **Molecular Biology and Biotechnology**, agree that the thesis entitled **“EARLY GENERATION SELECTION BASED ON GENETIC PARAMETERS AND MOLECULAR DIVERSITY IN PARENTAL LINES OF SOYBEAN [*Glycine max* (L.) Merrill]”** may be submitted in partial fulfillment of the requirements for the degree.



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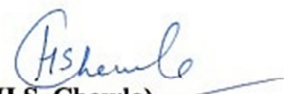
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LIST OF ABBREVIATIONS

ABLs	Advanced breeding lines
ANOVA	Analysis of variance
BPH	Brown Planthopper
cm	Centimetre
cM	Centimorgan
CTAB	Cetyl trimethyl ammonium bromide
dNTP	Deoxynucleotide triphosphate
EDTA	Ethylenediamine tetraacetic acid
EtBr	Ethidium bromide
g	Gram
GCV	Genotypic coefficient of variation
GSV	Grassy stunt virus
IRRI	International Rice Research Institute
°C	Degree Celsius
PCR	Polymerase chain reaction
PCV	Phenotypic coefficient of variation
QTL	Quantitative trait loci
RSV	Ragged stunt virus
RM	Rice microsatellite
SSR	Simple sequence repeat
SSST	Standard seed box screening technique
TBE	Tris-borate- EDTA
<i>viz.</i>	Namely
w/v	Weight/volume



Introduction

Soybean (*Glycine max* (L.) Merrill) is one of the most important and oldest seed legume in the world, contributing approximately 25% to the global edible oil production and about two-thirds of the world's protein concentrate for livestock feeding. Soybean is a self-pollinated crop, belonging to the family Leguminosae. It is an erect bushy plant with a well-defined main stem and branches, with numerous leaves. It is an exceptionally important oilseed crop due to the presence of 40 per cent protein and 20 per cent oil proving to be a nature's gift to mankind. The composition of amino acids makes the protein of soybean a 'complete protein', thereby justifying the title of 'miracle crop'. Based on per hectare production, soybean produces approximately thrice more protein than wheat, rice or maize. It is acknowledged as an excellent source of good quality unsaturated fatty acids (about 85%) and is very high in the essential fatty acids such as oleic acid (23%) linoleic acid (53%) and linolenic acid (7%) (**Fehr et al., 1992**). A recent escalation in research is due to the presence of soybean derived compounds such 'isoflavonoids', which are anti- cancerous, anti-inflammatory and have proved to reduce the level of cholesterol and bone respiration (**Smith and Ann, 2001**). It also has the potential to produce highest yield of protein per unit of land area. In these years of heightened fertilizer prices, the ability of soybean to deliver for its own nitrogen requirements through symbiotic nitrogen-fixing bacteria, *Bradyrhizobium*, thereby leaving a generous amount of nitrogen for subsequent crop is of equal interest. Despite having a flexibility in temperature requirements for its growth, soybean favours an optimum temperature of 30°C for growth and development while a seedbed temperature of 25–33°C for proper emergence of seedlings has found to be optimal.

The cultivation and use of soybean could be traced back to the beginning of China's agricultural age. Soybean, for centuries, has acted as a reliant source of meat, milk, cheese, bread, and oil for the people of Philippines, Japan, Indonesia, China, Manchuria, and Korea. This could be a practical possibility of it, having earned accolades like "Gold from soil" or "Cow of the field". China produced around 80% of the world's soybean around 1921. Soybean was introduced in India from China in

tenth century AD through the Himalayan silk routes and also brought in via Burma (now Myanmar) by Indonesian traders. This was followed by traditional cultivation of soybean on a small scale in Himachal Pradesh, Manipur, eastern Bengal, the Khasi Hills, the Naga Hills, the Kumaon region of Uttarakhand and regions of Madhya Pradesh. Also, the Indian subcontinent is reported to be the secondary center for domestication of the crop after China. India ranks fourth in area and fifth in world's production after USA, Brazil, Argentina and China.

Being the numero uno oilseed crop in India, soybean has become an important crop in a very short span of time covering approximately 11 million ha cultivable area. There are five agro-climatic zones for soybean cultivation in India viz. northern hill zone, northern plain zone, north eastern zone, central zone and southern zone respectively. Specific varieties have been released for each zone in accord to their respective agro-climatic considerations. A record upsurge in soybean cultivation has been observed since the past years with area which was just 0.03 m ha⁻¹ in 1970 reaching upto 11.40 m ha⁻¹ in 2016. Additionally, an enhanced mean national productivity has been observed from 430 kg/ha in 1970 to 1239 kg/ha in 2016 (**IISR, 2017**).

The chief states for soybean growth are Madhya Pradesh, Maharashtra, Rajasthan, Karnataka, Andhra Pradesh, and Chhattisgarh. These states altogether make a contribution of about 98% of the total soybean production in the country. Recent years have shown an upsurge in soybean growing areas covering southern parts of the country, in particular the states of Maharashtra, Andhra Pradesh, and Karnataka. Since the very beginning, Madhya Pradesh has retained the title of being the leader in terms of contribution to the soybean area and production. It currently contributes 47.3% of area (5.40 million hectare) and 40.5% of production (5.72 million tonnes) after which Maharashtra coming second making a contribution of 31.4% (3.58 million hectare) and 27.97% (3.95 million tonnes) in terms of total area and production of the country (**www.sopa.org**). The crop is well suited to be cultivated in most parts of India with states like northeast states, Himachal Pradesh and Jharkhand having good potential for soybean.

The estimates of world soybean area, production and productivity for 2016-17 was 121.93 million ha, 342.56 million tons and 2.81 t/ha, respectively. World productivity level has not yet been achieved in India (11.4 million ha⁻¹, 14.12 million

tons and 1.2 t/ha, respectively) where area, production and productivities are still low (IISR 2017). In Uttarakhand, the estimates of soybean area, production and productivity for 2016-17 is 11585 ha, 13355 metric ton and 1153 kg/ha, respectively. Low productivity in India is mainly due to the short growing period available in subtropical conditions, limited varietal stability and narrow genetic base of soybean cultivars (Singh and Hymowitz, 2001).

For a plant breeder, a proper understanding and estimation of genetic variability is a pre-requisite. But the continuous exploitation of the variability has narrowed down the genetic base of the cultivated varieties to such an extent that it resulted in an augmentation in the losses due to biotic and abiotic stress factors thereby becoming a major concern for plant breeders. Hence, it is of utmost priority to regenerate the variability among the genotypes. Variability can be created either through hybridization of genetically diverse parents or through induced mutation. Among the both hybridization is most commonly used and most preferred method for creation of variability. Exploitation of hybrid vigour in autogamous crop species like soybean is useful in improving yield potential of the existing cultivars by identifying potential cross combinations on the basis of heterosis aimed at isolating gene combinations. The primary objective of any breeding programme is to recover progenies which are superior to parent. This can be facilitated by incorporating transgressive breeding which can aid in increasing the soybean productivity. Transgressive segregation is the appearance of individuals with traits falling outside the parental range in segregating generations in both positive and negative direction and such plants are produced by the accumulation of superior genes from both the parents as a result of recombination. Heterosis or hybrid vigour concept was started with the studies reported by Shull (1908). Extent of heterosis for yield and its components helps the plant breeders in making correct decision about material selection method, type of variety and extent of testing. The study of heterosis, i.e. manifestation of heterozygosity, helps the breeders in eliminating less productive crosses in F₁ generation itself. The rejection of crosses showing no heterosis would enable the breeders to concentrate the attention to a few but possibly more productive crosses. The magnitude of heterosis provides a basis for genetic diversity and guide for the choice of desirable parents for developing superior F₁ hybrids so as to exploit hybrid vigour and/or for building gene pools to be employed

in breeding programme (**Sharma and Maloo, 2017**). In practical plant breeding standard heterosis is more important. For developing elite strains, the identification of genetically superior parents is an important prerequisite. For handling of segregating generations in selected crosses, individual plant selection on visual basis is quite common. However, it would be more advantageous if visual selection could be supplemented by artificial selection in early generations

For an efficient and conventional improvement in the crop, selection of yield attributing characters is important and selection in such characters is mainly dependent on the nature and magnitude of heritable variations. The competency of selection is not only dependent on the extent of genetic variability present in the population but also the heritability of concerned trait. Moreover, unidirectional selection for a trait may cause an unexpected dimension of other traits by direct and indirect effect via third variable. Therefore, it is highly important for a plant breeder to minutely observe the magnitude and nature of association among the traits for which amelioration is desired. The zenith among the possible objectives of all breeding programmes is high yield, but in general yield has low heritability due to which direct selection is not considered effective. Since, seed yield is a quantitative character, it is usually under the influence of various environmental factors and thus not an efficient character for selection. Hence, an understanding of the extent of relationship between yield and its various components is an important parameter for any plant breeder. This will inescapably expedite the selection process of desirable characteristics (**Jain *et al.*, 2015**). For the selection process of superior genotype, numerous biometrical techniques have been used consistently that can give knowledge regarding the relative contribution of various component traits towards seed yield. Taking an example, a technique named correlation coefficient is used to give us an insight into the association between different characters and thereby helping us to identify important characters that can be studied during selection. Thus, one must be well acquainted with correlation between grain yield and other attributing traits for an effective selection of suitable plant type along with concurrent advance in several other characters. Despite being very useful for quantification of size and direction of trait associations, correlation coefficients can be very much misleading in a way that a high correlation between two traits is a consequence of the indirect effect of other traits. Therefore, path coefficient analysis

(Sewall Wright, 1921) is suggested to be applied in order to determine the direct and indirect effect for one variable upon the other which further allows for the separation of correlation coefficient into direct and indirect components (Dewey and Lu, 1959). Hence, an amalgam of both the techniques viz. correlation co-efficient and path co-efficient analysis serves as a powerful tool to verify the character association in a particular crop and thus its ultimate effect on overall yield.

For any plant breeder, a productive breeding procedure is the one which escalates genetic gain per year. A breeding procedure in which the breeder conducts the test on the heterogeneous population in earlier generation rather than in late is known as 'Early generation testing'. Early generation testing, if successful, may help to identify and select potential cultivars in the early phase of breeding program itself thereby preventing any loss of preferable recombinants. Thus, selection would prove to be beneficial in F_2 and F_3 generations as these are largely heterogeneous populations. Nonetheless, it is only in the presence of the additive gene effects that early generation selection would be fruitful in those characters. Therefore, it would suffice to say that early generation selection has provided the breeder a level of convenience to perform selection at an early stage thereby saving labour, time and cost involved in testing the genotype up to late generations F_6 or F_7 .

In any of the crop improvement programmes, plant breeders make it a priority to estimate the accessible genetic variability. This is important to accurately distinguish between different genotypes in order to work out any breeding program, population-genetic analysis and genetic engineering and to determine the extent of variation within genotypes and between genotypes. This is useful for predicting potential genetic gains in a breeding programme and in setting up appropriate cross-breeding strategies. Interpreting the genetic divergence and relatedness among breeding materials has significant implications for improvement of crop plants. Molecular markers have been established as a most authentic method that accurately assesses the genetic variability. Being least affected by the environmental factors, DNA markers are reliably identified as favorable tool for examining the genetic diversity among germplasms (Lee, 1995). Due to a higher degree of polymorphism, simple sequence repeat (SSR) markers have been established as attractive tools that are being largely used in genome studies, marker-assisted selection and cultivar identification (Song *et al.*, 1999; Cregan *et al.*, 1999).

In consideration of the above facts as well as the importance of soybean crop, the present study was undertaken on fourteen F_2 and F_3 crosses and twenty parents with the following objectives.

1. To estimate the effectiveness of early generation selection in F_2 and F_3 based on genetic parameters
2. To estimate the manifestation of residual heterosis in F_2 and F_3 generations.
3. To examine the frequency of transgressive segregants in F_2 generation.
4. To assess the inter-character associations and direct and indirect effects of different component characters on yield.
5. To study molecular genetic diversity among the parents using the molecular marker technique.

*Review
of
Literature*

The primary element of any crop breeding programme is the genetic diversity, inbuilt or generated artificially. The entire concept of plant breeding is rested on the foundation of selection which becomes inefficient in any crop for the trait(s) under selection if this variability becomes non-existent. The inherent part of any planned crop breeding program are Correlation studies and Path-coefficient analysis which thereby facilitating a fundamental conceptualization of character association and contribution of different characters towards the enhancement of yield levels. This is the ultimate objective of all the crop improvement programs. The applicable literature available linking the various aspects of the present study on soybean are reviewed in order to obtain a thorough understanding of the subject and have been described under the following heads:

- 2.1. Early generation selection
- 2.2. Residual heterosis
- 2.3. Transgressive segregation
- 2.4. Inter-character correlation
- 2.5. Path coefficient analysis
- 2.6. Molecular genetic diversity

2.1. Early generation selection

Genetic variability has become a basic requirement for successfully carrying out any crop breeding programme. Hence, it is essential to have a thorough knowledge of genetic variability which renders crop breeding much easier by facilitating the selection of superior genotypes in different generations (**Skaloud and Kovacik, 1994**). The chief constituent of any agricultural production system is its genetic variability. (**Brown, 1978 and Frankel *et al.*, 1995**). Grain yield in soybean, as in other crops is a complex trait which is dependent on a number of variables (**Dong *et al.*, 2001**). In soybean, innumerable studies have been carried out till date which had accounted the nature and magnitude of variability.

Johansson (1909) ascribed the genetic and environmental components of variation to both heritable and non-heritable factors thereby concluding that the variation in a pureline is non-heritable since environmental factors were solely responsible for the variation.

The concept of splitting up of the genotypic variance into three components *viz.* additive, dominance and interaction components was given by **Fisher (1918)**. **Hayman and Mather (1955)** partitioned the epistatic component into three types *viz.* additive x additive, additive x dominance and dominance x dominance.

Heritability refers to the index of transmissibility, which measures the genetic relationship between the parents and their offsprings. Heritability generalizes as to how much emphasis must be laid on a particular trait for its selection. The ratio of additive genetic variance to the total phenotypic variance is known as heritability (**Wright, 1921**).

Lush (1949) divided heritability into broad sense and narrow sense. Broad sense heritability is the ratio obtained by dividing total genotypic variance by total phenotypic variance and is expressed in percentage. Narrow sense heritability is determined by dividing the additive genetic variance by total phenotypic variance and the ratio is expressed in percentage.

The difference between the genotypic values of the selected plants and, of the original population is known as genetic advance under selection. The genetic gain that can be obtained for a particular trait though selection is the result of its heritability, phenotypic standard deviation and selection differential (**Burton and De Vane, 1953**).

Puspendra and Ram (1987) used North Carolina Design I, correlation and regression techniques to analyze the heritability estimates from F₂ to F₅ generations of the two crosses *viz.* UPSM 534 x PK 86 and UPIR 1 x Bragg thereby obtaining large heritability values for plant height, seed weight and days to flowering which further suggested effective selection for these traits.

Singh et al. (1995) evaluated genetic variability, heritability and correlation coefficients in 51 soybean genotypes grown during *kharif* season 1987 for 8 yield attributing traits. Highest heritability was detected for 100 seed weight (94.5%),

followed by days to flowering (93.2%) and days to maturity (79.1%) in 18 vegetable soybean varieties.

Malik *et al.* (2006) concluded highly significant differences for genetic variability among 25 soybean genotypes studied for 16 yield and its attributing traits that included oil and protein contents. High heritability for days to 50% flowering, days to flowering completion, days to pod initiation, days to maturity, 100-grain weight, leaf area, plant height, oil and protein contents were accounted which implied the presence of additive type of gene action. The remaining characters represented moderate to low levels of heritability. High GCV and PCV values were reported for number of unfilled pods per plant (GCV = 45.88% and PCV = 55.59%) and number of shattered pods per plant (GCV = 63.09% and PCV = 75.11%).

Gupta and Punetha (2007) analyzed 33 genetically diverse genotypes of soybean and evaluated genotypic and phenotypic variability, heritability and genetic advance for 12 quantitative traits including seed yield and vigour. From the study, it was interpreted that the highest magnitude of genetic variability was displayed by number of pods per plant, followed by seed vigour, seed yield per plot and number of seeds per pod. It was concluded that the highest values of heritability (98.91%) and expected genetic advance (40.22%) were for number of pods per plant.

Balla and Elrayah (2010) assessed the genetic variability among 21 genotypes of soybean for which 6 traits were considered into study. Significant dissimilarities among genotypes for all the traits under study were brought out by ANOVA. Small to very large variations were reported among the magnitudes of PCV over GCV for all the corresponding traits. Minimum values of PCV and GCV were observed for days to maturity (17% and 16%, respectively), whereas maximum values varied among the characters. There was a significant variation for the estimates of heritability (h^2) from 43% (number of pods per plant) to 85% (grain yield). It was observed that the highest genetic advance as% mean (GAM) were for grain yield (17.9%), while the lowest was recorded for days to maturity (3.0%). It was the high estimates of heritability coupled with genetic advance that indicated the existence of sufficient amount of variability for selection to bring about the advancement of such traits.

Ramteke et al. (2010) studied important economic characters of 92 released varieties of soybean in India. The studied traits included plant height, days to 50% flowering, days to maturity, nodes per plant, branches per plant, 100-seed weight, grain yield, oil and protein contents. The genetic variability among these varieties was evaluated. Highly significant differences were recorded among the genotypes for all the characters under study. It was demonstrated that the characters like days to maturity, days to 50% flowering, plant height, nodes, oil and protein contents were highly heritable suggesting an additive gene action for the concerned characters and hence an improvement of these characters for effective selection.

Aditya et al. (2011) evaluated the genetic parameters by considering 8 quantitative traits among 31 soybean genotypes. The results revealed significant differences among the genotypes for all the concerned traits under the course of research. The magnitude of GCV and PCV were retrieved in the same range. The values for different traits ranged from 4.34% (days to 50% flowering) to 41.83% (seed yield per plant) for GCV and from 4.55% (days to 50% flowering) to 47.74% (seed yield per plant) for PCV. Highest heritability (91%) was observed for three characters viz. days to 50% flowering, number of primary branches per plant and 100-seed weight. High genetic advance as percentage of mean (GAM) was recorded for number of pods per plant (45.46%) and the lowest value for number of primary branches per plant (1.24%). High heritability in conjugation with high genetic advance broadens the scope for improvement of concerned characters through selection.

Bekele et al. (2012) estimated genetic variability among 49 soybean germplasm introductions on the basis of 17 characters including oil and protein contents. It was revealed that the estimates of PCV were significantly higher than that of GCV for all the characters under observation. The highest value of PCV (%) and GCV (%) were recorded to be 28.54% and 18.4% for plant height, followed by seed yield per plant (25.53% and 7.40%) and lodging (25.47% and 17.39%). It was observed that there were moderate to low levels of heritability for all the characters under study with the highest and lowest values observed for days to flowering (59.59%) and harvest index (0.00%). Highest value of genetic advance as percentage of mean (GAM) was observed for plant height (24.69%). This was followed by lodging (24.51%) and shattering

(23.60%), while the lowest values are recorded for harvest index (0.00%) followed by branches per plant (1.10%) and nodes per plant (2.26%).

Ghodrati (2013) evaluated 12 soybean genotypes during three crop growing seasons in order to study the genotypic variation and heritability in broad sense (h^2_b) for seed yield and other quality traits. The results revealed significant differences for seed yield and quality characters implying adequate genetic variability for efficient selection. High values for heritability in broad sense (81%, 76% and 74%) and genetic advance (0.35, 0.20, and 0.40) were recorded for the number of nodes per plant, days to flowering and plant height, respectively. The lowest values for heritability and genetic advance were reported for seed yield, 1000-seed weight, branches per plant, pods per plant, seeds per pod, number of seeds per plant, biological yield, harvest index, protein yield, oil and protein contents.

Pushpa Reni and Koteswara Rao (2013) evaluated the genetic variability for 45 soybean genotypes in order to estimate the variability, heritability and expected genetic advance for 13 traits including yield and the attributing traits. Analysis of variance displayed significant deviations among the genotypes for all the traits under observations. The study revealed high values of PCV (%) and GCV (%) for branches per plant (31.92% and 30.56%), pods per plant (38.19% and 37.26%), biological yield (23.98% and 22.10%), harvest index (24.70% and 22.72%) and yield per plant (40.44% and 38.51%). This implied that these traits have a broader adaptability with minimal environmental interference in their expression. High heritability (%) in conjunction with high expected genetic advance (GA%) was recorded for plant height, days to 50% flowering, number of branches per plant, pod length, number of pods per plant, number of seeds per pod, 100-seed weight, biological yield per plant, harvest index and seed yield per plant. This further concluded that additive gene action has a role in the expression of these traits and suggesting an enormous scope for trait improvement through direct selection.

Adsul and Monpara (2014) studied 100 germplasm lines of soybean and observed the selection indices and variability for 6 quantitative traits. It was recorded that a moderate to high amount of GCV values with high heritability and high genetic advance were estimated for all the traits under observation. This further suggested that

improvement in these traits through selection is highly recommended. Highest PCV (%) and GCV (%) values were reported for pods per plant (40.22% and 35.84%) followed by seed yield per plant (38.45% and 34.14%) and pod clusters per plant (32.64% and 27.53%). The range of estimates of heritability (broad sense) were from 86.91% (biological yield per plant) to 70.55% (harvest index) while for genetic advance as% mean (GAM), the range was from 65.80% (pods per plant) to 24.49% (harvest index).

Amrita et al. (2014) considered various genetic parameters from genetic variability to heritability, from correlation to path coefficient analysis etc. to study 26 advanced generation lines of soybean. When the observations recorded on 11 characters revealed significant differences among all genotypes. A comparison of magnitudes of GCV (%) and PCV (%) reported higher values for PCV (%) over GCV (%) for all characters under study. Number of branches per plant (32.05% and 29.40%) showed highest PCV (%) and GCV (%) values followed by seeds per plant (31.87% and 28.65%) and seed yield per plant (30.63% and 27.68%), while the lowest values for PCV (%) and GCV (%) were reported for reproductive phase days (5.59% and 4.69%). The estimates of heritability in broad sense (h^2_b) were high for all the characters under study with the values ranging from 95.87% (vegetative phase days) to 56.74% (seeds per pod). High estimates of heritability coupled with high genetic advance as% mean (GAM) were reported for plant height, branches per plant, pods per plant, seeds per plant, 100-seed weight, biological yield per plant and yield per plant indicating a possibility of improvement in these characters through direct selection.

Baraskar et al. (2014) studied the genetic variability, heritability and genetic advance among 61 genotypes of soybean for 15 yield contributing characters. The analysis of variance revealed significant dissimilarities for all the characters under consideration. Estimates of PCV and GCV revealed that the values of PCV were higher than that of GCV, with a narrow difference between these two estimates for all the traits, thereby indicating least influence of environment on the expression of these traits. High values of PCV and GCV were reported for clusters per plant (42.73% and 38.12%), seed yield per plant (33.46% and 22.95%), biological yield per plant (27.74% and 19.07%), number of pods per plant (27.23% and 16.56%) and plant height (22.96% and 20.53%) indicating adequate genetic variability in these traits for improvement

through selection. High estimates of heritability coupled with high genetic advance as% of mean (GAM) for plant height, primary branches per plant, pod clusters per plant, biological yield per plant, seed yield per plant and pods per plant. This suggested effective selection in these traits.

Baruah *et al.* (2014) estimated the genetic variability in 44 genotypes of soybean indigenous to North-eastern India. High heritability were observed in traits including seed yield and its component traits. The results revealed the traits to exhibit a wide variation among the genotypes. Highest PCV and GCV values were recorded for 100- seed weight (69.12% and 68.35%) followed by seed yield per plant (48.74% and 48.42%) and seed number per plant (48.49% and 48.30%), while for days to maturity (2.74% and 2.25%) and days to 50% flowering (8.96% and 7.35%) the lowest values were observed. The estimates of heritability exhibited highest value for seed number per plant (99.19%) whereas the lowest being reported for days to maturity (44.67%). Estimates of genetic advance (GA%) was shown to have highest value for 100-seed weight (139.24%) and lowest value for days to maturity (3.80%), respectively.

Hakima *et al.* (2014) obtained the genetic variability and expected genetic advance in the F₂ progenies of soybean from crosses comprising 3 parental combinations. They considered 8 characters. The observed mean variability for these characters ranged from 11.7% (branches per plant) to 52.6% (seed weight per plant). Among the F₂ progenies, estimates of variability for different traits under study were found to be low to moderate, whereas the range of their respective mean values were from 18.7% (seed weight per plant) to 56.1% (for both pods per plant and seed size). It was also observed that the estimates of expected genetic advance (%) ranged from low to moderate. *i.e.* from 12.3% (branches per plant) to 47.2% (pods per plant). From the results obtained, it was concluded that the agronomic characters like plant height, seed size, pods per plant and days to maturity exhibited high coefficients of variability in conjunction with high heritability and genetic advance. Thus, on the basis of selection for plant height, pods per plant and seed size, development of early maturing and high yielding soybean varieties was found to be practically possible..

Kumar *et al.* (2014) assessed nine soybean genotypes along with 3 checks *viz.* PS 1347, SL 688 and Bragg in order to evaluate the genetic variability and character

association for 11 characters. These characters included yield and its attributing traits. There were significant differences that were revealed among genotypes for all the characters under study after conducting by Analysis of variance. The values of PCV and GCV were observed to be coherent with the values of PCV recorded slightly higher than that of GCV. The variations in the values of PCV were found to be in the range from 2.08% (pod length) to 21.42% (plant height), while that of GCV varied from 1.58% (pod length) to 20.20% (seed yield per plant). There were higher estimates of heritability for majority of the characters. The highest observations were for biological yield per plant (99.80%), while the lowest were for pod length (50.00%). Estimates of genetic advance affirmed highest value for plant height (17.85%), while the lowest value was reported for pod length (0.14%). Thus, a direct selection of the characters illustrating high heritability and high genetic advance leading to satisfactory enhancement in the characters studied must be realized.

Malek *et al.* (2014) assessed genetic variability among 27 mutant genotypes of soybean and 4 parental genotypes. In consideration of 9 morphological traits, significant differences were observed among the mutants and parental genotypes for all the traits under study. There were eighteen mutants that performed superior over their parents with respect to grain yield and other morphological as well as yield contributing traits. There were narrow differences between phenotypic and genotypic coefficients of variation (PCV and GCV) that were recorded for greater number of the traits under experimentation thereby indicating environmental influence to be minimal. The highest and the lowest values of PCV and GCV that were observed for branches per plant were 38.11% and 35.03% and for days to maturity were 7.22% and 6.35%. The highest values of heritability were recorded to be 93.73% for 100-seed weight. This was further succeeded by plant height (87.74%) and branches per plant (84.70%). The lowest heritability was recorded to be 77.40% for days to maturity. The percent genetic advance was observed to be highest for branches per plant (66.33%), while it was reported to be lowest for days to maturity (11.50%). High heritability along with high GA (%) are the two parameters that must be considered as favourable aspects for any crop improvement program through phenotypic selection.

Sureshrao *et al.* (2014) studied 12 soybean genotypes in order to examine the genetic variability parameters after assessing 13 component traits for yield. The

revelations obtained from analysis of variance brought out significant differences for majority of the traits under study except for the number of grains per plant, thereby predicting the availability of massive amount of genetic variability. The estimates of PCV and GCV were in accord to the above prediction, with the highest values being reported for the number of pods per plant (PCV = 40.83% and GCV = 40.42%), while the number of grains per pod reported lowest values (PCV = 3.85% and GCV = 2.33%). The estimates of heritability were in the range from moderate to high values for all the traits under study. It was acknowledged that highest heritability was for days to maturity (98.50%) while the lowest value was recorded for number of grains per pod (36.70%). The estimates of genetic advance (GA%) exhibited highest value for the trait number of pod per plant (82.43%), while the lowest value was observed for the number of grain per pod (2.91%).

Badaya *et al.* (2015) evaluated the genetic variability and path analysis for 60 soybean genotypes on the basis of reproductive phase, not only but also estimated the quality traits for their affiliation with yield. The values of PCV and GCV ranged from 3.40% and 4.14% (protein content) to 25.38% and 26.93% (seed yield per plant). It was observed that the heritability was highest for days to full flowering (97.93%), while least for protein content (67.30%) and oil content (77.78%). The maximum values of genetic advance as percentage of mean (GAM) were recorded for seed yield per plant (49.28%), while the lowest were observed for protein content (5.75%) and oil content (8.67%). These low estimates of heritability and genetic advance for oil and protein contents implied that the expression of these traits could be due to non-additive gene action.

Kumar *et al.* (2015) calculated the extent of genetic variability after taking account of 42 genotypes of soybean so as to estimate agro-morphological traits. On applying, Analysis of variance for yield and its attributes, significant differences were demonstrated among all the genotypes for all the observed traits. On retrieving the results, it was revealed that the phenotypic and genotypic coefficients of variation (PCV and GCV) displayed near about identical trend of division. Highest PCV (21.30%) and GCV (19.24%) being exhibited for number of pod clusters per plant. High heritability was recorded for grain yield (87.43%), followed by number of clusters (81.62%) and number of pods (81.20%), whereas days to 50% flowering showed

negative heritability (-0.08%). It was demonstrated that estimates of genetic advance as percentage of mean (GAM) had higher values for number of clusters (35.81%), followed by number of pods (33.89%), and grain yield (25.07%). Higher values of heritability, along with competent grade of genetic advance, revealed a scope for trait improvement of through direct selection.

Dubey *et al.* (2015) determined the genetic variability among 50 soybean genotypes and the obtained results exhibited a higher phenotypic coefficient of variation (PCV) than that of genotypic coefficients of variation (GCV) for all the traits which were under experimentation. This range of magnitude between the values of PCV and GCV for most of the characters remained consistent. It was due to a lower levels environmental influence on the expression of traits under study. Higher values of heritability were recorded for maximum characters. Conjunction of high heritability (h^2_b) along with higher values of genetic advance as per cent of mean (GAM) were recognized for biological yield per plant, harvest index, number of seeds per plant, seed yield per plant and the number of pods per plant. These results concluded that improvement for these traits through direct selection is favourable.

Jain *et al.* (2015) not only estimated the genetic variability but also assessed correlation coefficient and path analysis among 41 soybean genotypes for 9 important yield and its related attributes. The estimates of PCV were observed to have greater value than those of GCV with only a slight deviation between both the estimates for all the traits under study. The largest value of GCV was observed for plant height, followed by number of primary branches and seed yield per plant. It was concluded that parameters, such as days to 50% flowering, 100-seed weight and seed yield per plant displayed higher estimates of heritability (%). Further, it was inferred that improvement of yield through selection based on these traits should be probable.

Mahbub *et al.* (2015) assessed the genetic variability among 28 genotypes of soybean for 11 morphological characters and significant differences were found among the genotypes for all the traits under consideration. Additive gene action was observed for characters like plant height, seed yield per plant, number of branches per plant, number of pods per plant, number of seeds per pod, and 100-seed weight. Therefore, a improvement of concerned characters through selection was found to be favourable.

They observed moderate to low values of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for all the traits concerned. Highest GCV was observed for seed yield per plant (31.45%), whereas highest heritability was observed for days to maturity (99.93%).

Manav and Arora (2017) determined yield and seedling characters of 45 germplasm accessions of soybean in order to determine genetic variability parameters at CCSHAU, Hisar during kharif season, 2014. A wide range of variability for different characters was considered. It was shown that the number of pods displayed largest variability. Minimum variability was shown by seedling dry weight. A close agreement was observed between GCV and PCV for traits viz. number of days to maturity, plant height and number of branches per plant. Out of 13 characters observed, number of pods per plant had displayed both highest heritability as well as maximum genetic advance.

Satpute *et al.* (2016) determined the genetic variability parameters in 47 soybean accessions at ICAR-IISR during *kharif*, 2017. The results revealed that number of seeds per pod and days to 50% flowering exhibited wide range of variations. On the other hand, traits such as seed yield per plant, number of nodes per plant, pods per plant, days to flowering and hundred seed weight have displayed highest PCV and GCV. Moderate to low estimates of PCV and GCV were reported for branches per plant, seeds per pod and days to maturity. Furthermore, they have observed that there was high heritability in conjunction with high genetic advance for days to flowering, days to pod initiation, days to maturity, plant height, number of nodes per plant, seed yield per plant.

Chandrawat *et al.* (2017) conducted an experiment with 41 soybean accessions and five checks (two local + three national checks). This was to estimate the genetic variability. They observed that the Analysis of variance has displayed significant variability for all the traits under consideration. High values of GCV and PCV were noted for characters viz., number of pods per plant (35.45, 38.62), plant height (23.49, 25.84), yield per plant (21.35, 24.86) and number of branches per plant (20.58, 24.22). There were six characters that have shown high heritability coupled with high genetic advance. These attributes included pods per plant, plant height, yield per plant, branches per plant, trypsin inhibitor content and 100 seed weight thereby indicating the existence of additive gene action.

Desissa (2017) conducted experiment with 16 soybean accessions in randomized complete block design with three replications in the season 2015-2016. The parameters that were included for investigation were on days to 50% flowering, Days to pod setting, Days to 95% maturity, plant height and number of branch per plant, number of pods per plant, number of seeds per pod, pod length, Leaf Area Index, Biological yield, hundred seed weight, Grain yield and Harvest index. In the experiment, mean values were computed and used by the researcher in order to estimate the Genotypic and Phenotypic Variance, Genotypic coefficient of variation (GCV), Phenotypic Coefficient of Variation (PCV), heritability and genetic advance percent of mean for each trait. Significant variation was displayed by all the characters and the coefficient of variation was having a comparably lower value. There was 70% higher heritability for all characters under consideration except for the number of branches per plant, leaf area index, harvest index and days to flowering, while expected genetic advance percent of mean ranged from low (1.98%) in harvest index to high (42.2%) in biological yield in ton/ha. It was revealed in this investigation, that high heritability with high genetic advance as percent of mean was found for plant height (84.59%, 21.3), pod length (89.2%, 35.3) and biomass yield (94.46%, 42.2), respectively. Also, high heritability in conjunction with moderate genetic advance was observed for number of pod/plant (89.8%, 11.43%), and days to 95% maturity (91.46%, 9.96), respectively.

After reviewing the literature on early generation testing in soybean, it was concluded by **Voigt and Weber (1960)** that selections from early generation testing were comparably superior in yield than those selected from pedigree and bulk method.

The progenies selected among the F₃, F₄ and F₅ progenies for yield were evaluated, by **Brim and Cockerham (1961)**. The yield was observed to be 30, 44 and 50 per cent greater, for F₃, F₄ and F₅ progenies respectively, than the expected gain after selecting among F₂ progenies. In conclusion, the investigation exhibited that selfing F₃ and F₄ generation before evaluation of progenies must be advantageous.

Horie (1967) assessed the hybrid F₂ population. Also, he investigated the feasibility to use of genetic parameters in breeding and the selection response in early generation.

Boerma and Cooper (1972) assessed the consequence of early generation yield selection in four crosses of F_2 derived soybean lines. There was gain in mean yield per generation for two crosses while in other crosses, no net gain in yield was revealed.

Boerma and Cooper (1975a) determined the efficiency and potency of three selection programs i.e., early-generation yield testing (EGT), pedigree selection (PS), and single-seed-descent selection (SSD) so as to confine high yielding lines. The selected lines were compared in each selection program but no consistent differences were observed in the mean of all selected lines, the mean of the five highest-yielding lines and the highest yielding line from each population. But the SSD method was observed to be the most effective procedure since it requires relatively less resolution for selection than the early generation testing. Additionally, pedigree method allows an accelerated advance of the early-generation segregating population as it doesn't take into consideration the expensive yield testing until later generations.

Wilcox and Schapaugh Jr. (1980) employed twelve soybean crosses for selecting the phenotypically superior plants in F_2 through F_4 generation. The visual selection of phenotypically superior plants from heterogeneous bulk population displayed no significant consequence on seed yield.

Costa *et al.* (2008) evaluated the broad sense and narrow sense heritability in F_3 populations which was deduced from six two-way crosses in soybean. The investigation revealed highly significant differences among families and wide variation in the experimental coefficient of variation (C_{Ve}), the C_{Vg}/C_{Ve} ratio and the heritability among different traits. The highest values were found for the number of pods, number of seeds and grain yield. Based on these results, it was concluded that determination of genetic parameters in early generation is favourable for directing the selection process in breeding experiments.

Carvahlo *et al.* (2009) manifested the advantage of using early generation testing for grain yield in soybean. They had exploited a population that was derived from a two-way cross between lines 14 and 38 and assessed one hundred $F_{2:4}$ and one hundred progenies $F_{4:6}$ in the 2006/07 growing season in a lattice square design in two locations with replicated 4 times. A 60% higher estimates of expected response to selection was recorded in the $F_{4:6}$ generation and it was deduced from these results that

early generation testing for grain yield in soybeans can be favourable for moderate selection intensities.

Karnwal *et al.* (2009) evaluated the efficacy of early generation selection in two interspecific crosses viz. (PK-472 x *Glycine soja*) x PK-472 and, (Bragg x *Glycine soja*) x Bragg for yield and its attribute. It was demonstrated that there were significant differences in the mean of the selected F₃ progenies for yield and its contributing traits, thereby suggesting the availability of genetic variability in both crosses for selection. On the basis of obtained results, the superiority could be deduced in terms of mean of selected progenies, number of progenies superior and / or / significantly superior to better parent and their respective yield, genetic advance over the bulk and better parent, genetic advance in F₄ generation in both the crosses, selection for dry matter, pods/plant, plant height, harvest index and yield *per se*. Thus, the above mentioned parameters are convincing enough for yield improvement in early generations in interspecific crosses of soybean.

Singh and Sharma *et al.* (2016) determined the efficacy of different selection standards to comply with, in early generation in two crosses of soybean viz. Pusa 16 x T 49 and Alankar x PK 262. The different selection standards used were; (i) selection of F₂ generation plants that have high and low mean values for different characters; (ii) randomly selected plants and; (iii) selection of plants based on an index that involve highest mean values for the different characters. The results thus obtained, by them were; (a) that the plants which were selected for single character were identified to have more number of F₄ progenies than those selected, on the basis of an index and random selection in both crosses, (b) plants selected for their high mean values further screened more number of F₄ progenies than having low means; (c) selection of plants in F₂ generation based on number of pods per plant examined to be most efficient selection criteria for seed yield improvement.

Eddakalathur *et al.* (2016) studied the F₂ generation of cross C-152 x IC 68786 for efficiency of early generation selection. The parameters such as test weight, days to 50% flowering, days to 50% maturity, pod length, plant height and number of seeds per pod were reckoned to have low GCV and PCV values in accord to the conclusion that these traits have lower variability in the material. Positively skewed

frequency distribution of F_2 population disclosed that the grain yield per plant, number of cluster per plant, days to 50% maturity, test weight and number of pods per plant displayed a positively skewed distribution while traits like plant height, number of seeds per pod, days to 50% flowering and pod length are shown to be negatively skewed in the frequency distribution curve.

Govintharaj *et al.* (2016) investigated the effectiveness of early generation selection in bacterial blight resistance genes; that were introgressed F_2 and $F_{2.3}$ population of the cross CB 174 R $\times$ IRBB 60 in rice. Selection differential was observed to be positive for all concerned traits. Also, the selection response was observed to be higher for number of grains; while realized heritability was revealed to be higher for number of grains and thousand grain weights. It was observed that expected selection response and predicted genetic gain is high for number of grains. The reports on parent-offspring correlation displayed low but significant association for number of productive tillers ($r=0.47^{**}$, $P<0.01$), single plant yield ($r=0.35^{**}$, $P<0.01$) and ($r=0.30^*$, $P<0.05$) panicle length in F_2 and $F_{2.3}$ generation, thereby suggesting favourable selection in early generation.

2.2. Residual heterosis

Heterosis is the superiority of F_1 over parents in terms of yield or some other characters. Heterosis depends upon the differences in allele frequency between the parents. In the manifestation of heterosis, importance of genetic diversity was reported by **Moll *et al.* (1962)** and **Moll *et al.* (1965)**. **East and Hayes (1912)** accredited the seed vigour of the F_1 to its heterozygosity. Thus, heterosis will amplify with increasing number of genes in which a plant is heterozygous. **Shull (1914)** was first define the term 'heterosis'; as superiority of the F_1 hybrid over both of its parents in terms of yield or some other characters. Usually, heterosis is the direct manifestation of increased vigour, size, growth rate, yield or some other traits. A number of investigators have accounted the extent of heterosis in soybean for differential development, yield and yield attributing characters. As early as **1924**, **Wentz and Steward** detected substantial amount of heterosis for seed yield and plant height in several inter-varietal soybean crosses.

Rao *et al.* (1978) studied nine F₁ hybrids derived from crosses that involved the varieties Local Black and Kalitur, as male parents; and six introduced varieties. Heterosis for percentage seed yield over that of the better parent was averaged 70.51%; with N49 X Local Black, Davis X Local Black, Monetta X Local Black, N49 X Kalatur and Davis X Kalatur exhibiting >100% heterosis. Classified on the basis of yield, height and number of seeds, pods and branches per plant; the crosses N49 X Local Black, N49 X Kalatur and Davis X Kalatur emerged as the most befitted for exploiting heterosis for these traits.

Thseng (1980) examined diallel cross of two determinate and two indeterminate varieties. Heterosis were evaluated for number of pods per main stem, number of seeds and seed yield in the F₁ of crosses between different types. Effects of non-allelic interactions detected for several characters were of higher amplitude in crosses between different varieties than those between same varietal types. In different varietal crosses, transgressive F₂ segregants for all traits under consideration except for the number of branches were carried into the F₃ and F₄ but; in crosses of the same type only those for height, number of pods per main stem and number of nodes were carried into the F₃ and F₄.

Guleria *et al.* (2000) examined 30 F₁ and F₂ soybean hybrids and their 13 parents for estimating the extent of heterosis for 7 agronomic traits (seed yield, number of pods/plant, internode length, number of primary branches/plant, plant height, days to flowering and days to maturity). The mean heterotic values for F₁ and F₂ hybrids were 22.06% and 11.45% for seed yield, respectively, over their better parents. A true heterotic effect was manifested for seed yield, where F₁ and F₂ hybrids had mean heterotic values of 56.67 and 53.3%, respectively, over the control. On the basis of specific combining ability effects and heterotic values, the best combinations of crosses were DS 83-20 x PB 1, DS 8 xPB 1 and Himso 558 A x Bragg.

Zhang and Yang (2000) evaluated three crosses between Chinese and American semi dwarf soybean genotypes and demonstrated that heterosis was predominant in the F₁; for many agronomic traits. There were marked differences that were observed between the parents with respect to branching giving rise to great variation in the progenies for this character. Heritability values for plant height, number of nodes on the main stem and 100-seed weight were comparably higher; as well as the heritability values for branch characters.

Wang *et al.* (2002) estimated F_1 seed yield heterosis among the 1326 highly heterotic cross combinations; at seven locations. The observations demonstrated that the average high parent heterosis (HPH), mid-parent heterosis (MPH) and control variety heterosis (CKH) was 6.8, 21.0, and 11.9%, respectively. The percentage of crosses with HPH and CKH over 20% and 18.3% was in the first yield test, whereas the average HPH and CKH was 22.5 and 21.1%, respectively. The percentage of crosses with HPH and CKH were over 20% was 22.1% in the second yield test. On examining the different patterns of crosses, it was indicated that the combinations made of distant parents might have greater heterotic values.

Patil (2003) examined seven crosses; involving Indira Soya, DSB-5, MAUS-64-1, AMS-97-1, SL-599, NRC-52, MAUS-47 as male and JS-335 as female, also along with their parents. The observations were noted down for all the plants of each cross for plant height, days to maturity, number of pods per plant, 100-seed weight and seed yield per plant. The mean squares due to genotypes were found to be significant for plant height and 100-seed weight, and the mean squares due to parents were observed to be significant for all traits except for number of pods per plant. The amplitude and orientation of useful heterosis varied considerably from cross to cross; and from character to character. Low to moderate level of heterosis allow minimal estimate for exploitation of heterosis at commercially. However, the cross JS-335 x NRC-52 had greatest performance as well as heterosis and; useful heterosis for 100-seed weight per plant and seed yield per plant and; commendable mean performance and useful heterosis for plant height, days to maturity and number of pods per plant thereby selecting it as the best cross.

Bhosle *et al.* (2005) investigated heterosis and inbreeding depression in soybean crosses, MACS 684 x MACS 124, MACS 684 x RSC 1 and PK 472 x RSC 2. The observations that were recorded for plant height, pod number, oil content and yield. There were significant differences displayed by Analysis of variance for plant height in MACS 684 x RSC 1 and PK 472 x RSC 2; and for oil content in MACS 684 x MACS 124. Pod number was estimated to be significant in MACS 684 x RSC; while yield was found to be significant for MACS 684 x MACS 124 and MACS 684 x RSC 1. Relative data on heterosis over mid parent and over better parent and inbreeding depression in the soybean crosses for 4 quantitative traits were also listed systematically.

Liang *et al.* (2005) examined the soybean isoflavone contents; and its components based on the NCII Mating Design in 8 soybean cultivars. There were found to be significant differences in the contents of isoflavone and its components among the different combinations that were derived from different parents. The results suggested that the tested traits were negative for heterosis except daidzein content. Based on the data of the general and specific combining abilities in average heterotic values; daidzin had displayed positive heterosis. It was suggested to use soybean cultivars with high isoflavone contents, as one of the parents in breeding programmes.

Ramana and Satyanarayana (2006) investigated 16 soybean hybrids derived from crossing four lines (LSb 1, LSb 3, DSb 1 and JS 90-41) and four testers (PK 472, JS 335, PK 1029 and MACS 201) in a line x tester mating design along with their eight parents; which were assessed for yield and their yield attributes in order to estimate heterosis. Heterosis was observed for all the characters under consideration. The hybrids, LSb 3 x PK 472, DSb 1 x PK 472, DSb 1 x PK 1029 and DSb 1 x MACS 201 reported to display significantly positive heterosis over mid and better parents for grain yield per plant. This was principally due to interdependency of component traits i.e. plant dry weight, harvest index, number of pods per plant and number of branches per plant. Positive heterosis over better parent was observed for oil content in the cross, LSb 3 x MACS 201; and for protein content in the cross, JS 90-41 x PK 472. These heterotic cross combinations could be taken advantage of to obtain superior segregants.

Burton and Brownie (2006) developed F₁ generation from two crosses; viz. Holladay/Hutcheson (Cross 1) and Brim/Boggs (Cross 2) by hand pollinations. Bulk selfing was used to generate inbred generations. The F₁, F₂, F₃, F₄ and F₅ generations were tested for yield in replicated bordered single row plots for multiple years and in multiple locations. The average yield of F₁ in Cross 1 was observed to be 16% greater than that of the highest yielding parent; and the average yield of F₁ in Cross 2 was found to be 5% greater than the highest yielding parent. There was significant inbreeding depression displayed by cross 1 when retroverted on percentage inbreeding; clearly indicating dominance for yield. Possible genetic bases for heterosis in soybean included gene complementation; or interaction of duplicate favorable loci in repulsion, linked dominant alleles that were inherited as a unit, a greater number of dominant alleles in the F₁ than either parent separately, multiple dosage-dependent regulatory

loci, and/or over-dominance. The existence of heterosis should establish the possibility of superior gene combinations. The magnitude of yield heterosis may be a standard parameter in order to select among biparental crosses.

Massey *et al.* (2007) evaluated heterosis for yield and yield attributes of soybean in the F₂ and subsequent generations among 10 crosses. The cross combinations varied significantly for all characters except number of seeds per pod. Among the F₂ generations, the highest negative residual heterosis, that were found to be significant, over the best parent (BP) and standard parent (SP) for number of days to maturity was recorded for PK 472 x PS 1024 and JS 335 x PK 416, respectively. The maximum residual heterotic response over BP was shown by PK 327 x PK 416. For number of seeds per pod, JS 335 x PK 416 and PK 472 x PK 416 were superior to BP. The maximum heterotic response over SP was displayed by PK 472 x PS 1024. JS 335 x PK 416 demonstrated the greatest significant positive residual heterosis for seed yield per plant. For harvest index and seed yield efficiency, JS 335 x PK 327, JS 335 x PK 416 and PK 472 x PS 1024 displayed significant positive residual heterosis over BP. On the other hand, PK 472 x PS 1024 exhibited significant positive residual heterosis over SP.

Patil *et al.* (2008) investigated fifteen crosses along with the parents that were involved in the crosses grown in a single block such that the plants of each cross were individually randomized. The observations were noted for all the plants of each cross with respect to the days to flower, days to maturity, plant height (cm), number of pods per plant and seed yield per plant. The mean squares due to genotypes were found to be adequately significant for days to flower, plant height, number of pods per plant and seed yield per plant; and the mean squares due to parents were significant for days to flower, plant height and seed yield per plant. The magnitude and direction of heterosis, heterobeltiosis and useful heterosis varied considerably from cross to cross; as well as from character to character. The crosses, viz. Bragg x IC-118013 and JS-80-21 x IC-118319 discovered to have maximum useful heterosis, heterobeltiosis and average heterosis for seed yield per plant, number of pods per plant and thus, selected as best crosses from this experiment.

Yin and Yi (2009) studied the hybrid heterosis, inbreeding depression and combining ability in F₁ to F₃ generations for 14 yield and quality traits among the

parental soybean materials. This was to set standard criterion for parental selection and early generation selection in breeding of hybrid cultivars and inbred line cultivars. A set of eight parental cultivars were chosen along with their 28 diallel crosses; that were tested in 2005. The observations were recorded on hybrid heterosis and inbreeding depression for yield-related traits, among them, yield heterosis was the found to be largest for number of pods per plant, followed by seeds per plant; while no heterosis for 100-seed-weight was apparent. The traits with high F_1 heterosis demonstrated high inbreeding depression in F_2 and F_3 , and hence, were not appropriate for utilization of heterosis in F_1 derived generations. No obvious hybrid heterosis were displayed in maturity and quality (protein and oil contents) traits. There were significant observations made for GCA x Generation and SCA x Generation interaction in yield; hence, the parental cultivars with high combining ability performed in F_1 were not necessarily with high combining ability in derived inbred generations; whereas no significant GCA x Generation and SCA x Generation interaction of quality traits were observed. Therefore, the combining ability performed in F_1 could predict that in derived inbred generations. The yield of the parental materials *per se* could not be used as an index of its GCA, but the protein and oil contents *per se* could be used to predict its GCA. The heterosis of yield was the largest among the traits concerned, but that in F_1 derived generations recessed.

Perez *et al.* (2009) conducted replicated yield trials in Iowa, USA, during 2005 and 2006 and examined the male sterility systems along with; insect-mediated cross pollination to generate hybrid soybean seeds. The chief objective was to estimate the agronomic performance of soybean F_1 hybrids; and to evaluate heterosis for yield and other agronomic traits of interest in the F_1 hybrids. The parental genotypes included' 2 male sterile, female fertile lines with the ms3 and ms9 mutations, in combination with a group of 6 high yielding male parental lines. A total of 12 F_1 hybrids were studied along with parental lines in 2005.

The range of mid parent heterosis (MPH) was from -29 to 32%, and high parent heterosis (HPH) varied from - 23 to 1.0%. In 2006; eleven hybrids were examined in total. The range of MPH values varied from -53 to - 21%; and HPH varied from -66 to -35%. Seed size and seed protein content displayed HPH for certain combinations. For traits that were linked to vegetative phase of the crop; as for example height and

lodging, positive MPH and HPH were observed. Thus, depending on the year and parent combinations, there were hybrids which performed better than the mid parent values, thereby indicating heterosis to be identified in soybean. Also, observed were significant differences for yield between hybrids of the ms 3 and ms 9 groups.

Sudaric *et al.* (2009) took 29 genotypes, 11 parental and 18 F₁ hybrids into consideration so as to estimate heterosis and heterobeltiosis for four grain yield attributes in soybean. This was to compare performance of the F₁ hybrids, with those of the parents. Positive heterosis and heterobeltiosis were checked for the pod number per plant (18.75%; 7.9%), seed number per plant (16.14%; 3.98%) and; the seed weight per plant (25.72%; 11.8%). There was lower value of positive heterosis (6.62%) and negative heterobeltiosis (-1.08%) determined for harvest index per plant. The cross combinations characterized; by high mean values and positive evaluations of heterosis for most analyzed traits (Ika x Vita, Podravka 95 x Ika, Ika x OS-1212-05) were populations from which selection of new superior lines were anticipated. Generally, the results of this study will impart to the efficacy of the breeding procedure in order to the increase genetic yield potential in the germplasm of domestic soybean.

Karnwal *et al.* (2009) analyzed two interspecific crosses viz. (PK-472 x *Glycine soja*) x PK-472 and (Bragg x *Glycine soja*) x Bragg for checking effectiveness of early generation selection in respect to yield and its attributing traits. The mean differences of the selected F₃ progenies for yield attributes were found to be significant, suggesting sufficient genetic variability that was available in both crosses for selection. Based on the superiority in terms of mean of selected progenies, the number of progenies superior and/or significantly superior to better parent with respect to yield and genetic advance; over the bulk and better parent and genetic advance in F₄ generation in both the crosses, 'selection for dry matter, pods/plant, plant height, harvest index and yield *per se* was set as a standard criterion for improvement in yield in early generation of interspecific cross of soybean. Four high yielding selected progenies of (PK-472 x *G. soja*) x PK-472 and; nineteen progenies of (Bragg x *G. soja*) x Bragg were observed to be free from yellow mosaic, bacterial pustule, rhizoctonia aerial blight, fungal complex and bihar hairy caterpillar that can be used; in breeding programme not only for resistance but also for varietal improvement.

Abirami *et al.* (2014) studied quality traits by estimating mid-parent heterosis, better parent heterosis and standard heterosis in 25 cross combinations in soybean. On the basis of these three heterotic values, the best cross was found to be co(Soy)3 x Williams for all concerned qualitative traits whilst two crosses viz., Co(Soy)3 x RKS 52 and Co1x NRC 66 were considered to be best for lower levels of phytic acid content from all of the twenty-five crosses investigated.

Arya *et al.* (2010) evaluated heterosis in 27 parental lines that also included one control/standard parent, PS 1092, and 35 F1 crosses in soybean. The data that was recorded was for plant height, basal pod height, number of primary branches per plant, number of nodes per plant, number of pods per plant, number of seeds per pod, grain yield per plant, dry matter weight per plant, harvest index, days to 50% flowering, days to maturity, 100-seed weight, oil and protein contents. Those F1's that were found to be promising, displayed higher value of heterosis in PS 1241 x PS 1330, PS 1241 x PS 1347, PS 1241 x PS 1428, PS 1021 x AGS 129, JS 335 x DS-98-14, PK 472 x JS 71-05, PK 515 x EC 389148 and MACS 450 x Hardee for yield and contributing traits in order to get better segregants; in advanced generations for selection in soybean.

Bhartiya *et al.* (2014) evaluated the magnitude as well as the direction of residual heterosis for yield and its component traits; in 15 F₃ cross combinations in soybean. They acknowledged that relative heterosis for the trait viz. seed yield per plant was highest in cross combination PS 1241x PS 1042 (78.1%) followed by Kalitur X PK 472 (68.5%) and PK 472 X UPSM534 (60.0%). In a similar manner, heterobeltiosis was observed to be maximum in PS 1241 X PS 1042 (76.8%), UPSM534 and PK472 (46.6%) coming next; and Kalitur and PK 472 (43.2%) next, thereby indicating early maturing and high yielding segregants cross PK 416 X VLS 47 found to be promising which exhibited significant residual heterosis over both mid and better parent for earliness as well as seed yield per plant.

Samant *et al.* (2014) conducted a replicated yield trial during *Kharif*, 2009 that comprised 48 genotypes (25F1 and 23 parents including one check / standard variety PS1347) of soybean and this experiment conducted in a Randomized Complete Block design in two replications. They evaluated heterosis for yield and its components. The heterosis was estimated in 25 F1's and for 16 yield and its contributing traits which are

as follows, days to flower initiation, days to 50% flowering, days to maturity, plant height, basal pod height, number of nodes per plant, number of primary branches per plant, number of pods per plant, number of seeds per pod, hundred seed weight, harvest index, seed yield efficiency, dry matter weight per plant, oil content, protein content and grain yield per plant. A higher magnitude of heterosis was found in different F₁'s and Doko X JS335, DOKO X JS9041, EC389148 X PS1092, JS335 X JS 90-41, UPSM534X PS1347, PK515 X AGS129, PK1029 X PS1241, PS1241 X DOKO, PS1347 X MACS450, PS1347X PS1241 and PS1368 X PS 1330 were concluded as most favourable genotypes.

Kaushar (2014) estimated the heterosis for twenty one crosses that were generated in line x tester method. In conclusion, the acknowledged the fact that high heterosis for seed yield is usually accompanied by heterosis for major yield contributing traits. Three of the F₂ crosses, PK1029 x JS335, PK1029 x PS1225 and PS1042 x PS1225 displayed significant positive better parent residual heterosis and only one F₂ cross, PK1029XJS335; showed significant positive residual heterosis over mid parent, better parent and standard parent for seed yield per plant. Among the 21 F₃ crosses, thirteen crosses displayed significant positive residual heterosis over mid parent, seven crosses over better parent but none of the crosses exhibited significant positive residual heterosis over standard parent. The overall mean values of different characters in conjunction with the mean residual heterosis percentage in F₂, all the characters except days to 50% flowering, days to maturity exhibited positive residual heterosis, while, in F₃, the number of primary branches per plant and dry matter weight displayed negative residual heterosis.

Nagarajan *et al.* (2015) generated twenty five F₁ hybrids by crossing five lines and five testers in a line × tester mating design which were further analyzed to obtain the degree of heterosis over mid, better and standard parents in a randomized block design conducted with two replications, this included one check/standard variety Co (Soy)3. The maximum standard heterosis was observed to be 56.69% for seed yield, whereas, the minimum standard heterosis was found to be 66.72% for phytic acid content. Four hybrids *viz.* RKS 18 × lpa 5-2, Co(Soy)3 × lpa 5-2, Co(Soy)3 × lpa 5-1 and Co(Soy)3 × lpa 13-1 have been shown to display high heterosis for seed yield and low for phytic acid content.

Rialch *et al.* (2017) analyzed 54 crosses for heterosis which were obtained after making cross combinations of 18 soybean lines with three testers. Heterosis was exhibited for almost all the characters. A highest value of positive heterosis over both mid parent and better parent was recorded for protein content, in crosses H-330 x Him Soya and for oil content, cross H-330 x Him Soya demonstrated highest significant heterosis over mid parent as well as better parent.

Sharma and Maloo (2017) examined heterosis and inbreeding depression for grain yield in three generations i.e., F_1 , F_2 and F_3 of soybean. On the basis of heterotic studies, it was concluded that PK 564 x PK 472, JS 71-05 x PK472, JS 79-81 x NRC 12, JS 71-05 x MACS 58 and JS 79-81 x MACS 58 were the best crosses economically for grain yield.

2.3 Transgressive segregation

There were studies that were conducted for quantitative traits in segregating hybrid populations that sometimes report the presence of extreme phenotypes with respect to those of either of the parental line (**DeVicente and Tanksley, 1993; Cosse *et al.*, 1995**).

The development of these extreme phenotypes is called as transgressive segregation, and it is a major mechanism by which extreme or novel adaptations that were observed in new hybrid ecotypes; or species are believed to originate. Transgressive segregation is a fundamental phenomenon that is specific to segregating hybrid generations; and refers to the proportion of individuals that have exceeded the parental phenotypic values either in a negative or a positive direction. When transgressive segregation becomes frequent, then the evolutionary role for hybridization can be explained in a more easy manner.

Thorne (1970) analyzed homozygous populations from 2-way adapted x exotic and 3-way (adapted x exotic) x adapted soybean crosses for 5 characters in 2 environments and for 4 other characters in one environment. There were significant differences that were observed with respect to parameters such as yield, time of maturity, resistance to lodging and oil and protein contents. Estimates of genetic variance for 3-way populations were found to be larger than those for 2-way populations; for seed yield as well as canopy width. They also considered phenotypic

and genotypic correlations for yield in order to select for protein and oil, protein alone and also for transgressive segregation for seed yield.

Miller (1976) analyzed 45 crosses by using female parent the high-protein cultivar. Heterosis was exhibited for protein in 13 F1 hybrids with an average; protein content of 1% above the high-protein parent. The crosses, D67-6117 X Tracy and D68-4641 X Hutton displayed highest specific combining ability for protein content. The F1 progeny matured late by at least two days than the later parent, and on an average was observed to be 4.2 cm taller than the taller parent. Transgressive segregation for parameters including protein, maturation date, height and flowering date took place in the F2 of some crosses. The average heritability estimates for all lines for these traits and as well as for the height of lower pod were discovered to be around 70, 50, 63, 76 and 46%, respectively.

Miku and Damaskin (1984) examined F2 hybrid populations in soybean and acknowledged the transgressive segregants for pods per plant along with yield per plant. The frequency of favourable transgressives for pods per plant was found to be 12.5 to 22.5; per cent for seeds per plant was found to be 10.2 to 24.5 per cent and; for yield per plant was 22.7 to 35.7 per cent.

Zhang *et al.* (1987) analyzed interspecific crosses in, *Glycine max* (Dongnong 33 and Dongnong 4), *G. gracilis* (Long 79-4004 and Long 79-3497-1) and *G. soja* (Ji50192). In 1985, the parents, F1-F3 and backcrosses were examined at Harbin. It was observed that the F1 generation was not entirely fertile. It was believed that the epistatic gene effects were important for all the characters studied, and this displayed a wide range of variation with a high genetic advance. Observations were taken on transgressive segregation for all the characters, except for the 100-seed weight and also the diameter of main stem in the F2 as well as the F3 generations.

Malik and Singh (1987) evaluated phenotypic coefficient of variation as well as the heritability for yield/plant, six yield-related and quality characters in the parents and; F2 of the crosses between *Glycine soja* and 3 varieties of *G. max*. Transgressive segregants for height, seed number/pod and yield were examined in the F2. It was acknowledged that the F2's were more variable than the parents. The highest mean heritability was for the seed weight (0.98), followed by seed number/pod, oil and protein contents and the next being pod number/plant (all >0.7).

Kapila and Gupta (1991) analyzed 20 crosses of F₂ population that resulted from crossing 10 diverse lines of soybean with two testers, as they were evaluated along with their parent in randomized block design in two replications. The residual heterosis were manifestation by measuring it over respective mid and better parent and was found to be location specific for all the traits, except for the trait 100 seed weight. Himso-40 x Lee, Himso-330 x Punjab-1 and Hardy x Punjab 1 were discovered to be as the promising crosses with best potential to select transgressive lines for bolder seed size and higher yield.

Halvankar and Patil (1992) analyzed 22 cross combinations along with their 7 parents for 8 economically important characters in soybean, in a randomized block design for manifestation of heterosis. The characters such as number of branches, pods per plant, number of seeds per plant, seed yield per plant displayed a high heterotic effect while, hundred seed weight exhibited poor heterotic response with respect to grain yield and other yield attributing traits. There were 5 cross combinations that were found to have potential to pass as segregating generations.

Bhatnagar and Karmakar (1995) examined 50 soybean varieties that were bred for cultivation in 5 agro-climatic zones; suggesting various sources of seed longevity, resilience to pod shattering as well as important diseases and pest that were being used in the domestic breeding trials. The consequence of hybridization of genetically divergent parent that were having high harvest index, high biomass yield, long seed filling duration and good GCA in transgressive segregants for higher seed yield (3.5-4.0 t/ ha).

Mansur *et al.* (1996) developed recombinant inbred populations from the soybean (*Glycine max*) parents, Minsoy and Noir 1. This soybean population was then used in assessing the genetic basis of several agronomic traits such as; days to flower, days to maturity, reproductive period, plant height, lodging score, height divided by lodging, seed protein content, seed oil content, seed size, yield, seed number, yield divided by height, leaf width, leaf length, and leaf area. Transgressive segregation was displayed for all of these traits in these recombinant inbreds.

Bailey *et al.* (1997) determined that pod dehiscence (shattering) before the crop harvest was an unwanted characteristic in soybean. Thus, they discovered a quantitative

trait loci that displayed resilience to pod dehiscence. They results that were acknowledged as the genomic location of one major and a few minor quantitative trait loci, that identified as epistatic interaction, further suggesting transgressive segregation. The observation was possibly the result of susceptibility alleles that were responsible for resistant parents.

Massey *et al.* (2008) assessed transgressive segregation in 10 F₂ cross combinations of soybean taking into consideration 12 characters. Analysis of variance displayed significant differences among the different F₂ cross combinations for all the concerned traits except for the number of seeds per pod. In all F₂ generations, except JS 335 x PK 327 and PK 327 x PK 416, transgressive segregants for days to maturity were established, indicating the presence of both positive as well as negative transgressive segregation. The involvement of additive, additive x additive epistatic effects along with dominance effects was suggested in the control of seed yield in these cross combinations; after analyzing the overall appearance of transgressive segregants in JS 335 x PK 327 and JS 335 x PS 1024,.

Lee *et al.* (2010) discovered the efficacy of Near Infrared Reflectance (NIR) spectroscopy analysis for single F₂ seeds in order to select for increased protein content from two populations that were developed from high as well as parents with average protein content. A normal distribution with transgressive segregation for protein concentration was displayed by the F₂ seeds that were derived from a single F₁ plant of each population

Aditya *et al.* (2014) raised 15 F₂ and F₃ generation of soybean crosses in a randomized block design along with their 16 parents and analysis were conducted for seven quantitative characters in order to identify and further isolate transgressive segregants. The cross PK 416 xVLS 47 and T 49xPK 472 was reported to display high frequency of transgressive segregation for plant height in F₂ (30%) and F₃ (25%) generations, respectively. The highest frequency of transgressive segregation for number of primary branches per plant in F₂ generation were exhibited by the cross PK 1029 x PK 1162 while, (*G. soja* x PK 262) x PK 1029) displayed highest frequency of transgressive segregation for the same character in F₃ generation. For the number of pods per plant' frequency of transgressive segregants was high and; equal in cross PS

1241 x PK 317 and T 49 x PK 472 in F2 generation whereas, cross T 49 x PK 472 exhibited high frequency of transgressive segregants in F3 generation. The frequency of transgressive segregants was highest in cross PK 1029 x PK 1162 in F2 generation, for hundred seed weight and seed yield per plant. The parents and crosses that were found promising for yield and other economic traits, may be used for future breeding programme.

Lee *et al.* (2014) developed the RIL population by crossing two Wyandot and PI 567301B in randomized complete block design with two replications for three agronomic characters viz. plant height, lodging and days to maturity and further analyzed the population so generated. They observed in their study, that transgressive segregation for days to maturity were found to be significant whereas no significant transgressive segregation was observed for plant height and lodging.

Kaushar (2014) assessed the utility of line x tester analysis for predicting prepotency of the parents in order to identify, on the basis of heterosis, the promising cross combinations and better transgressive segregants in soybean. It was reported that the highest frequency of positive transgressive segregants for seed yield per plant were observed in crosses, PS1042 X PS1347, PS1042 X PS1225 (80.5%), PK1029 X PS1225 (76%), CM60 X PS1225 while, in F3 crosses, CM60 X PS1225 (73.3%), DT21 X PS1347(65.5%), Doko X PS1225(55.2%) and PK1029 X PS1347(54.5%) high frequency of positive transgressive segregants for seed yield were exhibited. They concluded that harvest index have the most positive direct contribution towards yield per plot and this was followed by dry matter weight and number of pods per plant being next. These traits also displayed a significant and positive correlation with grain yield per plant.

Zhang *et al.* (2015) assessed continuous transgressive breeding for seed protein content by using marker assisted procedure in recombinant inbred line (RIL) population; so as to establish the effectiveness of marker assisted procedure in breeding for transgressive segregants. Their experimentation included selection of a transgressive segregant XG30 and WT133 with SPC 45.53% and 48.39% respectively, for trait improvement. Many transgressive progenies were obtained from the crosses involving WT133 and XG30, among which the recombinants with all three positive alleles A2_B2_L2_ comprised the highest SPC.

Hamawaki *et al.* (2015) performed the transgressive segregation analysis in two different locations *viz* Harrisburg and Dowell, for yield in the RIL population. During their experimentation, it was observed that the RIL population have displayed a higher performance in yield character by significant positive transgressive segregation for both the parents in Dowell but exhibited a much lower performance in yield against parents in Harrisburg; by a negative significant transgressive segregation.

2.4 Inter-character association (correlation) analysis

Correlation analysis is an approachable technique, which seeks knowledge about the degree of relationship between the important plant traits and is great indicator to anticipate the yield response in relation to the change of a particular character. The awareness about correlation between yield and its attributes is highly important in bringing about co-occurring response through selection in all such traits which are linked to each other.

Earlier workers have successfully reported positive associations between pods per plant, days to maturity and seed yield in soybean (**Jadhav *et al.*, 1995**).

Rajput *et al.* (2000) conducted analysis on the interrelationships between yield and growth parameters of soybean in Madhya Pradesh, India during *Kharif* seasons of 1995 and 1996. It was found out that, out of 78 character pair associations, 66 and 71 pairs were positively and significantly correlated during 1995 and 1996, respectively. Additionally, seed yield was observed to be positively and significantly correlated with all growth parameters especially the dry matter per plant, leaf area index, leaf area ratio, canopy growth rate, average growth rate and plant height, during both the years. The characteristic, pods per plant were among the yield components that were found to be most highly correlated with seed yield. The bulk of growth and yield parameters; displayed positive and significant correlations among themselves.

Thorat *et al.* (2001) evaluated the phenotypic and genotypic correlations of yield and its components by using 30 cultivars of soybean. It was demonstrated that the seed yield was positively correlated with the number of pods per plant and days to 50% flowering, but displayed a negative correlation with 100-seed weight. The negative correlations were also discovered for number of seeds per pod, oil and protein contents.

Jadhav *et al.* (2002) assessed the correlation and path coefficient analysis for different seed quality parameters like; moisture content, test weight and germination percentage in soybean cv. JS-335. On retrieving the results, it was disclosed that the test weight had the highest positive direct effect on seed germination.

Malik *et al.* (2006) analysed the correlation between 16 yield and its attributing characters that included, oil and protein contents among the 25 accessions of soybean. The conclusion made out was that of a significant and positive correlation of grain yield with number of pods per plant but turned out to be a negative correlation with days to 50% flowering and days to maturation. Thus, the outcome of selecting in the direction of more number of pods per plant would be higher yields in soybean.

Malik *et al.* (2007) carried out an analysis for the genotypic, phenotypic and environmental correlations between 16 yield and its attributing characters, also including oil and protein contents among 27 soybean genotypes. The results displayed that the estimates of genotypic correlation were comparatively higher than that of phenotypic and environmental correlations, suggesting a high degree of genetic association among the traits concerned. The observations revealed positive correlations for grain yield with branches per plant, days to 50% flowering, days to maturity, first pod height, plant height, leaf area and pods per plant signalling that high mean values for these traits may heighten the values for grain yield.

Ramteke *et al.* (2010) implemented correlation studies among the 92 released varieties of soybean in India. Various economically important characters were included under this study and yield were demonstrated to be significantly and negatively correlated with days to flowering and days to maturity. Also, 100-seed weight was found to be negatively correlated with days to flowering, days to maturity, plant height and nodes per plant but displayed a positive correlation with oil content. It was established that the protein content is positively correlated with the number of branches and days to 50% flowering; but negatively correlated with oil content.

Aditya *et al.* (2011) conducted studies for correlation analysis between 8 quantitative traits among 31 soybean genotypes. The revelations obtained proved that genotypic correlation coefficients have higher values than that for phenotypic correlation coefficients. Field parameters such as, grain yield per plant displayed a

highly significant and positive correlation with number of pods per plant ($r_g = 0.63$), dry matter weight per plant ($r_g = 0.491$), harvest index ($r_g = 0.488$) and number of primary branches per plant ($r_g = 0.403$) when considering at the level of the genotype; whereas, the remaining parameters exhibited non-significant correlation. It is at the phenotypic level, that the grain yield per plant displayed highly significant and positive correlation with the number of pods per plant ($r_p = 0.511$); and significant positive correlation was observed with dry matter weight per plant ($r_p = 0.410$) and harvest index ($r_p = 0.385$), but the rest of the traits were non-significantly correlated.

Koladiya *et al.* (2012) conducted correlation studies for 12 characters in the study, among 40 soybean genotypes. Thence, higher values of genotypic correlations were incurred over the phenotypic correlations for most of the characters under observation, thereby indicating about the possibility of a strong link between the character pairs at genotypic level. It was observed that a positive correlation is apparent for seed yield per plant; with days to 50% flowering, days to maturity, plant height and pods per plant.

Sarutayophat (2012) conducted association analysis among 22 genotypes of vegetable soybean for yield and its contributing characters. The reported results indicated towards a positive and significant correlation, for number of vendible pods per plant (0.821^{**}) and pod yield (0.520^*) along with plant height; and between number of marketable pods per plant and marketable pod yield (0.822^{**}). Also, green pod weight was found to be significantly and negatively correlated (-0.620^{**}) with plant height, and the negative correlation was consistent for number of marketable pods per plant (-0.588^{**}).

El-Mohsen *et al.* (2013) analyzed correlation and regression studies for seed yield and its attributes, among 6 soybean cultivars conducted under varying irrigated conditions. The correlation analysis brought out that the seed yield per hectare displayed a highly significant and positive correlation with number of branches per plant (0.676), number of pods per plant (0.845), number of seeds per pod (0.811), thousand seed weight (0.741) and seed yield per plant (0.615). On the other hand, a significant and negative correlation with oil content (-0.426) and protein content (-0.399) was revealed. Oil and protein contents were acknowledged to be highly

significant and negatively correlated (-0.661) with each other, suggesting a scope of selection for higher oil content that could cut down the protein levels in soybean.

Ghodrati (2013) carried out replication trials in three crop growing seasons for evaluation of 12 soybean genotypes for examining the genotypic and phenotypic correlation for seed yield and other quality parameters. The results disclosed higher magnitudes of genotypic correlation over phenotypic correlation, thereby indicating a strong alliance between each pair of traits that are being considered. It was demonstrated that around, 21.7% of genotypic and 25.5% of phenotypic correlations displayed significance at 5% probability. The results demonstrated a significant and positive genotypic and phenotypic correlations, that was marked between the traits viz. plant height, oil yield, protein yield and seed yield. Plant height displayed a highly significant and positive genotypic and phenotypic correlation with number of nodes per plant, pods per plant, seeds per pod and number of seeds per plant.

Moe and Girdthai (2013) carried out genetic correlation studies among 94 soybean cultivars; and the basis of these studies were physiological and agro-morphological characteristics. A consistently positive and significant correlations were discovered between yield and remaining agro-morphological traits under observation; excluding the number of seeds per pod.

Salimi *et al.* (2013) took into consideration 15 characters for the analysis assessed 19 of the soybean genotypes in order to evaluate the effect of drought stress on yield and its attributes by. The correlation analysis revealed that number of seed per plant showed highly significant and positive correlation with fresh weight of plant (0.737) and dry weight of plant (0.699), whereas it showed significant and positive correlation with days to maturity (0.536) and days to 50% flowering (0.517). Protein and oil contents exhibited both a negative as well as non-significant correlation (-0.139). However, it was reported that grain yield was non-significantly correlated, both negatively and positively, with protein (-0.068) and oil contents (0.129), respectively.

Attia (2014) valued 10 genotypes of soybean for grain yield and contributing characteristics, density of pubescence as well as the percent of trypsin inhibitor which was functionally equivalent as a resistant factor against percent defoliation. Further, it

was drawn to conclusion that out of 14 characters taken into consideration, it was the seed yield per plant that showed a significant and positive correlation with plant height (0.308), while it showed a highly significant and positive correlation with branches per plant (0.795), pods per plant (0.978), seeds per plant (0.828); as well as 100-seed weight (0.869). Nevertheless, a positive plus non-significant correlation was exhibited with percent oil content (0.058) while significant but negative correlation with percent protein content (-0.346).

Barh *et al.* (2014) carried out an investigation at the genotypic level, for the inter-character correlation coefficients. These coefficients were calculated between the 13 yield and yield contributing characters from the data obtained among 48 black soybean genotypes of Uttarakhand. The results disclosed the fact that the number of pods per plant, number of primary branches per plant, number of seeds per pod and 100-seed weight were shown to be highly significant plus positively correlated with seed yield per plant. On the other hand; it was established that, days to 50% flowering, days to maturity, plant height and protein content demonstrated negative correlations with seed yield per plant. Nevertheless, the oil and protein contents were indicated to be negatively correlated.

Malek *et al.* (2014) carried out genotypic and phenotypic correlation studies among 27 soybean mutants and 4 parent genotypes; between 9 morphological traits. They discovered that the degree and intensity of genotypic correlation coefficients were higher than that of phenotypic correlation coefficients. There were significant and positive correlations, both at phenotypic as well as genotypic levels, with seed yield per plant and seed yield per hectare for all the concerned traits except 100-seed weight. In conclusion they established, that except for the seed yield per plant, there was a significant and negative correlation displayed by 100-seed weight with all the concerned characters.

Ali *et al.* (2015) considered 8 economically important traits, in order to examine the character associations demonstrated between yield and its attributes in 10 soybean accessions. The correlation studies established a positive and significant correlation between seed yield, days to 50% flowering, days to maturity, pods per plant and 100-seed weight; while seed yield was disclosed to be positively correlated with pod length. Nevertheless, the seed yield demonstrated a negative correlation with plant height.

Aminifar *et al.* (2015) carried out character association studies and path analysis among 7 soybean cultivars viz. 033, 032, Sahar (all belonging to group maturity IV), Zan, Clark, Madari and L.17 (all belonging to group maturity III). Their studies manifested highly significant and positive correlation between seed yield and biological yield (0.996) in the maturity group IV; while in maturity group III, a highly significant and positive correlation with seed yield was exhibited with the weight of seeds per plant (0.997), biological yield (0.996) and plant dry weight (0.996). Additionally, seed yield was observed to be negatively and non-significantly correlated with oil and protein contents in maturity group IV but due to a significant and negative correlation of oil and protein contents with seed yield in maturity group III, it was suggested that selection for high oil and protein contents may result in depreciation of the grain yield in soybean.

Kumar *et al.* (2015) demonstrated by several correlation studies among various agro-morphological traits in soybean, taking into consideration 42 genotypes for the experiment. There were significant associations of seed yield with its component traits, as revealed by these studies. In conclusion, it was established that days to flowering was positively correlated with yield but negatively correlated with seed weight; while the number of branches per plant were positively correlated with yield.

Chandrawat *et al.* (2015) studied correlation coefficients and path analysis, for 11 quantitative traits among 41 germplasm soybean lines in addition to 3 national checks (Bragg, JS-93-05 and JS-335) and 2 local checks (MAUS-158 and MAUS-71). A higher influence of genetic factors was intimated in the development of a dependent variable (seed yield), considering the observations that proposed the magnitude of genotypic correlations being higher than the phenotypic correlations. There were positive as well as highly significant phenotypic and genotypic correlations observed for seed yield with that of hundred seed weight (0.363 and 0.451) and harvest index (0.582 and 0.662). However, there were highly significant and non-significant negative correlations displayed by seed yield per plant with that of protein content (-0.268 and -0.205); at the genotypic and phenotypic levels, respectively. Nevertheless, there was a non-significant, both positive (0.025) and negative (-0.016) correlations, with protein content at genotypic and phenotypic levels, respectively. Additionally, there was a positive but non-significant association of seed yield per plant with the rest of the traits such as days to 50% flowering, days to maturity and branches per plant.

Mahbub et al. (2015) established a significant positive genotypic and phenotypic correlation of seed yield with that of plant height, number of pods per plant, pod length, number of seeds per pod, 100-seed weight and branches per plant after carrying out correlation studies for 11 morphological characters, among 28 genotypes of soybean. In conclusion, they emphasized that characters such as plant height, pod length, seeds per pod and 100-seed weight are important parameters to improve seed yields in soybean.

Rodrigues et al. (2015) assessed 14 phenotypic traits that attribute to yield, in order to study the correlation among 15 soybean genotypes that were infected with Asian soybean rust (*Phakopsora pachyrhizi*). Highly significant and positive genotypic and phenotypic correlation coefficients were observed. They concluded that phenotypic correlations for seed yield, were observed to be highly significant and positive with total number of pods per plant (0.89) and number of pods with 2 (0.87) or 3 seeds (0.74), eliciting some interesting observations regarding the important traits to be selected for, in soybean for grain yield enhancement. Also, a strong environmental correlation between plant height at blooming and maturity, with grain yield and its components was intimated. There was a negative and non-significant phenotypic (-0.05) and genotypic (-0.07) correlation established between severity of rust infection and seed yield.

2.5 Path coefficient analysis

Wright (1921) drafted the theory of path analysis based on the assumption of standardized partial regression; analysis. Later; **Niles (1922); Li (1956); Turkey (1954) and Kempthorne (1957)** focused on its importance.

Dewey and Liu (1959) employed the technique of path coefficient to plant breeding for the first time and; observed that; it permits; a critical; examination of; specific forces; acting to; produce a particular correlation.

Gupta and Kataria (1971) observed days to maturity and leaves per plant as the most important components contributing; directly to; the manufacturing; process of; the plant; in soybean.

Lal and Haque (1971) found the 100-seed weight and number of pods as having positive direct effect on; seed yield; in soybean; but 100-seed; weight had; high negative; indirect effect; on seed; yield via all other variables except period of

flowering. Total leaf area and plant height had moderate direct effect on; seed yield; but had; high indirect; effect on; seed yield; via number; of pods.

Pandey and Torrie (1973) reported that the number of pods per unit area and number of seeds per pod were; important factors; in determining; seed yield; in soybean;. Seed yield; remained unaffected; by the density of the plant stand.

Chaudhary and Singh (1974) reported that the number of pods per plant and seed size had high direct effect; towards yield; in soybean;. Other characters; influenced; yield through; these two; primary components. However, seed size had a negative indirect effect on yield through the number of pods.

Patirana and Guzhov (1979) assessed number of seeds per pod and single seed weight as static components of yield in soybean.

Sharma (1979) reported in soybean that the plant height had a negative direct effect on yield but its indirect effect; through number; of pods; per plant; was fairly; high. The; number of; pods per; plant and; number of pod cluster per plant had an important direct and indirect contribution to yield.

Rajput *et al.* (1986) studied 36 soybean genotypes of diverse origins. They found that grain yield was positively; and significantly; correlated with; pods per; plant ($r=0.83$); and branches; per plant; (0.68). Pods per plant had the maximum direct effect on yield and also contributed indirectly through branches per plant, while; 100-grain; weight also; exerted a; high direct; positive effect.

Das *et al.* (1989) collected data on eight yield related traits in 32 strains of soybean grown for two consecutive years;. On the; basis of; these data; yield correlations; were derived;. Seed yield; was significantly correlated with plant height and number of pods and nodules per plant and seeds per pod. The major contribution; to yield; was number; of pods; per plant; and it; was estimated; that much; of the variation in seed yield was accounted for if selections were based on number of seeds per pod. The conclusion was; drawn in; favour of; selection for; these two; traits.

Mishra *et al.* (1994) evaluated six genetically diverse genotypes of soybean together with 15 F₂ and 15 F₃ hybrids for 10 yield characters in *Kharif*, 1992. Path coefficient analysis showed positive direct effect of 100-seed weight, number of seeds per plant and number of pods per plant on seed yield.

Wu *et al.* (1995) conducted path coefficient analysis and multivariate analysis and showed that among ordinary genotypes, seed yield was correlated with pods per plant, stem weight, plant height and branches per plant. Among high yielding genotypes, seed to stem ratio and also 100-seed weight, pods per plant and nodes per main stem were the main characters influencing seed yield.

Verma (1996) showed a direct positive effect of pod set on yield (0.89) and an indirect positive effect of flower produced per plant on pod set (0.62) and a negative direct of flower shedding on pod set (-0.79) and suggested that selection for higher number of flowers and a higher pod set would lead to increased yields in soybean.

Mehetre *et al.* (1997) concluded from field trials conducted in 1994-96 with 41 soybean genotypes that yield per plant was highly significant and positively correlated with number of branches per plant, leaf area, harvest index and 100-seed weight. Path coefficient analysis indicated that the number of branches per plant exerted the highest positive direct effect followed by contribution of root dry matter in yield, total dry matter per plant, root dry matter per plant, 100-seed weight, number of pods per plant, root length per plant and leaf area. The highest indirect positive effect was found from root length, number of pods per plant and leaf area.

Siahsar and Rezai (1999) studied yield contribution of 285 soybean lines and five control varieties. The genotypic and phenotypic correlations had similar trends. The number of pod per plant followed by number of lateral branches had the greatest phenotypic and genotypic correlations with seed yield. The importance of the direct effects of pods per plant, seeds per pod and 100-seed weight on seed yield was revealed and affirmed the importance of pods per plant.

Khan *et al.* (2000) did path coefficient analysis in 86 diverse maturity genotypes of soybean and revealed that pods per plant had the direct effect on seed yield followed by 100-seed weight. Pods per plant affected seed yield negatively via indirect effects of plant height, pod height, pod weight and seeds per pod.

Ball *et al.* (2001) assessed the direct and indirect contributions of plant population density for short season soybean. Although, population density had a large inverse association with pods per plant, the large direct effect of population density on yield was greater than its negative indirect effect via pods per plant. The direct effects

of pod number per plant and seeds per pod on yield were positive, whereas mass per seed had a negligible effect. Pods per fertile node differed between cultivars and it was reduced by increasing population density.

Jadhav *et al.* (2002) studied correlation and path coefficient analysis for different seed quality traits like, moisture content, test weight and germination percentage in soybean cv. JS-335. The results revealed that test weight had the highest positive direct effect on seed germination.

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

Miladinovic *et al.* (2004) determined the effects of yield, oil content and growing season duration on protein content in new soybean varieties seeds. They found high negative correlation between protein content and the other traits under investigation. Path coefficient analysis showed that only oil content had a significant direct effect on protein content. Their findings showed that despite its high heritability, protein content exhibited a strong interrelationship with other traits primarily oil content.

Yadav (2005) studied 48 genotypes of soybean (including 31 elite breeding lines and 17 parental lines) for twelve quantitative and eleven morphological characters in order to study genetic diversity and estimate the character associations for yield and its components and their direct and indirect effects on seed yield. Path analysis indicated that dry matter weight per plant, harvest index, number of pods per plant, plant height and basal pod height have positive direct effect in influencing seed yield. The dry matter weight affected seed yield both directly and indirectly.

Malik *et al.* (2006) evaluated 25 genotypes of soybean to investigate the path co-efficient analysis between 16 yield and its contributing characters, having included oil and protein contents. The characters such as chlorophyll content, number of

branches per plant, days to pod initiation, number of pods per plant and 100-seed weight reported to have exerted a direct and positive effect on yield. A direct effect of highest order was displayed by days to pod initiation (6.297). Also, direct and negative effects were shown on yield,; by the other attributes such as plant height, days to 50% flowering, days to flowering completion, first pod height, days to maturity, leaf area, oil content and protein contents.

Saharan *et al.* (2006) observed that the biological yield per plant and harvest index had high direct effect on seed yield per plant.

Arshad *et al.* (2007) established that among the 10 traits under observation, days to maturity, number of branches per plant, pod length, number of pods per plant and 100-seed weight exhibited positive and direct effects on seed yield, after evaluating 33 soybean genotypes for studying the path co-efficient analysis. They further intimated that these characters should be given priority during selection so as to enhance the soybean yield levels. It was further stated that positive selection for the remaining traits could result in impeded levels of yield, since these characters displayed a negative and direct effect on seed yield.

Malik *et al.* (2007) investigated 27 soybean genotypes, in order to conduct path co-efficient analysis for 16 yield and its contributing traits, which also included oil and protein contents. The results indicated that selection based on the following traits could lead to reduced grain yield viz. first pod height, days to 50% flowering, days to maturity, leaf area, branches per plant, 100-seed weight, protein and oil contents, since these traits were having negative and direct effects on yield,. Nevertheless, chlorophyll content, days to flowering completion, days to pod initiation, pods per plant and plant height displayed a direct and positive effect on grain yield. Largest direct effect were observed on seed yield by days to flowering completion (32.75) which was followed by days to pod initiation (19.46).

Nag *et al.* (2007) studied the path coefficient analysis and concluded that the number of seeds per plant had the highest positive direct effect on seed yield per plant followed by oil per cent, pod bearing length and 100-seed weight.

Karnwal and Singh (2009) studied twenty elite breeding lines of soybean were studied for path coefficient of eighteen economically important traits. Path coefficient

analysis indicated major role of pods per plant, total dry matter weight per plant, primary branches per plant, seed yield efficiency and 100- seed weight both directly and indirectly in influencing the seed yield. Therefore, main emphasis should be given on these traits during phenotypic selection for developing high yielding genotypes of soybean.

Oz et al. (2009) estimated yield and its components over different locations and years, for investigating the correlation and path analysis studies among 8 soybean cultivars. The studies on path co-efficient analysis established that a maximum direct and positive effect (0.473) by number of seeds per pod had on seed yield, followed by number of pods per plant (0.399), correlating to 57.0% and 50.4% of direct effects on seed yield, respectively. They concluded that number of pods per plant along with seeds per pod in soybean, could be accepted as a principal trait for enhancing yield; since stable expression of direct and positive effect of number of pods per plant have been established over the years and locations.

Showkat and Tyagi (2010) did the path coefficient analysis for 40 genotypes of soybean. The studies indicated that biological yield and harvest index were major characters influencing seed yield directly and indirectly. The results indicated that biological yield is responsible for manipulation of seed yield in soybean.

Machikowa and Laosuwan (2011) took into consideration studies on path co-efficient analysis for 8 characters after evaluating 14 soybean genotypes in order to study correlation and to assert the direct and indirect effects for these 8 characters through path co-efficient analysis. The results; thus, obtained exhibited; highest positive; and direct; effect number; of pods; per plant (1.203) on seed yield, followed by number of branches per plant (0.344). Additionally, most of the; characters exhibited; high indirect; effects through; pods per plant.

Badawy and Mehasen (2012) evaluated 5 genotypes viz. Crawford, Clark, Giza 22, Giza 35 and Giza 88 under 3 planting densities to estimate the interrelationships and path analysis between yield and its components. The study reported that 100-seed weight (15.51%) showed the highest direct effect on seed yield per plant, followed by number of pods per plant (14.04%), while the highest indirect effect on seed yield per plant was shown by number of pods per plant (26.47%) through 100-seed weight.

Haghi *et al.* (2012) studied the correlation and path analysis for yield, oil and protein contents under different levels of nitrogen starter and planting density by evaluating 4 genotypes of soybean *viz.* M9, L17, Williams and Clark considering 15 traits under study. The results from the path analysis revealed that pod number per plant (0.51) and seed diameter (1.00) showed high positive and direct effects of on seed yield, while majority of the remaining characters including oil (-0.0003) and protein (-0.0014) contents exerted negative and direct effects. 100-seed weight exhibited highest negative and direct effect on seed yield (-0.45).

Salimi and Moradi (2012) carried out path analysis for yield and its components under moisture stress and normal conditions among 19 genotypes of soybean. Results revealed that, under normal condition, direct and positive effects on grain yield were exhibited by fresh weight of plant (0.036), 100-seed weight (0.23) and number of seed per plant (0.88), whereas oil content (-0.18) exhibited direct negative effect on grain yield. The number of seed per plant had maximum direct effect (0.88) on grain yield. Similarly, under moisture stress, direct and positive effect on grain yield was shown by fresh weight of plant (0.105), pod length (0.255), 100-seed weight (0.48) and number of seed per plant (0.72), which could be determined as important yield components in soybean.

Abady *et al.* (2013) estimated heritability and genetic advance of genotypes for yield and yield related traits and to measure the extent of direct and indirect causes of association among traits through path coefficient analysis. They evaluated twenty soybean genotypes in a randomized complete block design. High heritability coupled with high genetic advance was recorded for number of nodules per plant, dry weight of nodules per plant, and seed yield per plot indicating the effectiveness of selection to improve these three characters. Based on path coefficient analysis, they reported that number of pods per plant, days to maturity and harvest index had positive direct effect on seed yield per plot. Number of branches per plant and plant height exerted positive and significant indirect effect on seed yield per plot through number of pods per plant; and plant height also exert positive and significant indirect effect on seed yield per plot through days to flowering and days to maturity

Aondover *et al.* (2013) studied the correlation and path analysis among 17 medium duration genotypes of soybean for 9 agro-morphological traits. The path

analysis revealed that, plant height (0.40), 300-seed weight (0.25) and branches per plant (0.24) showed positive and direct effect on seed yield, whereas first pod height (-0.67), pods per plant (-0.23), days to 50% flowering (-0.06) and days to maturity (-0.49) exhibited negative and direct effect on seed yield indicating that selection on the basis of latter might lead to reduced seed yields in soybean.

Li *et al.* (2013) carried out investigation for 30 genotypes of vegetable soybean for fresh pod yield; and rest; of the; yield attributes; to calculate; the correlation; and path; analysis among them;. Studies on; path coefficient; analysis have; disclosed that; number of; 3-seed pods; per plant (0.58); presented highest; direct and; positive effect; on fresh; pod yield; and this; was followed; by number; of 2-seed; pod per; plant (0.56); 2-seed pod; width (0.31), and; 100-fresh seed weight; (0.23). However; highest negative; and direct; effect on; fresh pod; yield was displayed; by plant; height (-0.36);

Amrita *et al.* (2014) carried out studies on phenotypic and genotypic path analyses for 11 traits after evaluation of 26 advanced generation lines of soybean. They acknowledged that pods per plant (3.174 and 0.173), biological yield per plant (2.220 and 0.944), seeds per plant (1.867 and 0.777) and harvest index (1.315 and 0.369) demonstrated positive direct effect at genotypic and phenotypic levels. Also, these traits displayed positive indirect effect through each other thereby suggesting improvement of these traits simultaneously and yield ultimately. However, negative and direct effects, both at genotypic and phenotypic levels, were displayed by 100-seed weight (-1.083 and -0.064) and seeds per pod (-1.528 and -0.373) on grain yield.

Arshad *et al.* (2014) evaluated fourteen early maturing soybean genotypes in 2011 using a randomized complete block design with 3 replications to verify direct and indirect effects which will be used for the selection of seed yield. The data regarding eight characters including branches per plant, nodes per plant, pods per plant, seeds per plant, 100 seeds weight, days to flowering, days from flowering to maturity and seed yield were evaluated for path coefficient analysis. They reported that pods per plant showed the highest positive direct effect on seed yield, followed by branches per plant. In addition, the indirect effects of most characters were high through pods per plant. The results obtained from genotypic correlations and path analyses showed that the efficiency of selection for seed yield in early maturing soybean should increase through the selection of pods per plant.

Chandel *et al.* (2014) studied the correlation and path analysis among 70 genotypes of soybean for 15 traits including seed yield. Results from the genotypic path analysis showed that highest positive and direct effect on seed yield per plant was exerted by biological yield per plant (1.268) followed by harvest index (0.942) and days to 50% flowering (0.115). However, clusters per plant, seeds per pod and 100-seed weight also exhibited positive and direct effect in lower magnitude on seed yield per plant as well as indirect effects through other traits under study. Hence, all these traits could be considered as important yield contributing characters in soybean. The study also showed that oil content (-0.022) and protein content (-0.036) exhibited direct and negative effects on seed yield per plant along with primary branches per plant, pods per plant, pods per cluster and pod length

Kaushar (2014) revealed that in F₂ and F₃, harvest index was the most positive direct contributor towards seed yield followed by dry matter weight, number of pods per plant. Since these characters also exhibited significant and positive correlation with seed yield per plant and hence, improvement in these component characters would result in the improvement of seed yield per plant. Therefore, during selection maximum emphasis should be given to the improvement of these component characters.

Malek *et al.* (2014) studied the path co-efficient analysis among 27 soybean mutants and 4 parent genotypes considering 9 morphological traits under study. Results obtained from the study showed that seeds per pod showed highest direct and positive effect (1.450) on seed yield per plant followed by 100-seed weight (1.350), days to maturity (1.184) and pods per plant (0.659) indicating that emphasis should be laid on these characters for yield enhancement during selection.

Aminifar *et al.* (2015) studied the character association and path analysis among 7 soybean cultivars *viz.* 033, 032, Sahar (all belonging to group maturity IV), Zan, Clark, Madari and L.17 (all belonging to group maturity III). They have found that in maturity group IV biological yield (1.04) and in maturity group III weight of seeds per plant (0.801) had the highest positive and direct effect on seed yields in soybean. These traits also showed high correlation with seed yield and hence, could be included as chief yield components in selection. However, plant dry weight (-0.501) showed negative and direct effect on seed yield.

Amit Kumar et al. (2015) studied 42 genotypes of soybean using agro-morphological traits and also conducted path-co-efficient analysis for the concerned traits. The results obtained showed that number of pod clusters per plant showed highest direct effect on yield (0.402) followed by number of pods per plant (0.313). Plant height showed little direct effect (0.003) as well as indirect effect on yield indicating that selection of taller genotypes did not show any significant effect on yield. This suggested that the selection of genotypes with more number of pods and pod clusters should be more rewarding over selection of tall genotypes.

Baraskar et al. (2015) carried out path co-efficient analysis for 9 characters among 61 soybean genotypes. Results revealed that biological yield per plant (0.817) showed maximum direct effect on seed yield followed by harvest index (0.483) and oil content (0.057). Therefore, selection based on these traits could be effective in enhancing yield levels. Maximum direct and negative effects on seed yield was shown by 100-seed weight (-0.098) followed by days to maturity (-0.092), primary branches per plant (-0.052) and plant height (-0.024).

Dubey et al. (2015) carried out path-co-efficient analysis for 13 characters including yield and its attributes among 50 genotypes of soybean. The study revealed that highest and positive direct effects were reported for number of pods per node (2.231) followed by number of nodes per plant (1.768), number of seeds per plant (0.770), number of branches per plant (0.360), biological yield per plant (0.338) and harvest index (0.280) on seed yield per plant. Hence, an inclusion of these characters as components in selection for higher seed yields was considered rewardable. However, highest negative and direct effect was exhibited by number of pods per plant (-3.609) followed by days to 50% flowering (-0.329) and days to maturity (-0.099).

Mahbub et al. (2015) studied the path-coefficient analysis among 28 genotypes of soybean for 11 morphological characters and reported that number of seeds per pod (1.20), 100-seed weight (0.739), pod length (0.072), days to maturity (0.062) and plant height (0.043) showed a positive direct effect on seed yield, whereas number of pods per plant showed the highest negative direct effect on yield (-0.040) followed by number of branches per plant (-0.031), days to first flowering (-0.010), number of seeds per pod (-0.004) and days to 50% flowering (-0.001).

Nagarajan *et al.* (2015) studied the genetic correlation and path analysis among soybean where they took 5 released varieties (lines) *viz.* Bragg, RKS 18, Co 2, Co (Soy) 3 and JS 335 along with 5 mutant lines (testers) *viz* Ipa 5-1, Ipa 5-2, Ipa5-3, Ipa 13-1 and Ipa 18 all as parents and crossed them in a line x tester design to generate 25 F₁'s which along with parents constituted the experimental material. The results from the study revealed that days to 50% flowering, number of pods per plant, number of branches per plant, number of pod clusters per plant, number of seeds per pod, harvest index and 100-seed weight exhibited positive and direct effect on seed yield, whereas days to maturity and plant height showed negative direct effect on seed yield. Hence, the study suggested that considerable importance should be given to the characters showing high positive and direct effects on seed yield to enhance overall yield.

Shruti *et al.* (2015) evaluated 13 genotypes of soybean to study the path analysis for 11 important yield and its contributing traits. They reported from the path analysis that harvest index showed highest positive and direct effect (0.504) on seed yield per plant followed by biomass (0.338), pod weight per plant (0.208) and days to 50% flowering (0.100). Whereas branches per plant (-0.074) and 100-seed weight (-0.004) showed negative direct effects on seed yield per plant. The path analysis also revealed that highest positive and indirect effect was shown by seed yield through pod weight per plant (0.415) followed by 100-seed weight (0.375), while pod length exhibited negative indirect effects through majority of the characters under study.

Ekka and Lal (2016) conducted experiment during *kharif* 2013, among the twenty genotypes. The genotypic; correlation studies; shown that pods per; plant (0.748**), seed index (0.665**), clusters per plant (0.489**), plant height (0.485**) and pod length (0.481**) showed positive significant association with grain yield per plant. Phenotypic correlation analysis has indicated that pods per plant (0.723**), seed index (0.586**), plant height (0.456**), clusters per plant (0.430*) and pod length (0.348*) showed positive significant association with seed yield per plant.

2.6 Molecular genetic diversity

Molecular diversity has been studied in plants for about three decades. The capacity of the molecular markers in revealing the genetic variability, existing in the different genotypes, is now worldwide accepted. It plays a vital role in enhancing global

food production by improving the efficiency of conventional plant breeding programs (**Kasha, 1999**). Simple Sequence Repeats (SSR), are relatively new class of DNA markers consisting of short run of tandemly repeated sequence motifs evenly distributed throughout the eukaryotic genomes. Simple sequence repeats are also known as microsatellites. The term microsatellite was coined by **Litt and Luty (1989)**. Owing to the high rate of variation in the number of repeat units, the polymorphism level shown by SSRs is high. Microsatellites or Simple Sequence Repeats based molecular markers are now the markers of choice in most areas of plant genetics (**Tautz and Renz, 1984; Tautz, 1989**). SSRs are currently considered as the molecular markers of choice, due to high level of polymorphism and information content, high reproducibility, codominance, abundant, rapid and simple genotyping assays (**Kong et al., 2000**).

A total of 391 simple sequence repeat (SSR) markers designed from genomic DNA libraries, 24 derived from existing GenBank genes or ESTs, and five derived from bacterial artificial chromosome (BAC) end sequences were developed. The 420 newly developed SSR loci were added to the 606 SSR loci published by **Cregan et al. (1999a)** and SRs were mapped in one or more of five soybean mapping populations: 'Minsoy' X 'Noir 1', 'Minsoy' X 'Archer', 'Archer' X 'Noir 1', 'Clark' X 'Harosoy', and A81-356022 X PI468916 (**Song et al., 2004**).

Sneller et al. (1997) detected genetic diversity in soybean from the analysis of 31 southern (MG V–VI) primary introductions (PIs), 15 southern (MG IV–VI) elite genotypes, and five northern (MG I–III) cultivars at 60 RFLP loci. They found that the greatest amount of genetic relative diversity was between the southern elite genotypes and the southern PIs.

Baranek et al. (2002) used random amplified polymorphic DNA (RAPD) technique to evaluate both genetic diversity among 19 soybean accessions included in the Czech National Collection of Soybean Genotypes and their potential as a new source of genetic variations for soybean breeding programs. Only 22 of all the 40 random primers used in RAPD reactions showed polymorphism acceptable for an effective characterization of these accessions. Altogether 122 highly reproducible RAPD fragments were generated, 55 of them were polymorphic (46%). However, because of the previously observed low degree of RAPD polymorphism in the case of *Glycine max*, fragments with low level of information were evaluated, too. Presented

results enable the selection of genetically distinct individuals. Such information may be useful to breeders willing to use genetically diverse introductions in soybean improvement process.

Hudcovicova *et al.* (2003) characterized sixty seven soybean genotypes of various origins by utilizing eighteen microsatellite markers and detected 188 alleles at the 18 SSR loci. From 4 to 21 alleles were found at each of these loci (average 10.4 per locus) and the gene diversity averaged 0.71. Differentiation of all 67 genotypes each from others has been successful by using of even only 6 of SSR markers (Sat001, Satt005, Satt038, Satt173, Satt177, Satt534) with gene diversity from 0.66 to 0.89. The cumulated probability of obtaining identical soybean SSR profile was 1.11×10^{-9} , which confirms a high potential of SSRs for differentiation of soybean accessions in collections. Clustering of genotypes partially reflects origin and pedigree of analysed soybean accessions.

Hua *et al.* (2005) detected genetic diversity of 158 Chinese summer soybean accessions collected from the primary core collection of *G. max* were used to analyze genetic variation at 67 SSR loci. A total of 460 alleles were detected, in which 414 and 419 alleles occurred in the 80 Huanghuai and the 78 Southern summer accessions, respectively. The average number of alleles per locus was 6.9 for all the summer accessions, and 6.2 for both Huanghuai and Southern summer accessions. Marker diversity (*D*) per locus ranged from 0.414 to 0.905 with an average of 0.735 for all the summer accessions, from 0.387 to 0.886 with an average of 0.708 for the Huanghuai summer accessions, and from 0.189 to 0.884 with an average of 0.687 for the Southern summer accessions. The Huanghuai and Southern summer germplasm were different in the specific alleles, allelic-frequencies and pair wise genetic similarities. UPGMA cluster analysis based on the similarity data clearly separated the Huanghuai from Southern summer soybean accessions, suggesting that they were different gene pools. The results indicate that Chinese Huanghuai and Southern summer soybean germplasm can be used to enlarge genetic basis for developing elite summer soybean cultivars by exchanging their germplasm.

Hu Genhai and Haiyan (2008) studied genetic diversity of 56 high oil soybean cultivars from China were analyzed by using 47 pairs of SSR primers. The results showed

that 289 alleles were produced by 47 pairs of SSR primers. The average allelic richness of polymorphic locus was 6.15. The index of genetic diversity ranged from 0.223 9 to 0.858 7, with an average of 0.6679. The genetic similarity coefficients among all high oil cultivars ranged from 0.117 to 0.926. It indicated that there actually existed sufficient genetic diversity among the high oil cultivars. Cluster analysis results showed that 56 high oil soybean cultivars could be classified into 6 groups by using the UPGMA method according to the genetic similarity coefficient and the cluster pattern was correlated to the geographical distribution of the high oil soybean cultivars to some degree.

Hwang *et al.* (2008) analyzed length polymorphisms of 377 simple sequence repeat (SSR) markers in 87 cultivated or wild soybeans, including Japanese elite cultivars and irreplaceable genetic resources. The average number of SSR marker in the 20 linkage groups was 18.9, with a range of 13 to 25. All SSR markers showed polymorphism on agarose gel electrophoresis, which revealed 1380 alleles for all accessions. The number of alleles at each locus ranged from 2 to 10, with an average of 3.7, and the polymorphic information content of each marker ranged from 0.02 to 0.86, with a mean of 0.44. Cluster analysis separated the accessions into three clusters. Most Japanese cultivars were found in cluster 1, which has further divided into three sub clusters that corresponded to the geographic origin of the cultivars. Most foreign cultivars and all wild accessions were present in clusters 2 and 3, respectively. Our data on the polymorphism of these SSR loci should facilitate the genetic mapping of agronomically important traits and the choice of appropriate markers for marker-assisted selection in soybean breeding programs in Japan.

Dayaman *et al.* (2009) assessed the genetic diversity level of forty five soybean accessions using 22 morphological traits and 11 SSR primers. The morphological traits and SSR markers used in the present study grouped the soybean accessions into 6 and 14 clusters correspondingly. The morphological diversity between CODE 34 and TS99-128 (similarity level 13%) was maximum while constructing the UPGMA based Dendrogram. Among these different clusters, the cluster III (MAUS61-2 and TNAU20052) and cluster VI (IC10755 and Himso1563) contained the minimum number of accessions indicating that these genotypes show maximum variability. The simple sequence repeat analysis generated 48 polymorphic alleles from 11SSR primers. The average number of SSR alleles generated was 4.45 per primer and the level of

polymorphism was 97.95%. The SSR primer Satt253 was highly informative with the PIC value of 0.909. The SSR marker data indicates the existence of a wide genetic diversity among the soybean accessions as compare to the morphological data. Soybean accessions were grouped into fourteen clusters based on SSR allele. Four accessions (NRC55, NRC43, NRC34 and IC10755) released from Indore, three accessions (TNAU20056, TNAU20048 and TNAU20037) released from Coimbatore and two accessions (SL525 and SL295) released from Ludhiana were grouped into a single cluster (cluster III). Thirteen SSR alleles were found to be significantly associated with 8 morphological traits. SSR alleles *viz.* Satt331.1.2, Satt371.5, Satt367.3 and Satt212.1 for pubescent density and SSR alleles Satt253.3 and Satt331.1.3.4.5 for number of pods per cluster. These markers will be useful for marker-assisted selection programs in soybean.

Kuroda *et al.* (2009) analyzed the genetic diversity of a wild soybean collection (1,305 accessions) plus Japanese cultivated soybeans (53 accessions) at 20 SSR marker loci. Higher levels of allelic diversity were found in wild soybeans (28 alleles per locus) than Japanese cultivated soybean (five alleles per locus). The genetic distance between wild soybeans from different regions reflected their proximity. Accessions from Russia consisted of a diverse array of alleles resulting in accessions being spread further apart in a PCA plot than accessions from other regions. Accessions of wild soybean from Korea included many rare alleles and thus had a high representation in the core collection. The two core collections developed here, traditional and mini, consisted of 192 accessions with 97% of the allelic diversity (14% of the whole collection) and 53 accessions with 62.4% of the allelic diversity (5% of the whole collection), respectively

Ristova *et al.* (2010) assessed genetic diversity and relationships of 23 soybean genotypes representing several independent breeding sources from South eastern Europe and five plant introductions from Western Europe and Canada using 20 SSR markers. In total 80 alleles were detected among 28 genotypes with an average of four alleles per locus and an average marker diversity of 0.585. Allele frequency distribution was characterized with a high proportion of alleles at very low frequencies with 11% of unique alleles. Cluster analysis clearly separated all genotypes from each other assigning them into three major clusters, which largely corresponded to their origin. Results of clustering were mainly in accordance with the known pedigrees.

Liu-YuLin et al. (2010) assessed 37 EST-SSR markers which were developed from 286 unigenes obtained from soybean cDNA library. Among the 286 markers designed for the 4 accessions of *Glycine max* and 6 of its wild progenitor (*G. soja*) within the subgenus *Soja*, 209 markers amplified DNA fragments, taking 73.1% and 37 markers appeared to be polymorphic, which was 12.9% of the total. The 37 loci detected a total of 142 alleles, while the PIC values varied from 0.194 to 0.794. Both the number of alleles per locus and PIC value were significantly related to the SSR motif. Six EST-SSR loci may be fixed for different alleles between *G. max* and *G. soja* since they were particularly polymorphic among the 6 *G. soja* accessions. A neighbor-joining tree placed the *G. max* accessions together as a group within the *G. soja*, though the average genetic distance among *G. soja* accessions was much higher. These new EST-SSRs markers will be useful for genetic diversity analysis, genetic mapping construction and gene discovery in *Soja* subgenus.

Shadakshari et al. (2011) studied genetic diversity using SSR markers, revealed that among the primers used, Satt207 and Satt135 produced a maximum of four alleles. PIG was highest for the SSR primer Satt207 which indicated that the primer Satt207 might be an effective and useful tool to determine the genetic differences among the soybean accessions and to study the phylogenetic relationship. The SSR marker profiles resulted in fifteen clusters at nearly 77 per cent similarity. Cluster V consisted of 15 accessions followed by VIII cluster with six genotypes. The formation of 15 clusters through SSR data revealed that the presence of genetic diversity at molecular level was high among the selected germplasm.

Tra et al. (2012) used 15 SSR primer pairs to analyze the genetic diversity of 50 soybean cultivars having different responses to rust. 14 primer pairs showed polymorphisms. There were 81 alleles have been amplified, amplified alleles of each SSR primer pairs ranged from 4 to 8. Polymorphic information contents of used primers ranged from 0.473 (Satt042) to 0.798 (Satt175). Among 15 SSR primer pairs, 10 have high Polymorphic information content (PIC=0.7). The soybean cultivars were grouped into two groups: Group I included, mainly soybean cultivars that are susceptible to rust, group II consisted mostly rust-resistant cultivars. Genetic distance between the two groups is 29%. This information could be used as the basis for selection of soybean cultivars resistant to rust for soybean production, as well as the

basis for the selection of soybean varieties with different genetic background for soybean breeding.

Zhang *et al.* (2013) identified 22 polymorphic EST-SSRs from grain soybean and used to assess the genetic diversity in 48 vegetable soybean accessions. Among the 22 EST-SSR loci, tri-nucleotides were the most abundant repeats, accounting for 50.00% of the total motifs. GAA was the most common motif among tri-nucleotide repeats, with a frequency of 18.18%. Polymorphic analysis identified a total of 71 alleles, with an average of 3.23 per locus. The polymorphism information content (PIC) values ranged from 0.144 to 0.630, with a mean of 0.386. Observed heterozygosity (H_o) values varied from 0.0196 to 1.0000, with an average of 0.6092, while the expected heterozygosity (H_e) values ranged from 0.1502 to 0.6840, with a mean value of 0.4616. Principal coordinate analysis and phylogenetic tree analysis indicated that the accessions could be assigned to different groups based to a large extent on their geographic distribution, and most accessions from China were clustered into the same groups. These results suggest that Chinese vegetable soybean accessions have a narrow genetic base. The results of this study indicate that EST-SSRs from grain soybean have high transferability to vegetable soybean, and that these new markers would be helpful in taxonomy, molecular breeding, and comparative mapping studies of vegetable soybean in the future.

Kaushar (2014) assessed SSR diversity of ten soybean genotypes and revealed that the Jaccard's similarity coefficient estimates between pair of different genotypes varied from 0.14 [between JS335 and DT 21] to 0.67 [between DS74 and PS1225] and [between PS1225 and CM60]. They reported that average number of alleles per primer was 1.85, while percentage of all bands showed that polymorphism was 100%. The UPGMA (unweighted pair group method with arithmetic mean) dendrogram constructed using Jaccard's similarity coefficient of SSR marker data divided 10 soybean genotypes into three main groups and further sub- divided into five clusters.

Kumar *et al.* (2015) investigated genomic DNA of six commercial Indian soybean varieties viz. JS95-60, JS93-05, NRC7, JS97-52, NRC37, JS335 and were amplified using ten simple sequence repeat (SSR) markers, Maximum similarity was observed between NRC7, JS93-05 and JS95-60. Two unique alleles were amplified in

the two varieties namely JS335 and NRC37 and four unique alleles in JS97-52. The researchers concluded that nine polymorphic markers used can distinguish the dominant cultivars from six non-trading varieties.

Gupta and Manjaya (2016) carried out the study for genetic variation at three SMV resistance loci in a set of SMV resistant and susceptible 23 soybean genotypes using the thirteen mapped SSR markers. With an average of 4.5 alleles per locus, 12 polymorphic SSR loci generated total 54 alleles. The number of alleles ranged from 2 to 7 and gene diversity for the polymorphic SSR markers ranged from 0.38 to 0.77 with an average of 0.60. They grouped the 23 soybean genotypes into three major clusters according to cluster analysis.

Rani *et al.* (2016) studied genetic basis of yellow mosaic virus disease in 41 soybean genotypes by using 58 simple sequence repeat primers. They found total 140 alleles with an average of 2.41 alleles per locus. PIC varied from 0.00 to 0.754 with an average of 0.357 and ten unique alleles were observed in the study. The genotypes were allocated in two major clusters separated at 41% similarity according to UPGMA (Unweighted Pairgroup method with Arithmetic Mean).



*Materials
and
Methods*



This chapter deals with all the information pertaining to the methodology including detailed explanation of procedures followed by the researcher in the study.

3.1 Experimental site

The present investigation was conducted during *Kharif* 2015 and 2016 at N. E. Borlaug Crop Research Centre, Govind Ballabh Pant University of Agriculture & Technology, Pantnagar, Udham Singh Nagar, Uttarakhand. Geographically, Pantnagar is situated at the latitude of 29° N, longitude 79.3° E and at an altitude of 243.84 meters above the mean sea level. The university falls under the subtropical zone and situated in the *Tarai* region at the foothills of *Shivalik* range of the Himalayas. The meteorological data as recorded during the study was congenial for crop growth and the same is presented in **Appendix-I**.

3.2 Experimental material

The experimental material in the present study comprised of thirty-six genotypes (fourteen F₂ crosses along with twenty parental lines and two checks) planted in randomized block design with two replications in *kharif* 2015 and F₃ generation were planted in compact family block design with two replications in *kharif* 2016 (comprising 14 F₃ crosses and each cross containing 10 lines of high yielding, 10 low yielding and 10 lines of bulk); are given in **Table. 3.1**.

Table 3.1 List of soybean genotypes with codes

S. No.	Cross/Parental line	Code
1.	PS 1583 x Pb1	C1
2.	PS 1583 x JS 335	C2
3.	PS 1583 x DS 12-5	C3
4.	PS 1583 x JS 20-29	C4
5.	PS 1583 x Bragg	C5
6.	PS 1584 x JS 20-69	C6

7.	PS 1584 x JS 20-41	C7
8.	PS 1042 x PS 1347	C8
9.	RVS 200-1 x PS 1092	C9
10.	JS 20-63 x JS 97-52	C10
11.	JS 20-69 x JS 20-59	C11
12.	JS 20-64 x JS 20-54	C12
13.	JS 20-29 x JS 20-55	C13
14.	PS 1225 x PS 1347	C14
15.	PS 1583	P1
16.	PS 1584	P2
17.	PS 1042	P3
18.	PS 1347	P4
19.	PS 1092	P5
20.	PS 1225	P6
21.	Bragg	P7
22.	JS 335	P8
23.	Pb 1	P9
24.	DS 12-5	P10
25.	JS 20-69	P11
26.	JS 20-41	P12
27.	JS 20-29	P13
28.	JS 20-63	P14
29.	JS 97-52	P15
30.	JS 20-59	P16
31.	JS 20-64	P17
32.	JS 20-54	P18
33.	JS 20-55	P19
34.	RVS 200-1	P20
35.	PS 19	Ch1
36.	SL-688	Ch2

3.3 Layout plan

The experimental material consisting of 36 genotypes (14 F_2 s, 20 parents and 2 checks) was planted in randomized complete block design with two replications during *kharif* 2015. During next year *i.e.* *kharif* 2016, the F_3 progenies of 14 crosses were planted in compact family block design with two replications, in addition to this 20 parents and two checks were also grown alongside with F_3 crosses for study of residual heterosis. In 2015, F_2 s were planted as bulk in 10 rows along with parents and checks in 3 rows of 4 meter with row to row distance of 45cm. In 2016, 30 rows (10 progeny rows of high yielding, 10 progeny rows of low yielding and 10 rows of bulk progeny) of 4 meter with 45 cm row to row spacing for each F_3 cross were planted in *kharif* 2016, while three rows of parents and checks were planted alongside the crosses. Plant to plant distance was maintained at 5 to 7 cm after thinning. The details of number of rows planted and number of plants was considered for recording observations on various characters in each generation/genotype are given below.

Genotype/ Generation	Number of rows planted	Number of plants observed
Parents and checks	3	5
F_2	10 rows(bulk)	50
F_3	30	125
High Yielding	10	5/row
Low Yielding	10	5/row
Bulk	10	25

3.4 Characters studied and observation procedure:

The observations were recorded on 50 plants of each F_2 crosses and five sample plants of the parents and checks, In F_3 generation data was taken from 5 randomly selected competitive plants from each row of high yielding and low yielding progeny row and 25 randomly selected plants from bulk row of crosses and five sample plants of the parents and checks.

A total of twelve quantitative characters were taken up for the present investigation which included discrete as well as continuous measurements for data recording. All the necessary observations were recorded at appropriate stages of crop growth which include plant height, basal node height, basal pod height, number of nodes per plant, number of primary branches per plant, number of pods per plant, number of seeds per pod, dry matter weight per plant, seed yield per plant and 100-seed weight. Observation on days to 50% flowering was recorded on whole plot basis and observation on derived character *i.e.* harvest index was also recorded for the treatments. The following were the parameters to be studied:

1. Days to 50 % flowering

The date when at least 50 % of the plants in a plot had at least one flower opened was noted and number of days to 50 % flowering was calculated.

2. Plant height (cm)

Plant height was measured in centimeters from ground level to the terminal point of the plant at maturity.

3. Basal node height (cm)

Basal node height was measured in centimeters from ground level to the first node at the base of the plant at maturity.

4. Basal pod height (cm)

Basal pod height was measured in centimeters from ground level to the first pod bearing node at the base of the plant at maturity

5. Number of nodes per plant

The number of nodes from ground level to terminal point of the main stem was counted from selected plants at maturity and the average number of nodes per plant was recorded.

6. Number of primary branches per plant

Branches coming out of the main stem of the selected plants were counted at maturity and the average value was worked out.

7. Number of pods per plant

All the seed bearing pods from selected plants were counted at maturity and the average number of pods per plant was recorded.

8. Number of seeds per pod

The number of seeds in ten randomly selected pods per plant was counted and the average number of seeds per pod was recorded.

9. 100-seed weight (g)

A sample of fully matured, well-developed, cleaned and sun dried hundred seed were taken from individual plant and their weight was recorded in grams.

10. Dry matter weight per plant (g)

Each selected plant was harvested separately from each plot. The weight of each plant was taken in grams. It was recorded when plants were completely dry in field. Root and leaves were not considered in dry matter weight per plant.

11. Harvest index (%)

Harvested plants were threshed separately and yield of representative plants was recorded separately and individually. Harvest index was calculated as per following formula:

$$\text{Harvest index}(\%) = \frac{\text{Economic yield}}{\text{Total biological yield above ground level}} \times 100$$

12. Seed yield per plant (g)

Seeds from selected individual plants were sun dried and weighed in grams. The seed yield per plant was recorded by taking the average of selected plants.

3.5 Statistical and genetical analysis

Means of the various observations were subjected to the following statistical/biometrical analyses for drawing appropriate conclusion from the present investigation.

1. Analysis of variance
2. Effectiveness of early generation selection on the basis of various genetic parameter
3. Estimation of residual heterosis

4. Transgressive segregation
5. Estimation of inter-character correlation
6. Estimation of path coefficient
7. Molecular marker analysis using SSR marker

3.5.1 (a) Analysis of variance for RCBD

The analysis of variance for each character was carried out for the randomized complete block design as suggested by **Fisher (1946)**. The replication wise mean values of 36 genotypes including 20 parents, 14 F_{2S} and 2 standard check varieties subjected to RCBD analysis. The model used was as follows:

$$Y_{ij} = \mu + t_i + b_j + e_{ij}$$

$$(i = 1, 2, 3, \dots, t)$$

$$(j = 1, 2, 3, \dots, r)$$

Where,

Y_{ij} = Observed response of i^{th} genotype in the j^{th} replication.

μ = General mean of population

t_i = Effect of i^{th} treatment

b_j = Effect of j^{th} block

e_{ij} = Random error of i^{th} genotype and j^{th} block

The analysis of variance Table was made as follows:

Source of variation	Degree of freedom	Sum of square	Mean of square	EMS	F- value
Replication	(r-1)	SS _r	$MS_r = \left(\frac{SS_r}{(r-1)} \right)$	$\sigma_e^2 + r\sigma_g^2$	
Treatment	(t-1)	SS _t	$MS_t = \left(\frac{SS_t}{(t-1)} \right)$	$\sigma_e^2 + r\sigma_g^2$	MSt/MSe
Error	(r-1) (t-1)	SS _e	$MS_e = \left(\frac{SS_e}{(r-1)(t-1)} \right)$	σ^2_e	
Total	(rt-1)				

Where,

r = Number of replications, t = Number of treatments, SS_r = Sum squares of replications, SS_t = Sum of squares of treatments, SS_e = Sum squares of error, MS_r = Mean squares for replications, MS_t = Mean squares for treatments, MSe = Mean squares for error

The significance of difference among the treatment means was tested by F test and whenever the 'F' test was found to be significant, critical difference (CD) was calculated to test the significance of difference between any two treatment means.

$$\text{C.D. (at 5 \%)} = (2MSe / r)^{1/2} \times t (5 \%) \text{ at error d. f.}$$

$$\text{C.D. (at 1 \%)} = (2MSe / r)^{1/2} \times t (1 \%) \text{ at error d. f.}$$

Standard error mean:

$$\text{SEM} = \sqrt{\frac{MSe}{r}}$$

Standard error of difference:

$$\text{SEd} = \sqrt{\frac{2MSe}{r}}$$

Coefficient of variance:

$$\text{CV (\%)} = \frac{\sqrt{EMS}}{\bar{X}} \times 100 \text{ or } \frac{SD}{\bar{X}} \times 100$$

Where

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

SD = Standard Deviation

3.5.1 (b) Analysis of Variance for CFBD

Observations for each character under study in two replications were averaged and tabulated for each of the fourteen families. The plot means of the characters was studied to the analysis of variance as prescribed for complete family block design and comparisons were made between families.

Analysis of variance for compact family block design

Source of variation	d.f	M.S
Replications	(r-1)	Mr
Families	(f-1)	Mf
Error(a)	(r-1) (f-1)	Me(a)
Between progenies within family	f(p-1)	Mp
Error (b)	f(r-1) (p-1)	Me(b)

Where,

r = number of replications

f = number of families

p = number of progenies per family

The families were tested against error (a) while progenies within families against error (b). The standard errors of difference (SEd) in case of pooled analysis were calculated as follows:

$$\text{SEd of means of two families (SEd between families)} = \sqrt{\frac{2M_{e(a)}}{rp}}$$

3.5.2. Effectiveness of early generation selection

The following statistical procedures were followed in this objective as outlined below:

3.5.2.1 Estimation of variability parameters

3.5.2.2 Intergeneration correlation coefficient

3.5.2.3 Intergeneration regression coefficient

3.5.2.4 Significance test of mean performance of selected lines

3.5.2.5 Realized heritability

3.5.2.1 The different parameters estimated include the following:

3.5.2.1.1 Estimation of Variance Components

Genotypic and phenotypic components of variance were estimated with the help of following formulae as suggested by **Burton and De Vane (1953)**.

$$\text{Genotypic Variance } (\sigma_g^2) = \text{MSSv} - \text{EMSS}/r$$

$$\text{Phenotypic variance } (\sigma_p^2) = \sigma_g^2 + \text{EMSS}$$

3.5.2.1.2 Coefficient of variability

The genotypic, phenotypic and environmental coefficients of variability were computed for each character as per method explained by **Singh and Chaudhary (1977)**.

$$\text{Genotypic Coefficient of Variation (GCV)} = \frac{\sigma_g}{\bar{X}} \times 100$$

$$\text{Phenotypic Coefficient of Variation (PCV)} = \frac{\sigma_p}{\bar{X}} \times 100$$

$$\text{Environmental Coefficient of Variation (ECV)} = \frac{\sigma_e}{\bar{X}} \times 100$$

Where,

σ_g = genotypic standard deviation

σ_p = phenotypic standard deviation

σ_e = environmental standard deviation

$\bar{X}$ = grand mean of the concerned character

3.5.2.1.3 Heritability (Broad Sense)

Heritability coefficient (h^2) was computed for each character as the ratio of genetic variance to the total variance as suggested by **Hanson *et al.* (1956)**.

$$h^2 = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where, σ_g^2 and σ_p^2 are genotypic and phenotypic variances, respectively.

3.5.2.1.4 Genetic Advance

Genetic advance (GA) for each character was computed by adopting the formulae given by **Johnson *et al.* (1955)**.

$$GA = h^2 KP$$

Where,

K = Selection differential which is equal to 2.06 at 5% intensity of selection
(**Lush, 1949**).

Genetic advance as per cent of mean (GAM)

$$GAM = \frac{GA}{\bar{X}} \times 100$$

Where,

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

3.5.2.2 Inter-generation correlation

Mean values of F₂ and F₃ generation for the twelve characters were used for the estimate of correlation between F₂ and F₃

3.5.2.2.1 Simple Correlation between F₂ vs. F₃ for all twelve characters

3.5.2.2.2 Correlation of lines selected for high value, low value and bulk for yield and yield attributing characters (dry matter weight per plant, number of pods per plant and harvest index) in F₂ and F₃ generations of each of fourteen crosses.

$$r_{xy} = \frac{Cov.XY}{\sqrt{Var.X \times Var.Y}}$$

3.5.2.3 Inter-generation regression

The parent progeny regression analysis was carried out by regressing the mean values of a character in the progeny (F₃) upon the value of a character in the parents (F₂). The regression coefficient (b) was calculated by using the formula suggested by **Singh and Chaudhary (1977)**.

Regression coefficient is used to measure the degree of dependence of one variable on the variable. Thus, regression coefficient of Y on X is the measure of change in Y for a unit change in X. Symbolically:

$$b = \text{Cov}(X, Y) / V(X)$$

Here, Y is the dependent variate and X is an independent variate,

In equation

$$\text{Cov}(X, Y) = [\sum (X_i - \bar{X})(Y_i - \bar{Y})] / (n - 1)$$

$$V(X) = \sum (X_i - \bar{X})^2 / (n - 1)$$

Test of significance:

To test the null hypothesis ($b=0$) is through the application of 't' test:

$$t_{\text{cal}} = b_{yx} / \text{S.E.}(b)$$

The calculated value is compared with tabulated t value at the 0.01 and 0.05 level of significance with the degree of freedom of the S.E. (b).

$$\text{S.E.}(b) = [\text{MSe} / V(X)]^{1/2} \quad \text{with d.f equal to MSe}$$

Where, MSe is the variance due to deviation from the regression and $V(X)$ is the variance of X.

3.5.2.4 Significance of mean performance of selected lines

3.5.2.4.1 The difference in mean performance of lines selected for high and low values for dry matter weight per plant, number of pods per plant, seed yield per plant and harvest index individually for each cross in each generation.

3.5.2.4.2 The difference in mean performance of lines selected for high values in F_2 and F_3 generation, likewise for lines selected for low values in F_2 and F_3 generations.

The significance of difference is tested by applying 't test' for (n-2) degree of freedom.

3.5.2.5 Realized heritability

It is the statistical tool which measures the magnitude of genetic improvement in a population achieved through selection. It is calculated by the formula given by **Singh and Chaudhary (1977)**

$$\text{Realized Heritability} = \frac{\text{Response to selection}}{\text{Selection differential}}$$

Response to selection is the difference of mean of progeny of selected individuals ($\overline{Xp}$) and the base population ($\overline{Xo}$)

Selection differential is estimated by difference in mean of the selected individuals ($\overline{Xs}$) from that of the base population ($\overline{Xo}$)

3.5.3 Estimation of residual heterosis:

Residual Heterosis, expressed as percent increase or decrease in the performance of segregating generation over the mid-parent (average or relative) heterosis, better parent (heterobeltiosis) and check parent (standard heterosis). It was computed for each character using the following formula:

$$\text{Relative heterosis} = \frac{\overline{F_2} - \overline{MP}}{\overline{BP}} \times 100$$

$$\text{Heterobeltiosis} = \frac{\overline{F_2} - \overline{BP}}{\overline{BP}} \times 100$$

$$\text{Standard heterosis} = \frac{\overline{F_2} - \overline{CP}}{\overline{CP}} \times 100$$

Where,

$\overline{F_2}$ = Mean performance of F_2 hybrid

$\overline{P_1}$ = Mean performance of parent one

$\overline{P_2}$ = Mean performance of parent two

$\overline{BP}$ = Mean performance of better parent

$\overline{CP}$ = Mean performance of check parent

$\overline{MP}$ = Mean mid-parental value i.e. $(P_1 + P_2)/2$

The significance of heterosis was tested with 't' as given below:

(a) For heterobeltiosis

$$t = \frac{\overline{F_2} - \overline{BP}}{\sqrt{2Me/r}}$$

- (b) For standard heterosis

$$t = \frac{\overline{F_2} - \overline{CP}}{\sqrt{2Me/r}}$$

- (c) For relative heterosis

$$t = \frac{\overline{F_2} - \overline{MP}}{\sqrt{3Me/2r}}$$

Where,

$\overline{F_2}$ = Mean of F₂ hybrid

$\overline{BP}$ = Mean of better parent

$\overline{CP}$ = Mean performance of check parent

$\overline{MP}$ = Mean of mid-parental value

Me = Error mean square

r = number of replication

3.5.4. Transgressive segregation:

Percentage of transgressive segregation in the F₂ generation for all the characters observed for each cross was obtained by defining extreme progeny types as transgressive segregants *i.e.*, the plants that exceeded their parental limits in either direction. Analysis and comparison was done based on their individual plant data.

The per cent value of transgressive segregants was calculated as per following formula:

$$\text{Transgressive segregants (\%)} = \frac{\text{Number of F}_2 \text{ progeny, exceed the parental limit}}{\text{Total number of F}_2 \text{ progeny}} \times 100$$

3.5.5. Estimation of correlation coefficient

The correlations between all the characters under study at genotypic, phenotypic and environmental levels were estimated according to the method given by **Searle (1961)** using the following formula:

1. Phenotypic correlation between characters X and Y

$$r_{xy}(p) = \frac{Cov.XY(p)}{\sqrt{Var.X(p) \times Var.Y(p)}}$$

2. Genotypic correlation between characters X and Y

$$r_{xy}(g) = \frac{Cov.XY(g)}{\sqrt{Var.X(g) \times Var.Y(g)}}$$

3. Environmental correlation between character X and Y

$$r_{xy}(e) = \frac{Cov.XY(e)}{\sqrt{Var.X(e) \times Var.Y(e)}}$$

Where, Cov. XY (p), Cov.XY (g), Cov. XY(e) denotes phenotypic , genotypic and environmental covariance between characters X and Y, respectively. Var X (p), Var. X(g), Var.(e) denote phenotypic , genotypic and environmental variance for character X and Var.Y(p), Var. Y (g) and Var.Y(e) denote phenotypic , genotypic and environmental variance for character Y, respectively.

$$\text{Test statistics, } t_{cal} = \frac{r \sqrt{n-2}}{\sqrt{1-r^2}} ; \quad (n-2) \text{ df.}$$

Where, n = number of genotypes.

3.5.6. Estimation of path-coefficient analysis

Path coefficients were obtained according to the procedure as suggested by **Wright (1921)** and as elaborated by **Dewey and Liu (1959)**.

Fourteen yield components were included in the path coefficient analysis to find their direct and indirect effects upon yield. Residual factor was also included in the causal system representing all other factors which might affect yield. The following equations are formed and solved for estimating direct and indirect effects.

$$r_{iy} = r_{i1} \cdot p_{1y} + \dots + p_{iy} + \dots + r_{in} p_{ny}$$

Where,

r_{iy} = denote coefficient of correlation between cause factor X_i and dependent character Y

r_{in} = denote coefficient of correlation among all possible combinations of causal factors, and

p_{iy} = denote direct effect of character X_i upon the character Y

Residual factor was obtained as follows:

$$p_z.Y_n = \sqrt{1 - R^2}$$

Where,

$$R^2 = \sum_{i=1}^n p_{iy}^2 + 2 \sum_{i < j}^n p_{iy} p_{jy} r_{ij}$$

Which is the square of the multiple correlation coefficient (R) and is known as coefficient of determination.

3.5.7 Molecular marker analysis using Microsatellite marker (SSR)

3.5.7.1 Experimental site

The molecular marker analysis work was carried out in the Molecular and Cytogenetic Laboratory of the Department of Genetics and Plant Breeding, GBPUA &T Pantnagar.

3.5.7.2 Research material

The research material comprised of twenty-two lines of soybean. The leaf samples were collected from the experimental field at three leaf stage and were stored in -80 degrees C deep freezer (New Brunswick Scientific TM Eppendorf Ltd.) until further use. The leaves were further utilized for the isolation of deoxyribonucleic acid (DNA). The extracted DNA was further purified and amplified for microsatellite (SSR) diversity analysis. The list of SSR marker used for molecular diversity study are listed in **Table 3.3**.

3.5.7.3 DNA extraction from soybean genotypes

For the molecular marker characterization study, genomic DNA was extracted from the collected genotypes of soybean under the present investigation.

3.5.7.3.1 Extraction of Genomic DNA

The genomic DNA was isolated for molecular characterization of genotypes studies by using the CTAB (Cetyl tri-methyl ammonium bromide) protocol given by **Doyle and Doyle (1990)** with slight modifications. The list of buffers and stocks solution is given in **Appendix-II**.

- 2.0 g of sterilized leaf material was weighed for DNA extraction
- Pre-weighed leaf material was ground in liquid nitrogen to a fine powder with the help of pre-chilled pestle and mortar.
- The powder was transferred to 2.5 ml centrifuge tubes containing 1.5 ml of pre-warmed extraction buffer. The spatula was used to dispense the material completely.
- The extraction buffer and powdered sample were mixed thoroughly by vortexing.
- Samples were incubated at 60°C for 40 min with occasional mixing by gentle swirling.
- After slight vortexing, spinning was done at 10,000 rpm at room temperature for 10 minutes in the centrifuge machine and the supernatant was collected in new centrifuge tubes.
- 1mL chloroform: isoamyl alcohol (24:1) was added to sample and was mixed by gentle inversion.
- The samples were centrifuged at 12,000 rpm for 15 minutes at room temperature.
- The aqueous phase was removed with a wide bore pipette, and transferred to a clean tube. Thereafter, 2/3 volume of isopropanol was added to the sample and mixed by quick gentle inversion and finally the tubes were kept overnight at -20°C.

3.5.7.3.2 DNA purification: RNase A treatment

Ribonuclease A is an end nuclease enzyme, having the capacity to digest RNA. DNase free RNase, supplied by Genei Pvt. Ltd., Bangalore was used. This RNase was supplied as a powder and dissolved easily in water.

Preparation

1 ml sterile de-ionized water (zero conductivity) was added to the vial containing RNase powder. Aliquots of 50µl were made in sterile Eppendorf tubes. The tubes were kept in boiling water at 100°C for 15 minutes; Eppendorf tubes were covered with a Paraffin film and stored at -20°C.

RNase treatment procedure

1. 4 µl RNase A was added to the Eppendorf tube containing 200 µl of extracted DNA and then incubated for 3 h at 37°C in a water bath.
2. The DNA was further extracted with equal volume of Phenol: Chloroform: Isoamyl alcohol (25: 24: 1, v/v) and centrifuged at 10,000 rpm for 12 min at 10°C.
3. The supernatant was taken into a fresh Eppendorf tube. 0.6 volume ice cold isopropanol and 0.1 volume of ice cold sodium acetate (3M) were added and the mixture was kept at -20°C for at least 2h.
4. The mixture was then centrifuged at 10,000 rpm at 10°C for 12 min.
5. The supernatant was removed using a micropipette and pellet was washed with 70% ethanol and dried completely.
6. The DNA pellet was redissolved in a minimum amount of TE buffer.

3.5.7.3.3 Quantification of Genomic DNA by U.V. Spectrophotometer

To measure the DNA concentration by using Eppendorf™ UV Biophotometer, the blank was set against TE buffer. The concentration was measured at 260/280nm by fixing the dilution in biophotometer machine. The concentration was displayed by equipment through quantifying the following equation:

$$\text{DNA Concentration } (\mu\text{g/ml}) = \frac{\text{O.D.} \times 50 \times \text{Dilution factor}}{1000}$$

O.D was recorded at 280 nm to calculate the ratio OD₂₆₀/OD₂₈₀. The ratio gives the amount of RNA (or protein) in the preparation. A value of 1.8 is optimum for best DNA preparation. A value of the OD₂₆₀/OD₂₈₀ ratio below 1.8 indicates the presence of proteins in the preparation and a value above 1.8 indicates that the sample has excess presence of RNA.

3.5.7.4 Polymerase chain reaction (PCR) in thermocycler

Molecular marker analysis involves the use of marker which is tightly linked with target gene and amplification through the PCR at the appropriate annealing temperature. PCR is a powerful, extremely sensitive technique based on the enzymatic amplification of DNA fragments that is flanked by oligo-nucleotide primers hybridizing to opposite strands of the target sequence. The PCR involves three basic steps which constitute a single cycle:

- Denaturation of the target DNA at 94⁰C
- Annealing of the primers to the template DNA (temperature based on marker used).
- Primer extension by addition of nucleotides to the 3' end of the primers by the enzyme DNA polymerase.

3.5.7.4.1 PCR ingredients

(i) Synthesis of the primers

An essential requirement of PCR is the availability of short oligo-nucleotides called primers having sequence complementarity to either end of the target DNA segment called template DNA to be synthesized. The primers used in the study were synthesized from Genei/Ocimum, Biosciences, Bengaluru, India.

- (ii) **Taq DNA polymerase:** *Taq* DNA polymerase is a thermo stable enzyme that replicates DNA at 72-74⁰C and remains functional even after incubation at 95⁰C. The enzyme has 5'→3' polymerase and 3'→5' exonuclease activity. The concentration of the enzyme was 5 U/μl. It was obtained from Merck India Ltd.
- (iii) **dNTP's:** The dNTPs used in the reaction were obtained from Merck India Ltd. as 2.5mM each (dATP, dGTP, dCTP, dTTP)
- (iv) **Assay buffer (10X):** Assay buffer (10X) contained 10 mM Tris-HCl (pH 9.0), 15 mM MgCl₂, 50 mM KCl and 0.01% gelatine.
- (v) **Primers:** 40ng primer was used for each PCR reaction that was selected from different chromosomes

3.5.7.4.2 Optimization of PCR parameters

There are a number of variables in a PCR which was optimized to give target amplification. These parameters are:

- Denaturation temperature and denaturation time
- Annealing temperature and annealing time
- Amounts of template and primer to be taken
- Concentration of MgCl₂ in the assay buffer
- The number of Cycles to be performed

Table 3.2: Reaction mixture for PCR amplification

	Component (conc.)	Final conc.	Single tube (µl)
1.	DNA template	50 ng/µl	2.0 µl
2.	dNTPs (10mM mix)	2.5 mM each	1.0 µl
3.	Taq polymerase (5unit/µl)	1 unit	0.2 µl
4.	Primer (F+R)	30 ng/µl	1.4µl
5.	Taq Buffer (10X)+ 25 mM MgCl ₂	1X	1.5 µl
6.	ddw		8.9 µl
		TOTAL	15 µl

Table 3.3: List of seventeen SSR primers:

Sl.No.	Primer	Ends	Sequence	Tm°C
1.	Satt146 forward	Left end	AAGGGATCCCTCAACTGACTG	59.8
	Satt146 reverse	Right end	GTGGTGGTGGTGAAAACCTATTAGAA	59.7
2.	Satt184 forward	Left end	GCGCTATGTAGATTATCCAAATTACGC	61.9
	Satt184 reverse	Right end	GCCACTTACTGTTACTCAT	52.4
3.	Satt187 forward	Left end	GCGTTTTAATTTATGATATAACCAA	53.1
	Satt187 reverse	Right end	GCGTTTTATCTCTTTTCCACAAC	57.6

4.	Satt197 forward	Left end	CACTGCTTTTTCCCCTCTCT	57.3
	Satt197 reverse	Right end	AAGATACCCCCAACATTATTTGTAA	56.4
5.	Satt200 forward	Left end	GCGATAAATGGTTAATGTAGATAA	54.2
	Satt200 reverse	Right end	GCGAAAGGACAGATAGAAAGAGA	58.9
6	Satt228 forward	Left end	TCATAACGTAAGAGATGGTAAAAC	56.4
	Satt228 reverse	Right end	CATTATAAGAAAACGTGCTAAAGAG	56.4
7	Satt267 forward	Left end	CCGGTCTGACCTATTCTCAT	57.3
	Satt267 reverse	Right end	CACGGCGTATTTTTATTTTG	51.2
8.	Satt268 forward	Left end	TCAGGGGTGGACCTATATAAAATA	57.6
	Satt268 reverse	Right end	CAGTGGTGGCAGATGTAGAA	57.3
9.	Satt277 forward	Left end	GGTGGTGGCGGGTACTATTACT	62.4
	Satt277 reverse	Right end	CCACGCTTCAGTTGATTCTTACA	58.9
10.	Satt281 forward	Left end	CCGGTCTGACCTATTCTCAT	57.3
	Satt281 reverse	Right end	CACGGCGTATTTTTATTTTG	51.2
11	Satt300 forward	Left end	GCGCCACACAACCTTTAATCTT	60.6
	Satt300 reverse	Right end	GCGGCGACTGTTAACGTGTC	61.4
12.	Satt433 forward	Left end	ATCAGCTGCATAAGTAAAGATACA	57.6
	Satt433 reverse	Right end	ACATGCTTGCAGAGGTGAATA	58.9
13.	Satt449 forward	Left end	GCGTGCTTCTTATATTAGGTGTTAGT	60.1
	Satt449 reverse	Right end	GCGCATTGGAGTTTTTGCTTTT	56.5
14.	Satt508 forward	Left end	GCGGCCTCCTCAAATAATAATAAT	58.1
	Satt508 reverse	Right end	GCGGTTAGGAATAGAAGATAGTTACATT	60.7
15.	Satt527 forward	Left end	GCGGTTACATCTTGCAAATAAATTAA	55.3
	Satt527 reverse	Right end	GCGGAATTTTGACATAAATTAATAAC	57.1
16.	Satt565 forward	Left end	GCGCCCGGAACCTGTAATAACCTAAT	63.2
	Satt565 reverse	Right end	GCGCTCTCTTATGATGTTTATAATAA	58.5
17.	Satt586 forward	Left end	GCGGCCTCCAACTCCAAGTAT	62.1
	Satt586 reverse	Right end	GCGCCCAAATGATTAATCACTCA	58.9

3.5.7.4.3 Determination of primer annealing temperature

Primer annealing temperature depends on its T_m value, which can be calculated using the following equation:

$$T_m (^{\circ}\text{C}) = 4 (G+C) + 2 (A+T)$$

Where A, T, G, and C stand for the number of corresponding nucleotides in the primer. Primer annealing may fail at a temperature much higher than T_m , whereas annealing temperature much below T_m may lead to non-specific amplification.

Table 3.4: PCR amplification cycle condition for SSR markers

Cycles	Denaturation		Annealing		Polymerization	
	Temp.	Time	Temp.	Time	Temp.	Time
First cycle	94 $^{\circ}$ C	5 min	-	-	-	-
35 Cycles	94 $^{\circ}$ C	30 sec	55-60 $^{\circ}$ c	30sec	72 $^{\circ}$ C	30sec
Last cycle	-	-	-	-	72 $^{\circ}$ C	10 min

3.5.7.5 Agarose Gel Electrophoresis

3.5.7.5.1 Procedure of gel electrophoresis

Horizontal gel electrophoresis unit was used for fractionating markers products on agarose gel. Agarose gel (2.5.0%) was prepared by dissolving an appropriate amount of agarose in 0.5X TBE buffer and EtBr for visualization of bands. Alternatively, for some of the markers, agarose gel combined with Metaphor high-resolution gel (1:2 respectively) was used for better resolution. For each well, DNA loading dye and DNA samples were mixed in 1:6 ratios and loaded with a micropipette. Electrophoresis was done at 80 V for 3hrs in 0.5X TBE electrophoresis buffer. The gel image was viewed and stored in gel documentation system.

3.5.7.6 Data analysis

The polymorphic products from microsatellite analyses obtained in gel photographs were used to score qualitatively and independently for presence (1) and absence (0) for each maker allele-genotype combination. The data entry was done into

a binary data matrix as discrete variables. Further data matrix was entered into NTYSYS-PC (Numerical Taxonomy and Multivariate Analysis System Programme. The data was analyzed using SIMQUAL (similarity for qualitative data) program that is used to calculate Jaccard's coefficient, a common estimator of genetic identity (**Jaccard, 1908**). These similarity coefficients were used to construct dendrograms using the un-weighted pair group method with Arithmetic average using (UPGMA) NTSYS program. The informativeness of the SSR markers in terms of polymorphism was obtained by calculating the polymorphism information content (PIC) (**Botstein *et al.*, 1980**). The polymorphism information content (PIC) value is a measure of polymorphism among varieties for a marker locus used in linkage analysis. Polymorphism information content (PIC) was computed by deducting the sum of square values for all the frequencies of different alleles produced by a single marker locus form using the formula.

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

Where Xi is the frequency of ith allele of a particular locus. PIC provides an estimate of the discriminatory power of a marker by taking into account, not only the number of alleles that are expressed but also the relative frequencies of those alleles. PIC value range from 0 (monomorphic) to 1 (very high discriminative, with many alleles in equal frequencies).



Results and Discussion



The results obtained from the present investigation have been presented and discussed under the following heads:

- 4.1 Analysis of variance and mean performance
- 4.2 Effectiveness of early generation selection using various genetic parameters
- 4.3 Estimation of Residual Heterosis
- 4.4 Transgressive segregation analysis
- 4.5 Estimates of inter-character correlation
- 4.6 Path coefficient analysis
- 4.7 Molecular marker diversity analysis

4.1 Analysis of variance and mean performance

Analysis of variance for the randomized complete block design was implied for all the twelve traits studied for appraising 36 genotypes *viz.* 14 F_{2s}, 20 parents and 2 standard checks, (PS 19 and SL 688) which is presented in **Table 4.1.3**. The mean of squares due to treatments were found significant for all the traits studied. The replication variances for all traits were found non-significant. The mean performance of 36 genotypes including 2 checks and the range of variation among them for all the characters studied are summarized in **Table 4.1.1**.

Analysis of variance for the compact family block design for twelve undertaken characters is presented in **Table 4.1.4** for fourteen crosses and their 21 progenies. The mean of squares due to families were found to be highly significant for all the twelve traits studied as well as for all the progenies of the respective families. However, the replication variances for all the traits were found non-significant. The mean performance of fourteen crosses and the range of variation among them for the traits studied are summarized in the **Table 4.1.2**. The results are summarized in detail in the ensuing pages:

1. Days to 50% flowering

A perusal of table for mean performance of parents and crosses for days to 50% flowering showed that in F₂ generation among parents and crosses, days to 50%

flowering ranged from 44.50(RVS200-1) to 56 days (PS19) with overall mean of 50.15 days, whereas in F₃ it ranged from 41.10(JS 20-69 X JS 20-59) to 52.75 days (PS 1225 X PS 1347) with mean value of 47.73 days.

2. Dry matter weight per plant (g)

Dry matter weight per plant ranged from 39.17 (RVS 200-1) to 97.50 g (PS 19) among the parents and the F₂ crosses with the overall mean of 60.43g, whereas in F₃ it ranged from 36.85 (RVS 200-1 x PS 1092) to 74.02 g(PS 1584 X JS 20-41), with mean value of 64.26 g.

3. Plant height (cm)

The range of plant height varied from 39.64 (RVS 200-1 x PS 1092) to 81.50 cm (PS 1584) among the 36 genotypes, showing the 59.43 cm as an overall mean, while in F₃ it ranged from 35.01(RVS 200-1 X PS 1092) to 64.55cm(PS 1583 X Bragg) with mean value of 53.93 cm.

4. Basal node height (cm)

Basal node height ranged from 2.15(JS 20-69) to 6.36 cm (RVS 200-1) in F₂ generation, having 4.14 cm as an overall mean, whereas in F₃ it ranged from 3.19(RVS 200-1 X PS 1092) to 4.39 cm (PS 1584 X JS 20-41) with overall mean value of 3.74 cm.

5. Basal pod height (cm)

Basal Pod height ranged from 3.88(JS 20-55) to 13.79 cm (Pb1) in both the parents and crosses with overall mean of 8.82 cm, whereas in F₃ it ranged from 4.5(RVS 200-1 X PS 1092) to 7.61 cm (JS 20-69 X JS 20-59), with an overall mean of 5.93 cm.

6. Number of nodes per plant

The number of nodes per plant ranged from 7.84(JS20-55) to 15.22(PS1583 X Pb1) among the genotypes and the overall mean was found to be 11.61, whereas in F₃ it ranged from 10.50 (PS 1583 X Bragg) to 14.96 (JS 20-69 X JS 20-59) with mean value of 12.24.

7. Number of primary branches per plant

Number of primary branches per plant ranged from 2.50 (PS 1583) to 5.92 (JS 20-69) in the F₂ generation with the overall mean of 3.93, whereas in F₃ it ranged from 3.39(PS 1042 X PS 1347) to 5.36 (PS 1584 X JS 20-69) with mean value of 4.34.

8. Number of pods per plant

Among the genotypes in F₂ generation, the number of pods per plant ranged from 44.82 (RVS200-1 X PS1092) to 110.83 (PS 19) having an overall mean of 65.61, whereas in F₃ it ranged from 40.13(RVS 200-1 X PS 1092) to 103.51(PS 1584 X JS 20-41) with mean value of 73.29.

9. Number of seeds per pod

In F₂ generation, number of seeds per pod ranged from 1.99(PS 1583 x JS 335) to 2.83(JS 20-69) with an overall mean of 2.39, whereas in F₃ it ranged from 2.22(RVS 200-1 X PS 1092) to 2.64(PS 1584 X JS 20-69) with mean value of 2.38.

10. Seed yield per plant (g)

Seed yield per plant ranged from 7.79(JS 20-55) to 29.76 g (JS 20-69) with the overall mean of 17.87 g, whereas in F₃ it ranged from 8.60(RVS 200-1 X PS 1092) to 29.66 g (PS 1584 X JS 20-41) with mean value of 20.20g.

11. 100-seed weight (g)

The range of 100-seed weight varied from 8.60 (PS1583xPb1) to 13 g (JS 20-64) with the overall mean of 10.98g in F₂ generation whereas in F₃ it ranged from 7.81(PS 1225 X PS 1347) to 9.78 g(JS 20-29 X JS 20-55) with mean value of 8.43g.

12. Harvest index (%)

Harvest index ranged from 14.86 (JS20-55) to 57 per cent (Pb1) with the overall mean of 30.03 per cent, whereas in F₃ it ranged from 23.18 (RVS 200-1 X PS 1092) to 37.26 per cent (PS 1583 X JS 20-29) with mean value of 29.89 per cent.

For any breeding programme to initiate, the knowledge and availability of genetic variability is the basic need, without which improvement of the existing lines is not possible. Therefore, genetic variability is the Holy Grail of any selection procedure. Higher the variability in the research material more will be the chances to perform selection and bring improvement in the available genetic material. The results from the analysis of variance data based on the genotypes showed that the significant amount of variability was present in the experimental material for all the twelve characters undertaken for study.

Table 4.1.1 Mean performance of yield and other characters in F₂ generation of soybean genotypes

Sn No.	Genotype	Days to 50% Flowering	Dry matter weight per plant (g)	Plant height (cm)	Basal node height (cm)	Basal pod height (cm)	Number of nodes per plant	Number of primary branches per plant	Number of pods per plant	Number of seeds per pod	Seed yield per plant (g)	100- seed weight (g)	Harvest index (%)
1	PS 1583	49.50	77.50	78.00	3.25	11.83	12.00	2.50	60.00	2.55	20.54	12.47	26.55
2	PS1584	49.50	72.50	81.50	4.25	11.50	9.97	4.09	78.00	2.63	16.09	11.63	22.26
3	PS1042	51.50	63.00	71.50	5.45	13.50	9.00	3.83	59.67	2.33	13.13	10.89	20.85
4	PS1347	50.00	67.00	73.50	4.13	12.25	9.84	3.23	64.00	2.50	13.63	11.24	20.35
5	PS1092	47.50	74.17	76.50	3.38	9.58	11.83	3.83	92.67	2.53	21.75	11.18	29.33
6	PS1225	50.50	65.83	75.50	3.06	7.33	12.00	4.00	106.50	2.38	26.56	10.36	40.35
7	Bragg	49.00	45.83	67.00	4.34	9.60	10.50	4.17	59.17	2.35	17.60	9.35	38.47
8	JS335	51.50	82.50	62.50	2.49	11.90	11.00	4.08	98.33	2.70	28.57	12.30	34.90
9	Pb1	49.50	46.67	63.00	3.50	13.79	14.45	3.83	78.00	2.75	26.47	11.02	57.00
10	DS 12-5	51.50	46.67	56.67	5.45	10.88	11.17	4.00	78.83	2.36	9.61	9.29	20.58
11	JS 20-69	51.00	59.00	49.00	2.15	12.00	14.27	5.92	61.50	2.83	29.76	11.72	50.45
12	JS 20-41	49.50	48.33	54.50	4.00	10.90	8.00	4.67	51.50	2.12	13.83	11.41	28.60
13	JS 20-29	48.50	70.83	51.50	3.15	5.25	10.33	4.10	60.33	2.60	23.97	12.27	34.14
14	JS 20-63	50.50	60.83	51.00	3.52	7.39	11.83	3.00	56.67	2.43	22.58	11.51	37.11
15	JS 97-52	48.00	71.67	70.00	3.59	10.20	13.17	5.33	48.33	2.70	25.99	11.42	36.26
16	JS 20-59	51.00	48.33	56.50	2.99	6.68	10.67	3.65	55.50	2.53	19.46	11.31	41.59
17	JS 20-64	51.00	71.67	66.17	2.71	5.21	12.00	5.33	76.00	2.53	27.19	13.00	38.63
18	JS 20-54	53.50	52.50	57.00	3.77	6.35	11.83	3.83	56.00	2.15	20.79	11.35	39.63
19	JS 20-55	52.00	52.50	57.50	5.99	3.88	7.84	3.83	49.83	2.51	7.79	9.61	14.86
20	RVS 200-1	44.50	39.17	46.50	6.36	6.75	8.17	4.17	62.17	2.80	11.46	9.58	29.34
21	PS 19	56.00	97.50	81.50	2.46	9.58	12.00	4.50	110.83	2.23	26.14	11.67	26.81
22	SL688	53.50	93.33	61.00	2.44	6.15	13.67	4.39	87.17	2.47	25.43	12.22	27.78
23	PS 1583 x Pb1	51.50	60.40	55.21	6.15	8.13	15.22	4.38	55.44	2.36	12.57	8.60	20.97
24	PS 1583 x JS 335	49.50	56.40	56.40	5.22	7.73	13.28	3.44	56.66	1.99	14.45	10.07	25.66
25	PS 1583 x DS 12-5	47.50	42.30	57.83	4.81	10.16	12.50	3.30	51.84	2.02	12.61	9.14	29.90
26	PS 1583 x JS 20-29	50.00	57.30	49.55	4.60	8.48	12.72	3.38	68.12	2.12	16.87	11.76	31.74
27	PS 1583 x Bragg	52.00	71.40	50.44	4.42	6.76	13.02	4.16	69.77	2.36	18.31	11.74	25.82
28	PS 1584 x JS 20-69	47.50	41.20	51.43	4.23	7.38	12.56	3.28	58.12	2.17	19.37	12.01	47.11
29	PS 1584 x JS 20-41	49.50	65.80	52.76	4.27	7.50	9.94	4.18	57.98	2.20	12.02	10.92	18.20
30	PS 1042 x PS 1347	50.50	48.92	48.99	4.38	9.16	12.10	3.14	52.34	2.21	12.84	10.56	26.27
31	RVS 200-1 x PS 1092	49.00	46.20	39.64	4.74	7.51	9.20	3.43	44.82	2.25	8.77	9.36	18.98
32	JS 20-63 x JS 97-52	52.00	55.40	57.14	4.10	10.03	13.26	3.46	59.68	2.27	12.45	11.38	22.48
33	JS 20-69 x JS 20-59	50.50	64.50	50.97	4.56	8.67	14.04	4.04	54.52	2.34	15.37	12.16	23.97
34	JS 20-64 x JS 20-54	51.00	45.00	51.91	5.50	7.33	8.60	4.08	46.14	2.20	8.73	10.44	19.55
35	JS 20-29 x JS 20-55	48.50	54.90	47.31	5.37	8.33	11.41	3.10	61.60	2.28	11.59	10.01	21.11
36	PS 1225 x PS 1347	47.50	58.30	61.90	4.10	7.73	14.46	3.74	73.76	2.27	19.19	10.53	33.39
	GM	50.15	60.43	59.43	4.14	8.82	11.61	3.93	65.61	2.39	17.87	10.98	30.03
	S.Em.±	0.57	2.22	1.08	0.18	0.41	0.48	0.19	2.37	0.1	0.66	0.25	1.42
	S.E(d)	1.14	4.44	2.16	0.37	0.81	0.97	0.37	4.75	0.20	1.32	0.49	2.85
	C.D. 5%	2.32	9.04	4.39	0.75	1.66	1.98	0.76	9.67	0.40	2.69	1.01	5.80
	C.D. 1%	2.76	10.75	5.22	0.89	1.97	2.35	0.91	11.50	0.47	3.20	1.20	6.90
	C.V.(%)	2.27	7.34	3.63	8.93	9.22	8.36	9.52	7.23	8.21	7.38	4.50	9.48

GM= General mean, S.Em= Standard error mean, S.E(d) = Standard deviation C.D= Critical difference, C.V= Coefficient of variation

Table 4.1.2 Mean performance of yield and other characters in F₃ generation of soybean genotypes

Sn No.	Genotype	Days to 50% Flowering	Dry matter weight per plant (g)	Plant height (cm)	Basal node height (cm)	Basal pod height (cm)	Number of nodes per plant	Number of primary branches per plant	Number of pods per plant	Number of seeds per pod	Seed yield per plant (g)	100- seed weight (g)	Harvest index (%)
1	PS 1583 x Pb1	51.02	51.51	63.43	3.52	6.97	10.76	4.49	60.07	2.25	13.10	8.18	26.78
2	PS 1583 x JS 335	50.27	56.62	53.09	4.30	5.34	10.77	4.65	65.02	2.30	15.96	7.89	28.00
3	PS 1583 x DS 12-5	48.70	63.44	53.36	3.70	6.62	11.10	4.41	78.17	2.47	19.78	7.98	30.35
4	PS 1583 x JS 20-29	50.74	69.30	49.15	3.47	5.46	11.90	4.75	85.33	2.35	25.82	8.38	37.26
5	PS 1583 x Bragg	48.58	67.61	64.55	3.85	6.27	10.50	4.46	71.26	2.44	21.74	8.16	31.94
6	PS 1584 x JS 20-69	46.46	88.26	57.55	3.72	5.80	10.90	5.36	100.05	2.64	31.64	8.49	34.61
7	PS 1584 x JS 20-41	48.53	74.02	60.39	4.39	6.11	13.48	4.69	103.51	2.44	29.66	9.47	31.01
8	PS 1042 x PS 1347	46.22	52.09	45.19	3.22	5.27	12.92	3.39	54.57	2.35	15.22	8.49	29.30
9	RVS 200-1 x PS 1092	45.62	36.85	35.01	3.19	4.50	14.26	3.45	40.13	2.22	8.60	8.33	23.18
10	JS 20-63 x JS 97-52	42.17	59.42	60.07	3.36	6.63	12.02	3.73	61.88	2.36	18.80	7.98	31.14
11	JS 20-69 x JS 20-59	41.10	72.86	55.04	3.81	7.61	14.96	5.04	74.44	2.49	21.77	8.05	28.88
12	JS 20-64 x JS 20-54	45.17	65.29	50.93	3.36	5.09	12.01	3.84	83.28	2.34	20.90	9.10	32.04
13	JS 20-29 x JS 20-55	50.93	73.28	53.00	4.24	5.55	11.69	4.14	80.79	2.37	20.18	9.78	25.83
14	PS 1225 x PS 1347	52.75	69.11	54.27	4.30	5.83	14.14	4.46	67.65	2.36	19.72	7.81	28.16
	GM	47.73	64.26	53.93	3.74	5.93	12.24	4.34	73.29	2.38	20.20	8.43	29.89
	S.Em.±	0.29	0.83	2.15	0.25	0.31	0.21	0.30	2.69	0.03	0.27	0.35	0.38
	S.E(d)	0.40	1.18	3.04	0.35	0.44	0.30	0.42	3.81	0.05	0.39	0.49	0.54
	C.D. 5%	0.88	2.57	6.64	0.77	0.95	0.65	0.91	8.31	0.10	0.85	1.07	1.18
	C.D. 1 %	0.98	2.85	7.37	0.85	1.05	0.73	1.01	9.22	0.11	0.94	1.18	1.31
	C.V. (%)	0.85	1.83	5.64	9.39	7.33	2.44	9.64	5.19	1.88	1.91	5.79	1.80

GM= General mean, S.Em= Standard error mean, S.E(d) = Standard deviation C.D= Critical difference, C.V= Coefficient of variation

Table 4.1.3: Analysis of variance for yield and other characters in F₂ generation of soybean

Mean Sum of square													
Source of variation	df	Days to 50% Flowering	Dry matter weight per plant (g)	Plant height (cm)	Basal node height (cm)	Basal pod height (cm)	Number of nodes per plant	Number of primary branches per plant	Number of pods per plant	Number of seeds per pod	Seed yield per plant (g)	100- seed weight (g)	Harvest index (%)
Replication	1	0.125	2.24	0.862	0.008	0.771	0.155	0.106	39.216	0.028	0.891	0.008	7.498
Treatments	35	8.738**	399.879**	229.425**	2.417**	11.522**	7.662**	0.926**	542.979**	0.094**	81.82**	2.365**	189.933**
Error	35	1.296	19.679	4.646	0.136	0.661	0.94	0.14	22.513	0.038	1.741	0.244	8.105

**Significant at 1% level of probability

*Significant at 5% level of probability

Table 4.1.4: Analysis of variance for yield and other characters in F₃ generation of soybean

Source of Variation	Mean Squares	Replication	Family	Error (a)	Progeny	Error (b)
df		1	13	13	280	280
Days to 50% flowering		.138	23.652**	0.163	3.378**	2.600
Dry matter weight per plant (g)		188.835	312.638**	1.388	1300.597**	29.328
Plant height (cm)		368.909	117.684**	9.261	101.244**	20.613
Basal node height (cm)		23.683	0.353**	0.123	1.124**	0.620
Basal pod height (cm)		2.134	1.375**	0.189	4.704**	2.114
Number of nodes per plant		0.386	4.317**	0.09	4.005**	1.425
Number of primary branches per plant		5.266	0.665**	0.175	1.336**	0.798
Number of pods per plant		190.867	586.907**	14.487	1888.6**	46.511
Number of seeds per pod		0.172	0.023**	0.002	0.065**	0.022
Seed yield per plant (g)		13.242	74.985**	0.15	199.768**	3.303
100 seed weight(g)		3.119	0.729**	0.239	1.823**	0.526
Harvest index (%)		14.420	25.26**	0.292	112.212**	6.407

**Significant at 1% level of probability * Significant at 5% level of probability

4.2. Effectiveness of early generation selection on the basis of various genetic parameters

Seed yield is one of the quantitative characters for which improvement is most desirable in any plant breeding programme but due to its complex nature and due to influence of various environmental factors, the selection of the character is not much effective in comparison to the other characters. Therefore, breeders practice selection on the different component characters which directly or indirectly affects the seed yield per plant for making selection effective for the prime character. In order to practice selection on the component characters, first objective would be to identify those characters and for this purpose a statistical tool is being applied *i.e.* correlation. Correlation coefficient gives a linear relationship between the two variables and henceforth could be used as an important genetic parameter to estimate the relationship not only between two characters but also between two variables. Likewise, regression can be used to estimate the degree of direction predicted by the correlation. Both correlation and regression are reliable parameters as these are not much affected by the environmental factors and hence could be used as important parameters to check the efficiency of selection of characters in early generation. To estimate the gain achieved through selection for high and low yield and yield components, response to selection and realized heritability can also be estimated to identify those crosses which performed well in the early generation as to select the superior ones and reject the inferior ones. In self-pollinated crops, identification of high yielding genotypes is a major issue for the plant breeders mainly in the segregating generation. As a large number of recombinants available for a single cross, there is greater risk of losing the superior gene combinations when selection is practiced in the later generations, therefore, early generation selection could be a greater advantageous practice to identify superior gene combinations and preventing these combinations from getting rejected or lost in later generations. Thus, the effectivity of early generation selection is decided by various genetic parameters, which are being described below:

4.2.1. On the basis of variability parameters observed in both F_2 and F_3 generation

4.2.2 On the basis of inter-generation correlation

4.2.3. On the basis of regression of F_2 vs. F_3

4.2.4 On the basis of difference in mean performance of selected lines in F_2 and F_3

4.2.5. On the basis of realized heritability

4.2.6 On the basis of mean performance of crosses for seed yield in F_2 and F_3

Seed yield is one of the most complex quantitative traits governed by large number of genes. The expression of this trait largely depends upon the action and interaction of its number of components. Being the direct selection ineffective for seed yield, the indirect selection for yield components had been advised to form an effective selection strategy aimed at its improvement.

4.2.1 Genetic variability parameters

Coefficient of variation, heritability and genetic advance

Effective selection depends on the existence of the genetic variability. The heritability refers to as an index of transmissibility, to measure the genetic relationship between the parents and their offsprings. Heritability infers as to how much emphasis should be placed for selection in case of a particular trait.

Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for the various traits were also observed. These results indicated that variability was primarily due to genotypic differences. Therefore, selection based on these characters is expected to be effective

The estimates of phenotypic (PCV), genotypic (GCV) and environmental (ECV) coefficients of variation along with heritability, genetic advance and genetic advance as per cent mean (GAM) as obtained for all the quantitative characters in F₂ and F₃ are summarized in **Table 4.2.1a and 4.2.1b**, respectively. In general, the results obtained showed that the magnitudes of PCV were higher than that of both GCV and ECV for all the characters under study in both the generation. The PCV and GCV values were classified into 3 categories given below as indicated by **Sivasubramanian and Menon (1973)**.

Low (0-10%) Moderate (10-20%) High (20% and above)

4.2.1.1a Phenotypic coefficient of variation (PCV)

The estimates of phenotypic coefficient of variance (PCV) revealed moderate to high values for majority of the characters included. The highest value of PCV was recorded for seed yield per plant (36.03%) followed by harvest index (33.14%), basal

node height (27.33%), basal pod height (26.34%), number of pods per plant (25.63%) and dry matter weight per plant (23.97%). Number of primary branches per plant (18.59%), plant height (18.21%) and number of nodes per plant (17.87) showed the moderate value of PCV (%), whereas the lowest estimate of PCV (%) was recorded for days to 50% flowering (4.47%) as presented in **Table 4.2.1a**. However in F₃ generation, the highest value of phenotypic coefficient of variance PCV (%) showed by only two characters *i.e.*, seed yield per plant (30.34%) and number of pods per plant (23.66%). Moderate value of PCV (%) was recorded for seven characters like dry matter weight per plant (19.5%), number of primary branches per plant (15.39%), basal pod height (14.92%), plant height (14.78%), basal node height (13.04%), number of nodes per plant (12.15%) and harvest index (12.07%). 100-seed weight (8.25%), days to 50% flowering (7.23%) and number of seeds per pod (4.67%) showed the lowest estimate of PCV (%), as given in **Table 4.2.1b**.

4.2.1.1b Genotypic coefficient of variation (GCV)

The estimates of genotypic coefficient of variance (GCV) exhibited a similar trend of distribution like phenotypic coefficients of variation (PCV) in F₂ with majority of characters being included under moderate to high categories. Highest value of GCV was observed for seed yield per plant (35.26%) followed by harvest index (31.75%), basal node height (25.82%), basal pod height (24.70%), number of pods per plant (24.59%) and dry matter weight per plant (22.82%). Moderate values of GCV (%) was observed for plant height (17.84%), number of primary branches per plant (15.96%) and number of nodes per plant (15.80%) meanwhile, days to 50% flowering (3.85%) exhibited the lowest values for GCV (%) as presented in **Table 4.2.1a**. The estimates of genotypic coefficients of variance (GCV) in F₃ generation revealed that highest value of GCV (%) had showed by seed yield per plant (30.28%) and number of pods per plant (23.08%), whereas characters like dry matter weight per plant (19.41%), plant height (13.66%), basal pod height (12.99%), harvest index (11.93%), number of nodes per plant (11.79%) and number of primary branches per plant (11.39%) exhibited moderate values of GCV (%). Lowest value of GCV (%) showed by basal node height (9.05%), days to 50% flowering (7.18%), 100-seed weight (5.87) and number of seeds per pod (4.27%), as given in **Table 4.2.1b**.

Table 4.2.1a: General Mean (GM), Range, Standard Error of Mean (SEm) and Variability parameters in F₂ generation of soybean

Character	GM	Range	SEm±	PCV(%)	GCV(%)	ECV(%)	h ²	GA	GA value % mean
Days to 50% Flowering	50.15	44.50-56.00	0.81	4.47	3.85	2.31	0.74	3.42	6.82
Dry matter weight per plant (g)	60.43	39.17-97.50	3.14	23.97	22.82	6.87	0.91	27.04	44.75
Plant height (cm)	59.43	39.64-81.50	1.52	18.21	17.84	3.56	0.96	21.40	36.01
Basal node height (cm)	4.14	2.15-6.36	0.26	27.33	25.82	9.18	0.89	2.08	50.27
Basal pod height (cm)	8.90	3.88-13.79	0.58	26.34	24.70	10.64	0.88	4.25	47.73
Number of nodes per plant	11.61	7.84-15.22	0.69	17.87	15.80	7.84	0.78	3.34	28.76
Number of primary branches per plant	3.93	2.50-5.92	0.26	18.59	15.96	9.11	0.74	1.11	28.23
Number of pods per plant	65.61	44.82-110.83	3.36	25.63	24.59	6.46	0.92	31.88	48.60
Number of seeds per pod	2.39	1.99-2.83	0.14	10.78	6.99	8.09	0.42	0.22	9.35
Seed yield per plant (g)	17.87	7.79-29.76	0.93	36.03	35.26	5.91	0.96	12.71	71.10
100-seed weight (g)	10.98	8.60-13.00	0.35	10.40	9.38	4.50	0.81	1.91	17.41
Harvest index (%)	30.03	14.86-57.00	2.01	33.14	31.75	9.19	0.92	18.82	62.68

GM= General mean, S.Em= Standard error mean, , P.C.V= Phenotypic coefficient of variation, G.C.V = Genotypic coefficient of variation, E.C.V= Environmental coefficient of variation, h²= Heritability, G.A.= Genetic advance, G.A.(%)= Genetic advance expressed as percent of mean

Table 4.2.1b: General Mean (GM), Range, Standard Error of Mean (SEm) and Variability parameters in F₃ generation of soybean

Character	GM	Range	SEm±	PCV (%)	GCV (%)	ECV (%)	h ²	GA	GA value % mean
Days to 50% Flowering	47.73	41.10-52.75	0.29	7.23	7.18	0.84	0.98	7.01	14.69
Dry matter weight per plant (g)	64.26	36.85-88.26	0.83	19.50	19.41	1.83	0.99	25.59	39.82
Plant height (cm)	53.93	35.01-64.55	2.15	14.78	13.66	5.64	0.85	14.02	26.00
Basal node height (cm)	3.74	3.19-4.39	0.25	13.04	9.05	9.39	0.48	0.48	12.94
Basal pod height (cm)	5.93	4.50-7.61	0.31	14.92	12.99	7.33	0.75	1.38	23.29
Number of nodes per plant	12.24	10.50-14.96	0.21	12.15	11.79	2.44	0.90	2.81	22.82
Number of primary branches per plant	4.34	3.39-5.36	0.30	15.39	11.39	9.64	0.58	0.78	17.93
Number of pods per plant	73.29	40.13-103.51	2.69	23.66	23.08	5.19	0.95	34.00	46.39
Number of seeds per pod	2.38	2.22-2.64	0.03	4.67	4.28	1.88	0.83	0.19	8.06
Seed yield per plant (g)	20.20	8.60-31.36	0.27	30.34	30.28	1.91	0.99	12.58	62.25
100-seed weight (g)	8.43	7.81-9.78	0.35	8.25	5.87	5.79	0.19	0.51	5.86
Harvest index (%)	29.89	23.18-37.26	0.38	12.07	11.93	1.80	0.97	7.27	24.32

GM= General mean, S.Em= Standard error mean, , P.C.V= Phenotypic coefficient of variation, G.C.V = Genotypic coefficient of variation, E.C.V= Environmental coefficient of variation, h²= Heritability, G.A.= Genetic advance, G.A.(%)= Genetic advance expressed as percent of mean

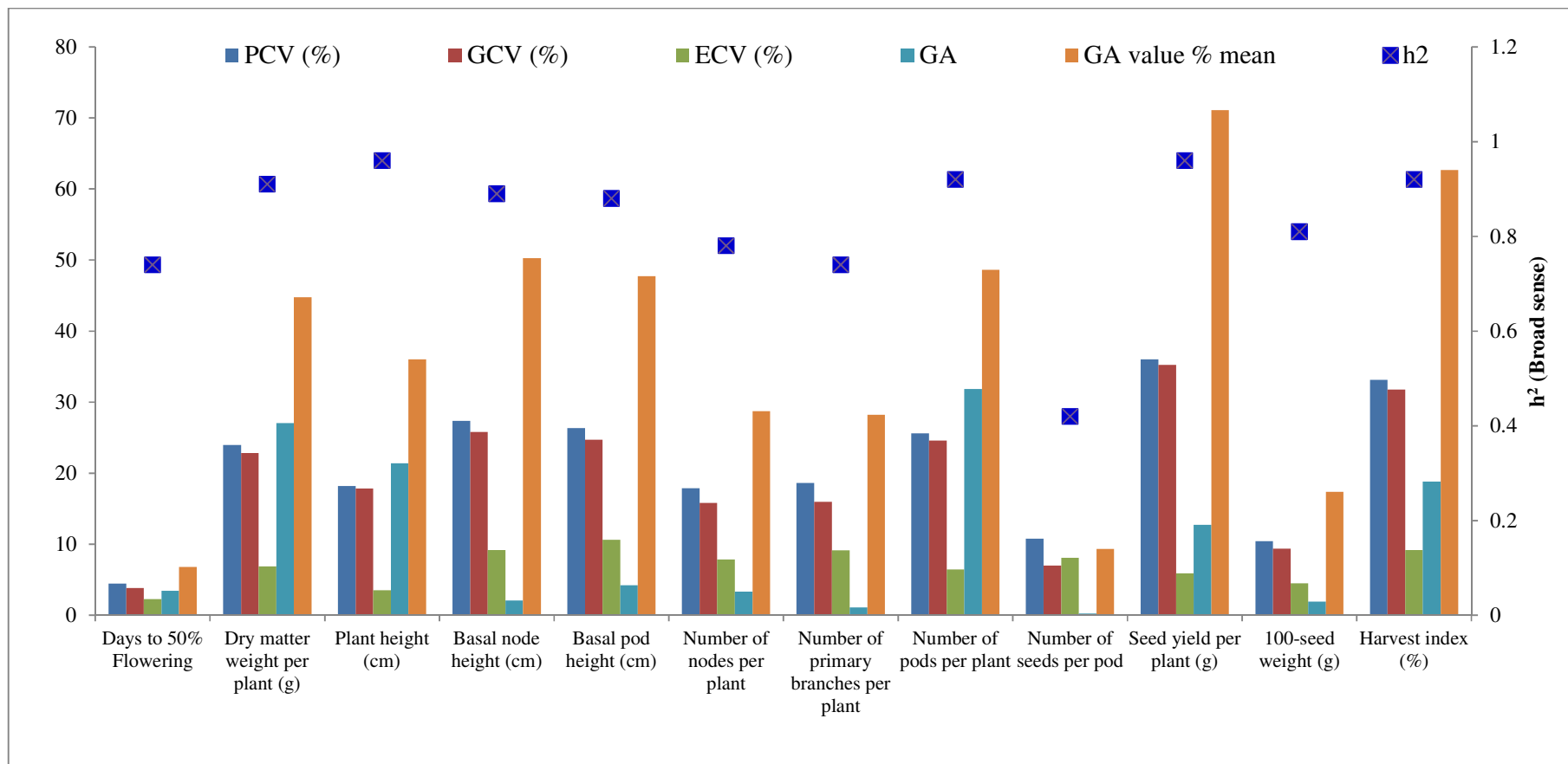


Fig. 4.2.1a: Diagrammatic representation of genetic variability in F₂

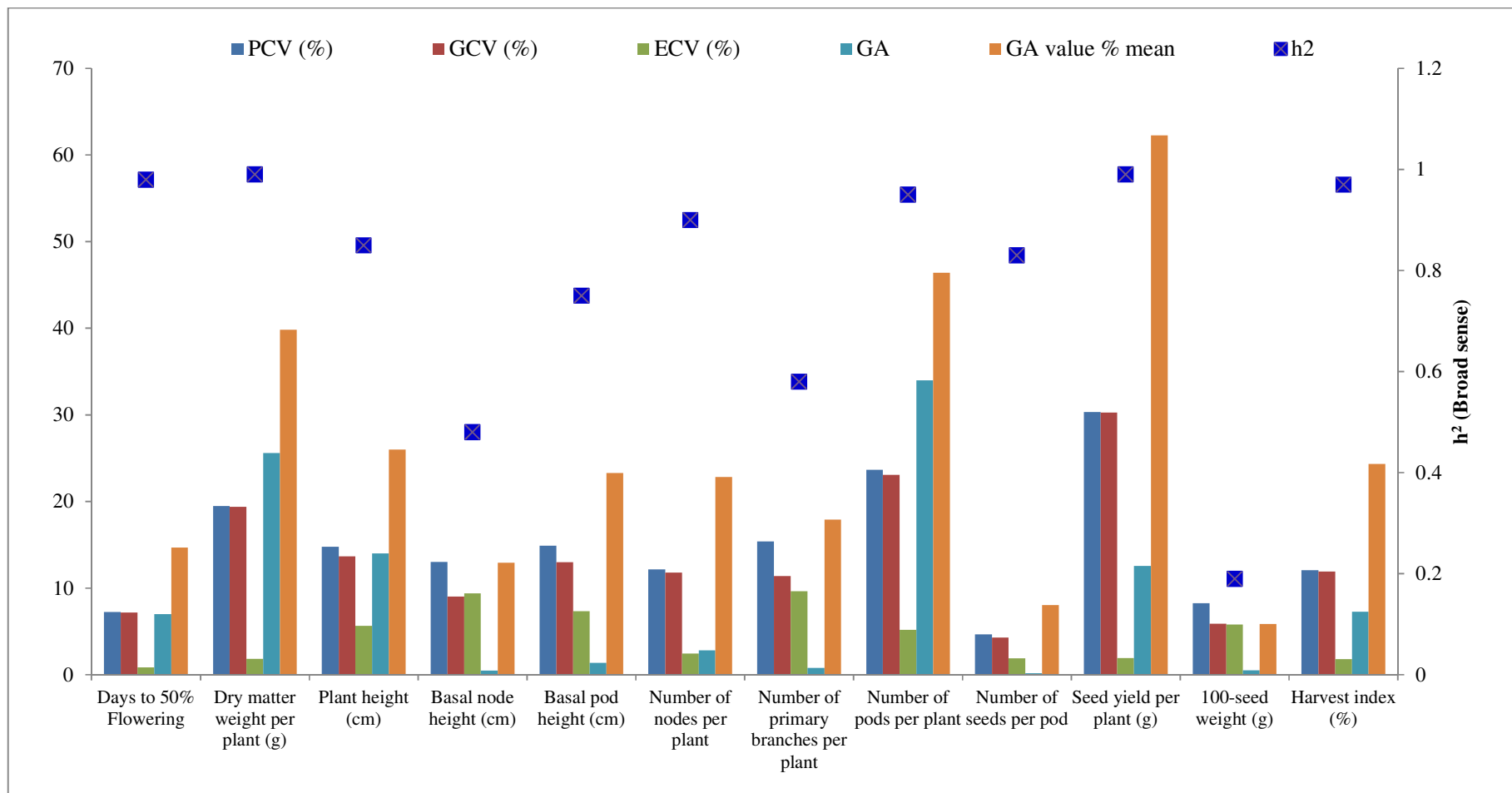


Fig. 4.2.1b: Diagrammatic representation of genetic variability in F₃

4.2.1.1c Environmental coefficient of variation (ECV)

It could be observed from the results obtained in F_3 that the values of ECV (%) were comparatively low as compared to those of PCV (%) and GCV (%) for majority of characters under study. The highest values of ECV were observed for basal pod height (10.64) followed by harvest index (9.19%), basal node height (9.18), number of primary branches per plant (9.11%), number of seeds per pod (8.09%), number of nodes per plant (7.84), dry matter weight (6.87%), number of pods per plant (6.46%) and seed yield per plant (5.91%), whereas, the lowest values of ECV were recorded for days to 50% flowering (2.31%) and plant height (3.56%) as presented in **Table 4.2.1a**. The lowest values of ECV in the expression of a particular character indicate that it is least influenced by environment and hence, improvement of all such characters is easy as they show a stable response to selection based on phenotype. The study of ECV in F_3 generation revealed that all the characters exhibited low values of ECV which indicates that all the characters are least influenced by the environment. The values of ECV of all the characters are observed as number of primary branches (9.64%), basal node height (9.39%), basal pod height (7.33%), 100-seed weight (5.79%), plant height (5.64%), number of pods per plant (5.19%), number of nodes per plant (2.44%), seed yield per plant (1.91%), number of seeds per pod (1.88%), dry matter weight per plant (1.83%), harvest index (1.80%) and days to 50% flowering (0.84%) as given in **Table 4.2.1b**.

A general comparison of estimates revealed higher values of PCV over GCV and ECV, with the values of GCV deviating only slightly from those of PCV. All the characters except days to 50% flowering showed a greater contribution of GCV values towards PCV values with a negligible impact of ECV in both the generations. This indicated a minimal influence of environment and hence, a maximum role of genetic factors in the expression of such characters, which could be highly rewarding during selection (**Datt Shiv et al. 2011 and Dubey et al. 2015**). **Jain et al. (2015)** and **Joshi (2015)** also reported high estimates of PCV and GCV in comparison to ECV. They reported near equal and high estimates of PCV and GCV for pods per plant, 100-seed weight, biological yield and seed yield per plant and reported moderate estimates of PCV and GCV for number of seeds per pod. **Manav and Arora (2017)** also reported high value of GCV and PCV for number of pods per plant whereas moderate values of GCV and PCV for plant height, number of primary branches per plant, 100-seed weight

and number of seeds per pod. Similar results of low GCV and PCV for days to 50% flowering and moderate value of 100-seed weight were reported by **Baraskar *et al.* (2014)** and **Singh *et al.* (2017)**. This suggests that selection on the basis of phenotypic performance should be effective enough to bring about considerable improvement of these characters (**Aditya *et al.*, 2011**).

4.2.1.2. Heritability and genetic advance

Heritability is the degree of transmissibility of characters from one generation to the other. The concept of heritability plays a key role in determining whether the phenotypic differences observed among individuals are due to differences in their genetic constitution or simply a result of environmental factors (**Comstock and Robinson, 1948**). **Johnson *et al.* (1955)** suggested that heritability values coupled with the estimates of genetic advance would be more useful during the selection programmes than heritability considered alone.

The estimates of heritability were also classified into 3 categories given below as suggested by **Robinson *et al.* (1949)**.

Low (0-30%) Moderate (30-60%) High (60% and above)

Genetic advance as per cent mean was also classified into 3 categories shown below as suggested by **Johnson *et al.* (1955)**.

Low (0-10%) Moderate (10-20%) High (20% and above)

A critical perusal of heritability estimates given in the **Table 4.2.1a** revealed that in F₂ generation seed yield and plant height exhibited highest heritability value (96%) followed by number of pods per plant and harvest index (92%). High heritability values were also observed for dry matter weight (91%), basal node height (89.50%), basal pod height (88%), 100-seed weight (81%), number of nodes per plant (78%), number of primary branches per plant (74%) and days to 50% flowering (74%). However, moderate heritability was observed for number of seeds per pod (42%). The estimates of genetic advance (%) were found to be highest and lowest for number of pods per plant (31.88%) and number of seeds per pod (0.22%), respectively. The values of genetic advance for the remaining characters were recorded for dry matter weight per plant (27.04%), plant height (21.40%), harvest index (18.82%), seed yield per plant

(12.71%), basal pod height (4.25%), days to 50% flowering (3.42%), number of nodes per plant (3.34%), basal node height (2.08%), 100-seed weight (1.91%) and number of primary branches per plant (1.11%).

The estimates of genetic advance expressed as per cent of mean were observed to be highest for seed yield per plant (71.10%) followed by harvest index (62.68%), basal node height (50.27%), number of pods per plant (48.60%), basal pod height (47.73%), dry matter weight (44.75%), plant height (36.01%), number of nodes per plant (28.76%) and number of primary branches per plant (28.23%). High estimates of genetic advance as per cent mean indicated the preponderance of additive genetic effects in expression of these characters. Therefore, selection for these characters in segregating generations based on phenotypic performance would be likely more effective. However, moderate levels of genetic advance as percent of mean were observed for 100-seed weight (17.41%), whereas number of seeds per pod (9.35%) and days to 50% flowering (6.82%) showed low estimates of genetic advance as per cent mean. However in F_3 generation, the highest value of heritability was shown by seed yield per plant (99%) dry matter weight (99%) followed by days to 50% flowering (98%), harvest index (97%), number of nodes per plant (94%), plant height (85%), number of seeds per pod (83%) and basal pod height (75%). Moderate value of heritability was shown by number of primary branches per plant (58%), 100-seed weight (50%) and basal node height (48%).

The estimates of genetic advance (%) in F_3 generation were found highest and lowest for number of pods per plant (34%) and number of seeds per pod (0.19%), respectively. The values of genetic advance for the remaining characters were recorded for dry matter weight per plant (25.59%), plant height (14.02%), seed yield per plant (12.58%), harvest index (7.27%), days to 50% flowering (7.01%), number of nodes per plant (2.81%), basal pod height (1.38%), number of primary branches per plant (0.78%), 100-seed weight (0.51%) and basal node height (0.48%). The estimates of genetic advance expressed as per cent of mean in F_3 were observed to be highest for seed yield per plant (62.25%) followed by number of pods per plant (46.39%), dry matter weight per plant (39.82%), plant height (26%), harvest index (24.32%), basal pod height (23.29%) and basal node height (12.94%). However, characters like number of primary branches per plant (17.93%) and days to 50% flowering (14.69%) exhibited

moderate values of genetic advance as per cent of mean. Low values of GA expressed as per cent of mean was shown by 100-seed weight (5.86%) and number of seeds per pod (8.06%) as shown in **Table 4.2.1b**. High estimates of genetic advance as per cent mean indicated the preponderance of additive genetic effects in expression of these characters. Therefore, selection for these characters in segregating generations based on phenotypic performance would be likely more effective.

Majority of the characters under study including plant height (cm), number of nodes per plant, number of pods per plant, dry matter weight per plant (g), harvest index (%), basal pod height (cm) and seed yield per plant (g) exhibited high values of heritability along with high estimates of genetic advance as per cent mean in both the generations. This strongly indicated the preponderance of additive gene action involved in the expression of these characters and hence, there exists an ample scope for the improvement of concerned traits through selection. These results were in accordance with **Agarwal *et al.* (2001)** who reported high GCV for plant height and number of branches per plant and also observed high heritability (broad sense) and genetic advance as per cent of mean (GAM) for all characters under study except days to maturity. **Sureshrao *et al.* (2014)** also reported high estimates of heritability and genetic advance as per cent mean for plant height, pods per plant, biological yield, harvest index, seed yield per plant and seed yield per hectare. **Mahbub *et al.* (2015)** reported high heritability and high genetic advance as per cent mean for plant height, number of pods per plant and seed yield per plant. Similar results were reported by **Rajarithinam *et al.* (1996)**; **Malik *et al.* (2006)**; **Karnwal and Singh (2009)**; **Patil *et al.* (2011)**, **Amrita *et al.* (2014)** and **Singh *et al.* (2017)**.

High heritability coupled with moderate genetic advance as per cent mean was recorded for 100-seed weight in F₂ generation and days to 50% flowering in F₃ generation. **Datt Shiv *et al.* (2011)** and **Singh *et al.* (2017)** also reported high heritability and moderate genetic advance for days to 50% per cent flowering.

High heritability coupled with low genetic advance as per cent mean was observed for days to 50% flowering in F₂ generation and for number of seeds per pod, 100-seed weight in F₃ generation indicating the influence of dominant effects on the expression of such characters. Hence, progeny testing or heterosis breeding could be employed for the improvement of these characters in soybean. **Desissa (2017)** also

reported high heritability and low genetic advance for days to 50% flowering and 100-seed weight in soybean.

The results obtained in the present study were comparable with the earlier findings of **Zhu (1992); Rasaily *et al.* (1986); Ghatge and Kadu (1993); Jagtap and Mehetre (1994); Rao *et al.* (1998), Jain and Ramgiry (2000) and Manav and Arora (2017).**

Relationship between the Heritability of F₂ and F₃ generation

Heritability is the parameter which determines the degree of transmission from parent to their progeny from one generation to the another generation. The heritability estimates of the twelve characters taken for the study had shown a range from high to low in both the generation. The characters having high heritability had higher chances of transmissibility from one generation to other as these characters are mainly being governed by the additive genes. As discussed earlier, heritability along with genetic advance gives a reliable and true estimate for the genetic nature of the character. Hence, heritability and genetic advance had been taken as parameters to decide on the affectivity of the early generation selection.

Out of the twelve characters undertaken, seven characters had showed the high value of heritability along with high estimate of genetic advance as per cent mean. The characters which exhibited the high estimate of heritability and genetic advance in both the F₂ and F₃ generation were dry matter weight per plant, plant height, basal pod height, number of nodes per plant, number of pods per plant, seed yield per plant and harvest index. Hence, it indicates that these characters are governed by the additive genes and thus direct selection for these characters in the early segregating generation can bring the desired improvement.

4.2.2a Inter-generation correlation

The simple inter-generation correlations in fourteen crosses of soybean for all the quantitative characters were computed on the basis of information in **Table 4.2.2a**. The result on parent offspring correlation reveals that most of the characters had showed non-significant correlation in both the directions.

Table 4.2.2a: Intergeneration correlation coefficient between different crosses for twelve characters

Sn No	Character	PS 1583 x Pb1	PS 1583 x JS 335	PS 1583 x DS 12-5	PS 1583 x JS 20-29	PS 1583 x Bragg	PS 1584 x JS 20-69	PS 1584 x JS 20-41
1	Days to 50% flowering	0.709**	0.725**	0.871**	-0.148	0.703**	0.834**	0.829**
2	Dry matter weight per plant (g)	-0.341	0.063	0.227	-0.093	-0.071	0.509*	0.251
3	Plant height (cm)	0.748**	0.459*	0.497*	0.728**	0.670**	0.612**	0.557**
4	Basal node height (cm)	0.181	-0.179	0.159	-0.219	0.385	-0.311	0.167
5	Basal pod height (cm)	0.230	0.148	0.290	-0.132	0.413	-0.154	-0.103
6	Number of nodes per plant	0.069	-0.404	0.247	-0.049	0.156	-0.122	0.196
7	Number of primary branches per plant	-0.355	-0.071	-0.081	-0.342	0.214	-0.092	-0.143
8	Number of pods per plant	0.516*	0.611**	0.613**	0.602**	0.498*	0.483*	0.448*
9	Number of seeds per pod	-0.276	-0.176	0.313	-0.419	-0.272	-0.165	-0.392
10	Seed yield per plant (g)	0.702**	0.458*	0.648**	0.693**	0.576**	0.840**	0.700**
11	100- seed weight (g)	-0.283	-0.302	-0.430	-0.667**	-0.385	-0.522*	-0.266
12	Harvest index (%)	0.412	0.430	0.390	0.404	0.229	0.483*	0.144

Sn No	Character	PS 1042x PS 1347	RVS 200-1 x PS 1092	JS 20-63 x JS 97-52	JS 20-69 x JS 20-59	JS 20-64 x JS 20-54	JS 20-29 x JS 20-55	PS 1225 x PS 1347
1	Days to 50% flowering	0.681**	0.154	0.735**	0.282	0.936**	0.761**	0.618**
2	Dry matter weight per plant (g)	0.373	-0.004	-0.165	-0.199	-0.123	0.395	0.049
3	Plant height (cm)	0.668**	0.568**	0.622**	0.799**	0.764**	0.531*	0.535*
4	Basal node height (cm)	0.043	0.116	-0.094	0.226	0.329	-0.292	0.018
5	Basal pod height (cm)	0.301	0.007	-0.340	0.281	0.668**	-0.092	-0.220
6	Number of nodes per plant	0.192	-0.499*	-0.121	-0.433	0.105	0.168	-0.027
7	Number of primary branches per plant	0.284	-0.161	0.111	0.097	-0.012	-0.092	0.184
8	Number of pods per plant	0.573**	0.471*	0.519*	0.407	0.461*	0.589**	0.719**
9	Number of seeds per pod	-0.125	0.138	-0.333	-0.238	-0.249	0.110	-0.323
10	Seed yield per plant (g)	0.353	0.319	0.585**	0.718**	0.622**	0.759**	0.646**
11	100- seed weight (g)	-0.517*	0.395	0.245	-0.359	-0.083	-0.020	-0.354
12	Harvest index (%)	-0.016	0.311	0.623**	0.717**	0.453*	0.627**	0.657**

**Significant at 1% level of probability

*Significant at 5% level of probability

(1) Days to 50% flowering

Mostly all the crosses had showed positive significant parent off spring correlation for days to 50% flowering. The highest value of positive significant correlation had been showed by cross JS 20-64 X JS 20-54 (0.936) and the lowest significant value by cross PS 1225 X PS 1347 (0.618), whereas two crosses, RVS 200-1 X PS 1092(0.154) and JS 20-69 X JS 20-59 (0.282) showed positive non-significant correlation between F_2 and F_3 for days to 50% flowering, while cross PS 1583 X JS 20-29 (-0.148) showed non-significant negative correlation between F_2 and F_3 generations.

(2) Dry matter weight per plant

The inter-generation correlation value for dry matter weight per plant was observed non-significant in almost all the crosses. Out of 14 crosses, seven crosses had exhibited positive correlation whereas only one cross PS 1584 X JS 20-69 (0.509) showed significant positive correlation between the two generations indicating that selection for this character in early generation is not effective.

(3) Plant height

All the 14 crosses had revealed significant positive inter-generation correlation estimate between F_2 and F_3 generation for plant height. The range of correlation value varied from 0.799 (JS 20-69 X JS 20-59) to 0.459 (PS 1583 X JS 335). The maximum number of crosses showed positive significant inter-generation correlation value for this character indicating that selection in early generation for plant height is highly effective.

(4) Basal node height

The parent-off spring correlation range for basal node height was from -0.311(PS 1584 X JS 20-69) to 0.329 (JS 20-64 X JS 20-54) and nine crosses showed positive correlation value but were non-significant. Similarly, five crosses showed negative correlation but not one of the cross showed significant inter-generation correlation value for basal node height, imposing that this character is not at all suitable for early generation selection.

(5) Basal pod height

For basal pod height, the range of inter-generation correlation value was from -0.340 (JS 20-63 X JS 97-52) to 0.668 (JS 20-64 X JS 20-54). Eight crosses had

showed positive correlation between F_2 and F_3 but only one cross out of eight crosses displayed significant inter-generation correlation, whereas seven crosses exhibited non-significant negative inter-generation correlation value. This indicates that basal pod height is also not much effective for the selection in early segregating generation.

(6) Number of nodes per plant

The parent offspring correlation range for this character was observed from -0.499 (RVS 200-1 X PS 1092) to 0.247 (PS 1583 X DS 12-5). Out of fourteen, five crosses exhibited positive but non significant inter-generation correlation, whereas nine crosses displayed negative inter-generation correlation and among these only one cross RVS 200-1 X PS 1092 showed significant negative correlation between F_2 and F_3 generation. Thus, early generation selection in number of nodes per plant is not effective.

(7) Number of primary branches per plant

The range of inter-generation correlation for this character was observed from -0.355 (PS 1583 X Pb1) to 0.214 (PS 1583 X Bragg). Five crosses exhibited positive value of inter-generation correlation but all were non-significant. Similarly, nine crosses displayed non-significant negative inter-generation correlation indicating the unsuitability of the character for early generation selection for improvement to be accomplished.

(8) Number of pods per plant

Out of fourteen crosses, thirteen crosses had showed positive significant inter-generation correlation for number of pods per plant. Highest correlation value was shown by cross, PS 1225 X PS 1347 (0.719) and the lowest inter-generation correlation by cross, PS 1584 X JS 20-41 (0.448). The range of inter-generation correlation for the character as varied from 0.407 (JS 20-69 X JS 20-59) to 0.719 (PS 1225 X PS 1347), indicates that this character can be improved by practicing selection in early segregating generation.

(9) Number of seeds per pod

Out of the 14 crosses, only three crosses exhibited positive inter-generation correlation while eleven crosses displayed negative value of inter-generation correlation. However, results obtained presented that none of the cross had significant value of parent offspring correlation, making early generation selection ineffective for

this character. The range of inter-generation correlation was -0.419(PS 1583 X JS 20-29) to 0.313 (PS 1583 X DS 12-5) for number of seeds per pod.

(10) 100-seed weight

The range of inter-generation correlation for the character was -0.667 to 0.395 and only three crosses showed the significant value but in negative direction. Thus, the selection of the character 100-seed weight is not effective for early generation.

(11) Harvest index

Out of fourteen crosses, six crosses displayed positive significant inter-generation correlation between F_2 and F_3 for harvest index. The highest value of correlation was revealed by cross JS 20-69 X JS 20-59 (0.717) followed by PS 1225 X PS 1347 (0.657), JS 20-29 X JS 20-55 (0.627), JS 20-63 X JS 97-52 (0.623), PS 1584 X JS 20-69 (0.483) and JS 20-64 X JS 20-54 (0.453). Although six crosses exhibited significant positive inter-generation correlation value for the character still it indicates that the character is not much suitable for early generation selection.

(12) Seed yield per plant

For seed yield per plant, twelve crosses had showed positive significant inter-generation correlation value and the range of inter-generation correlation value varied from 0.319(RVS 200-1 X PS 1092) to 0.840 (PS 1584 X JS 20-69). The highest value of significant correlation was showed by cross, PS 1584 X JS 20-69 (0.840) and the lowest value being showed by cross PS 1583 X JS 335 (0.458), while two crosses, PS 1583 X Pb1(0.353) and RVS 200-1 X PS 1092 (0.319) showed non-significant parent offspring correlation value.

4.2.2b Correlation between the selected lines of F_2 and F_3 generations

The study of simple inter-generation correlation between the lines selected for high values and between the lines selected for low values had been analyzed on seed yield per plant as selection of F_2 plants for high value and low values had been performed on the basis of *per se* performance of plants for this character only, while three other characters, dry matter weight per plant, number of pods per plant and harvest index had been taken into account on the basis of correlation studies and path coefficient analysis performed separately in F_2 and F_3 . These three characters had exhibited positive correlation with seed yield per plant in both the generations and also

had high value of direct effect on seed yield per plant. The inter-generation correlation was calculated separately for the lines selected for high and low value of yield and yield attributing characters and is summarized in **Table 4.2.2b**.

The results obtained from the simple correlation analysis are being described below for the four characters taken for this study:

For dry matter weight per plant, six crosses had showed positive correlation between the lines selected for high value of F_2 and F_3 generations, maximum in PS 1042 X PS 1347 (0.296), while only three crosses had exhibited positive correlation between the lines selected for low value of F_2 and F_3 generation, of which maximum value was found in RVS 200-1 X PS 1092 (0.169).

For number of pods per plant, six crosses had showed positive correlation between the lines selected for high values of F_2 and F_3 generations. The crosses are PS 1583 X JS 335 ($r=0.345$), PS 1583 X JS 20-29 ($r=0.272$), JS 20-69 X JS 20-59 ($r=0.127$), JS 20-64 X JS 20-54 ($r=0.037$), JS 20-29 X JS 20-55 ($r=0.118$) and PS 1225 X PS 1347 ($r=0.337$), while nine crosses exhibited positive correlation between the lines selected for low value of F_2 and F_3 generations, maximum in PS 1042 X PS 1347 ($r=0.566$) followed by cross, JS 20-63 X JS97-52 ($r=0.558$), PS 1583 x Bragg ($r=0.475$), PS 1583 X Pb1 ($r=0.416$), PS 1583 X DS 12-5 ($r=0.386$), PS 1225 X PS 1347 ($r=0.382$), JS 2064 X JS 20-54 ($r=0.313$), PS 1583 X JS 335 ($r=0.151$) and RVS 200-1 X PS 1092 ($r=0.064$). The crosses PS 1583 X JS 335, JS 20-64 X JS 20-54 and PS 1225 X PS 1347 had showed positive correlation between both the lines selected for high value as well as lines selected for low value of F_2 and F_3 generations.

The value of inter-generation simple correlation for harvest index was found positive between the high value lines for six crosses, JS 20-69 X JS 20-59 (0.704), PS 1584 X JS 20-41($r=0.557$), PS 1583 X JS 20-29 ($r=0.324$), PS 1225 X PS 1347 ($r=0.296$), JS 20-29 X JS 20-55 ($r=0.205$) and PS 1584 X JS 20-69($r=0.168$).Whereas seven crosses had showed positive inter-generation correlation between the lines selected for low values and maximum correlation been exhibited by cross PS 1225X PS 1347 (0.602) followed by JS 20-63 X JS 97-52(0.291), PS1583 X JS 335 (0.273), PS 1584X JS 20-69 (0.230), PS 1042 X PS 1347 (0.197), PS 1583 X Bragg (0.179) and PS 1583 X Pb1 (0.030). Two crosses, PS 1584X JS 20-69 and PS 1225 X PS 1347 had showed positive simple correlation for both the lines selected for high harvest index and lines selected for low harvest index.

Table 4.2.2b: Simple correlation coefficient between high value group of F₂ vs high value group of F₃ and between low value group of F₂ vs low value group of F₃

S.No.	Cross	Number of pods per plant		Seed yield per plant (g)		Dry matter weight per plant (g)		Harvest index (%)	
		F ₂ & F ₃ HY	F ₂ & F ₃ LY	F ₂ & F ₃ HY	F ₂ & F ₃ LY	F ₂ & F ₃ HY	F ₂ & F ₃ LY	F ₂ & F ₃ HY	F ₂ & F ₃ LY
1	PS 1583 x Pb1	-0.366	0.416	0.070	-0.076	-0.218	-0.209	-0.058	0.030
2	PS 1583 x JS 335	0.345	0.151	-0.464	0.394	-0.220	-0.207	-0.239	0.273
3	PS 1583 x DS 12-5	-0.051	0.386	0.066	-0.332	-0.126	-0.436	-0.373	-0.323
4	PS 1583 x JS 20-29	0.272	-0.700*	-0.069	-0.118	0.168	-0.310	0.324	-0.516
5	PS 1583 x Bragg	-0.403	0.475	-0.182	-0.556	-0.007	-0.446	-0.599	0.179
6	PS 1584 x JS 20-69	-0.369	-0.077	0.597	0.372	0.003	-0.116	0.168	0.230
7	PS 1584 x JS 20-41	-0.168	-0.100	0.700*	0.434	-0.346	-0.127	0.557	-0.084
8	PS 1042 x PS 1347	-0.316	0.566	-0.093	0.071	0.296	0.16	-0.494	0.197
9	RVS 200-1 x PS 1092	-0.235	0.064	-0.482	-0.337	0.051	0.169	-0.560	-0.029
10	JS 20-63 x JS 97-52	-0.131	0.558	0.466	0.384	-0.113	-0.034	-0.022	0.291
11	JS 20-69 x JS 20-59	0.127	-0.271	0.297	-0.140	0.167	-0.489	0.704*	-0.151
12	JS 20-64 x JS 20-54	0.037	0.313	0.157	0.549	-0.062	-0.423	-0.148	-0.011
13	JS 20-29 x JS 20-55	0.118	-0.268	0.399	-0.431	0.191	-0.176	0.205	-0.150
14	PS 1225 x PS 1347	0.337	0.382	-0.114	0.233	-0.418	0.073	0.296	0.602

**Significant at 1% level of probability

*Significant at 5% level of probability

HY= High yielding, LY= Low yielding

For seed yield per plant, the degree of simple correlation was positive between eight crosses ranging from 0.066 to 0.700 and eight crosses had displayed positive correlation between the lines selected for high value of F_2 and F_3 . The maximum correlation was exhibited by cross, PS 1584X JS 20-42 (0.700) followed by PS 1584X JS 20-69 ($r=0.597$), JS20-63 X JS 97-52 ($r=0.466$), JS 20-29 X JS20-55 ($r=0.399$), JS 20-69 X JS 20-59 ($r=0.297$), JS 20-64 X JS 20-54 ($r=0.157$), PS 1583 X Pb1 ($r=0.070$) and PS1583 X DS 12-5 ($r=0.066$). The value of inter-generation simple correlation between lines selected for low values were found positive between seven crosses, JS 20-64 X JS 20-54 ($r=0.549$), PS 1584 X JS 20-41 ($r=0.434$), PS 1583 X JS35($r=0.394$), JS 20-63 X JS97-52 ($r=0.384$), PS1584 X JS 20-69 ($r=0.372$), PS 1225 X PS 1347 ($r=0.233$) and PS 1042 X PS 1347 ($r=0.071$). Four crosses had showed positive inter-generation correlation between both the lines selected for high value as well as lines selected for low value which are; PS 1584X JS 20-69, PS 1584 X JS 20-41, JS 20-63 X JS97-52 and JS 20-64 X JS 20-54. Although, all the crosses displayed non-significant positive correlation between group of high value of F_2 and F_3 and between group of low value of F_2 and F_3 but if we take non-significant correlation into consideration, three crosses showed positive correlation for maximum number of characters for both the group are JS 20-64 X JS 20-54 (for number of pods per plant and seed yield per plant), PS 1225 X PS 1347 (for number of pods per plant and harvest index), PS 1584 X JS 20-69 (for seed yield per plant and harvest index).

Weiss *et al.* (1947) also reported positive phenotypic correlation between the F_3 and F_4 lines of soybean. Similar findings were also reported by **Thorne (1974)**, who revealed positive correlation between yield of F_3 and F_6 derived lines of soybean. The study of inter-generation correlation done by different workers in different crops also reported the similar pattern. In barley, **Mackenzie and Lambert (1960)** reported the range of correlation (0.11 to 0.81) between yield of F_2 and F_5 lines. In wheat, **Whan *et al.* (1981)** also reported positive correlation for yield at different selfing generations.

Barman and Borah (2012) also reported the positive inter-generation correlation in rice for days to 50% flowering and plant height. Similar finding were also reported by **Kahani and Hittalmani (2016)** in rice for plant height and days to 50% flowering. The positive and significant inter-generation correlation was also reported for seed yield per plant in rice by **Dhanraj *et al.* (1987)**, **Jangale *et al.* (1987)**, **Kumar *et al.* (2009)**, **Barman and Borah (2012)** and **Govintharaj *et al.* (2017)**.

4.2.3 Parent-offspring regression analysis

Regression is another estimate to predict the effectiveness of selection accurately beside correlation. It is a statistical procedure which estimates the linear relationship that relates two or more variables. The parent progeny regression analysis is mainly done to estimate the heritability of the character undertaken. Yield is a complex character which is affected by a number of component characters and increasing the yield is a primary desire of any researcher in a breeding programme. Correlation coefficient (r), measures only the degree (intensity) and nature (direction) of association between characters. Regression coefficient (b), quantifies the rate of change in dependent variable for unit change in the independent variable (**Abd El-Mohsen *et al.*, 2013**). Therefore, studies on inter-generation correlation and regression analysis had been taken to obtain a proper insight of affectivity of selection in F_2 generation for yield and other characters.

Inter generation regression analysis was done for all the 12 quantitative characters and is presented in **Table 4.2.3**. The results of the inter-generation regression studies were found in correspondence with the inter-generation correlation analysis and are presented below for all 14 crosses.

For days to 50% flowering, the range of inter-generation regression was -0.212 (PS 1583 X JS 20-29) to 1 (JS 20-64 X JS 20-54). Twelve crosses had given highly significant inter-generation regression, indicating that the character is suitable for selection in early generation, while two crosses, PS 1583 X JS 20-29(-0.212) and RVS 200-1 X PS 1092 (0.096) showed non-significant inter-generation correlation values. Similarly for plant height, all the 14 crosses had given positive significant regression value, ranging from 0.424 (JS 20-29 X JS 20-55) to 1.368 (JS 20-69 X JS 20-59). For harvest index, the range for inter-generation regression was from -0.007 (PS 1042 X PS 1347) to 0.361 (JS 20-69 X JS 20-59) and six crosses had showed significant regression values maximum in JS 20-69 X JS 20-59 (0.361) followed by JS 20-29 X JS 20-55 (0.33), PS 1584 X JS 20-69 (0.313), PS 1225 X PS 1347 (0.279), JS 20-64 X JS 20-54 (0.197) and JS 20-63 X JS 97-52 (0.193). Seed yield per plant showed inter-generation regression range from 0.242 (RVS 200-1 X PS 1092) to 1.53 (JS 20-29 X JS 20-55). Twelve crosses out of fourteen crosses exhibited positive significant parent progeny regression value, indicating that early generation selection is highly effective for seed yield per plant.

Table 4.2.3 Inter-generation regression coefficient between F₂ vs F₃ in soybean for fourteen crosses

Cross	Days to 50% flowering	Dry matter weight per plant (g)	Plant height (cm)	Basal node height (cm)	Basal pod height (cm)	Number of nodes per plant	Number of primary branches per plant	Number of pods per plant	Number of seeds per pod	Seed yield per plant (g)	100-seed weight (g)	Harvest index (%)
PS 1583 x Pb1	0.678**	-0.513	1.13**	0.217	0.163	0.035	-0.496	-0.49	-0.24	0.409**	0.046	0.173
PS 1583 x JS 335	0.748**	0.148	0.628**	-0.135	0.072	-0.38	-0.047	-0.047	-0.179	0.358**	0.163	0.217
PS 1583 x DS 12-5	0.792**	0.797	0.676**	-0.276	0.166	0.25	-0.107	-0.107	0.421	0.841**	-0.001	0.153
PS 1583 x JS 20-29	-0.212	-0.15	0.853**	-0.16	-0.057	-0.03	-0.262	-0.262	-0.204	0.56**	-0.244	0.144
PS 1583 x Bragg	0.714**	-0.099	0.761**	0.146	0.364	0.079	0.27	0.27	-0.24	0.66**	-0.063	0.123
PS 1584 x JS 20-69	0.733**	-0.343	0.911**	-0.13	-0.084	-0.078	-0.162	-0.162	-0.099	1.30**	0.039	0.313**
PS 1584 x JS 20-41	0.687**	0.416	0.875**	0.112	-0.064	0.238	-0.147	-0.147	-0.458	1.05**	0.011	0.094
PS 1042 x PS 1347	0.409**	0.577	1.053**	0.022	0.182	0.168	0.194	0.194	-0.054	0.306	-0.101	-0.007
RVS 200-1 x PS 1092	0.096	-0.004	0.643**	0.04	0.005	-0.335	-0.168	-0.168	0.076	0.242	0.629	0.168
JS 20-63 x JS 97-52	0.776**	-0.323	0.746**	-0.032	-0.282	-0.108	0.072	0.072	-0.331	0.57**	0.131	0.193**
JS 20-69 x JS 20-59	0.282	-0.268	1.368**	0.139	0.206	-0.443	0.08	0.08	-0.19	0.74**	-0.117	0.361**
JS 20-64 x JS 20-54	1**	-0.39	0.955**	0.287	0.358**	0.372	-0.015	-0.015	-0.147	1.136**	-0.257	0.197**
JS 20-29 x JS 20-55	0.787**	1.4	0.424**	-0.3	-0.048	0.282	-0.164	-0.164	0.08	1.53**	-0.273	0.33**
PS 1225 x PS 1347	0.607**	0.073	0.501**	0.013	-0.089	-0.003	0.206	0.205	-0.195	0.41**	-0.151	0.279**

**Significant at 1% level of probability *Significant at 5% level of probability

The characters, dry matter weight per plant, plant height, basal node height, basal pod height, number of nodes per plant, number of primary branches per plant, number of pods per plant, number of seeds per pod and 100-seed weight exhibited non-significant inter-generation regression in both positive and negative values and therefore, are not recommended for practicing early generation selection as the selection would be ineffective for these characters. In soybean, **Suwarto *et al.* (2013)** also reported positive inter-generation regression for plant height and days to 50% flowering. In rice, **Barman and Borah (2012)** reported positive and significant inter-generation regression for plant height and yield per plant. Similar findings for seed yield, plant height and days to 50% flowering was also reported by **Kahani and Hittalmani (2016)** in rice.

4.2.4 On the basis of mean performance of lines

In order to test the selection effectivity in early generation, selection response was also estimated by determining the difference between the high and low yield and yield components of both the generations for fourteen crosses (**Bhatt, 1977**). Visual selection was performed in the F_2 generation on the basis of yield of the individual lines. The top most high yielders were advanced as high yielding lines and the bottom lowest yielders were advanced as low yielding lines in the next generation, rest of the F_2 plants were bulked to constitute the bulk progeny in the F_3 generation. The mean differences of the traits for the lines selected for high and low values were compared by using t-test. These differences were computed for four characters *viz.*, dry matter weight per plant, number of pods per plant, seed yield per plant and harvest index and is presented in **Table 4.2.4(a) to 4.2.4(n)**

The results from the **Table 4.2.4(a) to 4.2.4(n)** indicated that there were significant differences between the lines selected for high and low values of the traits, dry matter weight per plant, number of pods per plant, seed yield per plant and harvest index. These differences were observed in F_2 generation and in F_3 generation as well. However, the differences between the lines selected for high and low value in harvest index and dry matter weight per plant was not significant for all the crosses in F_3 generation. This inferred that characters, harvest index and dry matter weight per plant is not completely effective for early generation selection as the genotypic level of the trait varied due to the environmental factors making its selection ineffective. The other

two traits, number of pods per plant and seed yield per plant had showed significant differences and thus, can be selected in the early generations effectively and significant differences among high and low value lines can be attributed to positive and significant response to selection for the all fourteen crosses.

The mean performance of lines selected for high value, low value as well as bulked lines was studied in order to evaluate the performance of parents *i.e.*, F_2 and their selected progeny *i.e.*, F_3 . In order to compute the efficiency of the breeding methods in the early generation, mean performance of lines selected for high values and bulked progeny were compared. The comparison was made on the basis of the phenotypic performance showed by the F_2 and F_3 for dry matter weight per plant, number of pods per plant, seed yield per plant and harvest index and was given in **Table 4.2.4 (a) to 4.2.4(n)**. Henceforth, comparison was mediated in

- (i) F_2 (parents selected for high value) vs. F_3 (high value lines)
- (ii) F_2 (parents selected for low value) vs. F_3 (low value lines)
- (iii) F_3 (selected lines) vs. Bulk progeny
- (iv) F_2 mean vs. Bulk progeny

4.2.4.1 Dry matter weight per plant (g)

For dry matter weight per plant, the mean performance of thirteen crosses for lines selected for high value in F_3 generation had higher mean performance than the F_2 lines selected for high value, whereas eleven crosses of lines selected for low value showed lesser mean performance than the mean performance of lines selected for low value in F_2 generation. Eleven crosses had exhibited higher mean performance in bulked progeny than the high value group of F_3 generation, indicating the greater efficiency of bulk method than the pedigree method for this character. The comparison between the F_3 bulked progeny and F_2 mean revealed that mean performance of F_3 bulked progeny of thirteen crosses had higher value than the F_2 mean for dry matter weight per plant. The cross PS 1042 X PS 1347 (85g) was with highest mean value of dry matter weight among the fourteen F_2 crosses, while JS 20-29 X JS 20-55 (129g) showed highest mean value among the bulked progeny of fourteen crosses.

4.2.4.2 Number of pods per plant

The results on number of pods per plant revealed that the mean performance for lines selected for high value in F_3 generation was greater than the respective lines of high value in F_2 generation for six crosses, PS 1584 X JS 20-69, PS 1584X JS 20-41, PS 1583 X DS 12-5, PS 1583X JS 20-29, JS 20-64 X JS 20-54 and JS 20-29 X JS 20-55, whereas four crosses, PS 1583 X Pb1, PS 1584 X JS 20-69, RVS 200-1 X PS 1092 and PS 1225 X PS 1347 had showed the mean performance of lines selected for low value was lesser than the mean performance of lines of low value in F_2 generation. This indicated that lines showing high values for this character in F_3 had greater number of pods per plant than their parents *i.e.*, F_2 and similarly, the lines selected for low value had shown lesser yield in comparison to the F_2 generation.

The general trend of comparison in the performance of bulk and lines selected for high value in F_3 was that, out of fourteen crosses, ten crosses showed the high value of number of pods per plant in bulked progeny than the high value group, proving that for number of pods per plant bulk method is more beneficial than the pedigree method. The comparison between the mean value of F_3 bulked progeny and F_2 mean revealed that thirteen crosses of F_3 bulked progeny had displayed higher value than the F_2 mean. Among the fourteen F_2 crosses, PS 1225 X PS 1347 (77.96) had highest mean value for number of pods per plant, while JS 20-29 X JS 20-55 (184.5) had highest mean value among the F_3 bulked progeny.

4.2.4.3 Harvest index (%)

The study on harvest index revealed that only two crosses, PS 1584 X JS 20-41 (30.73%) and JS 20-64 X JS 20-54 (34.94%) in F_3 high group showed high value of harvest index than the F_2 lines selected for high value, while only one cross, PS 1584 X JS 20-69 (28.19%) in low group had displayed lower harvest index value than F_2 lines selected for low value. The comparison between the mean value of F_3 bulk and F_2 mean for harvest index revealed that the ten crosses of F_3 bulked progeny had displayed higher value than the F_2 mean. Among the fourteen F_2 crosses, PS 1583 X JS 20-29 (42.27%) had highest mean value for harvest index, while PS 1584 X JS 20-69 (48.76%) had highest mean value among the F_3 bulk.

4.2.4.4 Seed yield per plant (g)

For seed yield per plant, eight crosses of F_3 high value group showed higher seed yield per plant than the F_2 lines selected for high seed yield per plant. The maximum yield was exhibited by cross, PS 1584 X JS 20-69 (42.63 g) followed by PS 1583 X JS 20-29 (33.40 g), JS 20-69 X JS 20-59 (29.79 g), PS 1584 X JS 20-41 (29.75 g), PS 1583 X DS12-5 (28.69 g), JS 20-29 X JS 20-55 (28.57 g), PS 1583 X Bragg (27.73 g) and JS 20-64 X JS 20-54 (25.91 g) in F_3 high group. The lowest seed yield per plant in F_3 high group was exhibited by cross, RVS 20-1 X PS 1092 (10.13 g) and six crosses had showed the lowest value of seed yield in comparison to the lines selected for low value in F_2 generation.

Out of fourteen crosses, bulked progeny of ten crosses showed higher seed yield per plant than their respective lines selected for high values in F_2 generation. The comparison between the mean value of F_3 , bulked progeny and F_2 mean for seed yield per plant revealed that all the fourteen crosses of F_3 bulked progeny had displayed higher value than the F_2 mean. Among the fourteen F_2 crosses, PS 1584 X JS 20-69 (20.7 g) had highest mean value for seed yield per plant, while PS 1584 X JS 20-69 (50.12 g) again had showed highest mean value among the F_3 bulk.

The comparison of different selected lines in F_2 and F_3 generations revealed that out of four, three characters (dry matter weight per plant, harvest index and seed yield per plant) had given maximum mean performance by the crosses in F_3 generation rather than in F_2 generation and for the breeding method the bulk method was proved to be more phenotypically superior than the pedigree method. **Surek *et al.* (2004)** also reported significant differences in mean of low and high groups for seed yield per plant, 1000 grain weight and number of grains per panicle but not for number of productive panicles per square meter. Similar findings were also reported by **Rasmusson and Cannall (1970)** in barley. **Benbelkacem *et al.* (1984)** had also reported significant difference between high and low progeny groups for tiller number in barley. In soybean, **Singh and Sharma (2016)** reported the findings of high difference of mean performance of F_2 plant selected for high and low expression of 100-seed weight, seed yield, biological yield while the difference were found moderate to low for number of pods per plant and number of seeds per pod. **Torrie (1958)** reported the seed yield of bulk selection greater than the pedigree method for intermediate and late maturity classes in soybean. **Ivers (1975)** reported effectiveness of bulk family selection and single line family selection to be greater than the pedigree method and random selection in soybean.

Table 4.2.4a: Mean performance of selected lines in F₂ generation, the ten highest, the ten lowest and bulked lines in F₃ generation of PS 1583 x Pb1

Sn No	Characters	F ₂				F ₃			
		Mean	High	Low	Difference	High	Low	Difference	Bulk
1	Number of pods per plant	43.96	82.2	40.2	42.00**	77.98	35.96	42.02**	121.93
2	Seed yield per plant (g)	13.74	22.89	6.33	16.56**	17.12	8.28	8.84**	20.94
3	Dry matter weight per plant (g)	50	57.5	68.5	-11	59.79	37.27	22.52*	110.83
4	Harvest index (%)	27.48	41.16	9.86	31.30**	31.08	23.27	7.82**	18.9

**Significant at 1% level of probability, *Significant at 5% level of probability

Table 4.2.4b: Mean performance of selected lines in F₂ generation, the ten highest, the ten lowest and bulked lines in F₃ generation of PS 1583 x JS 335

Sn No	Characters	F ₂				F ₃			
		Mean	High	Low	Difference	High	Low	Difference	Bulk
1	Number of pods per plant	56.72	89.4	39.8	49.6**	79.23	46.58	32.65**	107
2	Seed yield per plant (g)	15.52	25.29	8.19	17.1**	20.79	10.53	10.26**	21.72
3	Dry matter weight per plant (g)	55.00	59.75	53	6.75*	64.75	46.8	17.95*	73.33
4	Harvest index (%)	28.22	42.46	15.69	26.77**	32.3	23.55	8.75**	29.65

**Significant at 1% level of probability, *Significant at 5% level of probability

Table 4.2.4c: Mean performance of selected lines in F₂ generation, the ten highest, the ten lowest and bulked lines in F₃ generation of PS 1583 x DS 12-5

Sn No	Characters	F ₂				F ₃			
		Mean	High	Low	Difference	High	Low	Difference	Bulk
1	Number of pods per plant	48.24	83.8	40.3	43.5**	104.86	49.45	55.41**	98.17
2	Seed yield per plant (g)	11.51	23.81	4.7	19.11**	28.69	10.73	17.96**	20.9
3	Dry matter weight per plant (g)	45.00	47	34.75	12.25**	82.89	43.6	39.29**	67.33
4	Harvest index (%)	25.58	51.81	14.31	37.50**	34.77	25.88	8.89*	31.05

**Significant at 1% level of probability, *Significant at 5% level of probability

Table 4.2.4d: Mean performance of selected lines in F₂ generation, the ten highest, the ten lowest and bulked lines in F₃ generation of PS 1583 x JS 20-29

Sn No	Characters	F ₂				F ₃			
		Mean	High	Low	Difference	High	Low	Difference	Bulk
1	Number of pods per plant	60.24	97.2	37.6	59.6**	109.41	58.87	50.55**	109
2	Seed yield per plant (g)	20.08	27.52	6.31	21.21**	33.4	17.53	15.87**	32.78
3	Dry matter weight per plant (g)	47.50	61.5	59	2.5	82.78	51.61	31.18**	111.17
4	Harvest index (%)	42.27	47.01	11.5	35.51**	40.96	34.33	6.62	29.61

**Significant at 1% level of probability, *Significant at 5% level of probability

Table 4.2.4e: Mean performance of selected lines in F₂ generation, the ten highest, the ten lowest and bulked lines in F₃ generation of .PS 1583 x Bragg

Sn No	Characters	F ₂				F ₃			
		Mean	High	Low	Difference	High	Low	Difference	Bulk
1	Number of pods per plant	68.18	112	44.4	67.6**	84.33	54.83	29.5**	104.67
2	Seed yield per plant (g)	19.32	24.19	8.05	16.14**	27.73	14.95	12.78**	29.72
3	Dry matter weight per plant (g)	77.50	69.25	68.25	1	79.86	49.87	29.99**	122.5
4	Harvest index (%)	24.93	36.38	14.33	22.06**	34.77	29.89	4.88	24.23

**Significant at 1% level of probability, *Significant at 5% level of probability

Table4.2.4f: Mean performance of selected lines in F₂ generation, the ten highest, the ten lowest and bulked lines in F₃ generation of PS 1584 x JS 20-69.

Sn No	Characters	F ₂				F ₃			
		Mean	High	Low	Difference	High	Low	Difference	Bulk
1	Number of pods per plant	59.48	114.1	35.9	78.20**	123.86	71.98	51.88**	142.61
2	Seed yield per plant (g)	20.70	30.79	12.53	18.27**	42.63	18.79	23.84**	50.12
3	Dry matter weight per plant (g)	50.00	64.95	42.25	22.70**	106.61	68.45	38.17**	102.78
4	Harvest index (%)	41.40	48.43	32.96	15.47**	39.6	28.19	11.40**	48.76

**Significant at 1% level of probability, *Significant at 5% level of probability

Table 4.2.4g: Mean performance of selected lines in F₂ generation, the ten highest, the ten lowest and bulked lines in F₃ generation of PS 1584 x JS 20-41

Sn No	Characters	F ₂				F ₃			
		Mean	High	Low	Difference	High	Low	Difference	Bulk
1	Number of pods per plant	59.16	90	38.9	51.10**	105.22	61.79	43.42**	50.5
2	Seed yield per plant (g)	13.62	21.36	6.5	14.87**	29.75	17.34	12.41*	16.65
3	Dry matter weight per plant (g)	50.00	79.5	59	20.50**	94.12	56.11	38.00**	52
4	Harvest index (%)	27.24	27.73	11.46	16.27**	30.73	31.16	-0.43	32.27

**Significant at 1% level of probability, *Significant at 5% level of probability

Table 4.2.4h: Mean performance of selected lines in F₂ generation, the ten highest, the ten lowest and bulked lines in F₃ generation of PS 1042 x PS 1347

Sn No	Characters	F ₂				F ₃			
		Mean	High	Low	Difference	High	Low	Difference	Bulk
1	Number of pods per plant	51.48	78.1	39.5	38.60**	62.86	44.07	18.79**	76.5
2	Seed yield per plant (g)	15.66	23.18	5.96	17.22**	18.25	11.73	6.52**	19.62
3	Dry matter weight per plant (g)	85.00	51.25	44.85	6.40*	59.67	43.27	16.39*	64.33
4	Harvest index (%)	18.42	45.81	13.77	32.04**	30.55	27.94	2.61	30.58

**Significant at 1% level of probability, *Significant at 5% level of probability

Table 4.2.4i : Mean performance of selected lines in F₂ generation, the ten highest, the ten lowest and bulked lines in F₃ generation of RVS 200-1 x PS 1092.

Sn No	Characters	F ₂				F ₃			
		Mean	High	Low	Difference	High	Low	Difference	Bulk
1	Number of pods per plant	42.40	69.6	33.6	36**	50.12	25.68	24.43**	84.61
2	Seed yield per plant (g)	9.19	13.89	4.16	9.73**	10.13	6.17	3.97**	17.42
3	Dry matter weight per plant (g)	55.00	40	48.5	-8.50*	38.1	31.82	6.28	74.67
4	Harvest index (%)	16.71	35.54	8.74	26.79**	27.34	19.02	8.32**	23.32

**Significant at 1% level of probability, *Significant at 5% level of probability

Table 4.2.4j: Mean performance of selected lines in F₂ generation, the ten highest, the ten lowest and bulked lines in F₃ generation of JS20-63 x JS 97-52

Sn No	Characters	F ₂				F ₃			
		Mean	High	Low	Difference	High	Low	Difference	Bulk
1	Number of pods per plant	58.88	89.4	46.5	42.90**	72.04	48.93	23.11**	89.63
2	Seed yield per plant (g)	13.37	23.18	7.47	15.71**	22.49	13.85	8.63**	31.12
3	Dry matter weight per plant (g)	55.00	52.75	59.25	-6.5	64.74	50.18	14.56	98.5
4	Harvest index (%)	24.31	45.76	12.86	32.89**	35.37	26.86	8.52**	31.58

**Significant at 1% level of probability, *Significant at 5% level of probability

Table 4.2.4k: Mean performance of selected lines in F₂ generation, the ten highest, the ten lowest and bulked lines in F₃ generation of JS 20-69 x JS 20-59

Sn No	Characters	F ₂				F ₃			
		Mean	High	Low	Difference	High	Low	Difference	Bulk
1	Number of pods per plant	49.16	90.7	33.7	57.00**	84.62	60.53	24.10**	111.67
2	Seed yield per plant (g)	16.06	27.07	8.23	18.83**	29.79	12.34	17.44**	35.63
3	Dry matter weight per plant (g)	42.50	62.75	68.75	-6	87.89	53.92	33.97**	111.83
4	Harvest index (%)	37.79	44.19	12.96	31.23**	34.59	22.88	11.70**	31.88

**Significant at 1% level of probability, *Significant at 5% level of probability

Table 4.2.4l: Mean performance of selected lines in F₂ generation, the ten highest, the ten lowest and bulked lines in F₃ generation of JS 20-64 x JS 20-54.

Sn No	Characters	F ₂				F ₃			
		Mean	High	Low	Difference	High	Low	Difference	Bulk
1	Number of pods per plant	42.60	66.4	35.7	30.70**	95.07	65.07	30.01**	145.25
2	Seed yield per plant (g)	9.35	14.37	4.56	9.81**	25.91	14.63	11.29**	33.28
3	Dry matter weight per plant (g)	55.00	43.75	46.5	-2.75	76.22	49.51	26.71*	113.67
4	Harvest index (%)	17.00	33.68	10.06	23.62**	34.94	29.41	5.53**	29.3

**Significant at 1% level of probability, *Significant at 5% level of probability

Table 4.2.4m Mean performance of selected lines in F₂ generation, the ten highest, the ten lowest and bulked lines in F₃ generation of JS 20-29 x JS 20-55 .

Sn No	Characters	F ₂				F ₃			
		Mean	High	Low	Difference	High	Low	Difference	Bulk
1	Number of pods per plant	60.72	82.7	40.4	42.30**	103.72	47.46	56.26**	184.5
2	Seed yield per plant (g)	11.61	19.16	7.28	11.88**	28.57	9.8	18.77**	39.76
3	Dry matter weight per plant (g)	50.00	60.5	50	10.50**	96.43	44.53	51.89**	129
4	Harvest index (%)	23.22	32.28	15.17	17.11**	29.24	21.91	7.33**	30.85

**Significant at 1% level of probability, *Significant at 5% level of probability

Table 4.2.4n: Mean performance of selected lines in F₂ generation, the ten highest, the ten lowest and bulked lines in F₃ generation of PS 1225 x PS 1347

Sn No	Characters	F ₂				F ₃			
		Mean	High	Low	Difference	High	Low	Difference	Bulk
1	Number of pods per plant	77.96	118.3	52.7	65.6**	85.53	49.93	35.60**	65.96
2	Seed yield per plant (g)	19.58	30.08	7.23	22.85**	24.68	14.32	10.36**	23.97
3	Dry matter weight per plant (g)	57.50	67.65	51.95	15.70**	76.85	61.9	14.95*	88.5
4	Harvest index (%)	34.05	45.42	14.54	30.88**	32.44	23.99	8.45**	27.09

**Significant at 1% level of probability, *Significant at 5% level of probability

4.2.5. On the basis of realized heritability

Realized heritability had been calculated separately for the lines selected for high and low value. Therefore, two values of realized heritability had been calculated for high and low group of yield and yield attributing characters. The result of realized heritability for twelve characters is presented in **Table 4.2.5** which revealed that the character for which maximum crosses had showed high value of realized heritability was days to 50% flowering followed by number of pods per plant, seed yield per plant, 100-seed weight, plant height, while minimum number of crosses had displayed high and positive realized heritability for basal node height, basal pod height, number of nodes per plant, number of seeds per pod, dry matter weight per plant and number of primary branches per plant.

Study of realized heritability on high group of days to 50% flowering showed that thirteen crosses displayed high value, while only one cross exhibited moderate value of realized heritability ranging from 12.37(PS183 X Pb1) to 0.33 (PS 1583 X DS 12-5). In low group, all the fourteen crosses had given high value of realized heritability ranging from 0.58 (PS 1583 X JS 335) to 1.76 (PS 1584 X JS 20-69).

For number of pods per plant, range of realized heritability for high group was from 0.42 (JS 20-64 X JS 20-54) to 4.68 (RVS 200-1 X PS 1092). Twelve crosses had showed high value of realized heritability (h) and two crosses had showed moderate level of realized heritability of high group (r_h). Whereas, the result for realized heritability for low group (r_l) showed that nine crosses had exhibited high value of realized heritability while one cross (RVS 200-1 X PS 1092) had displayed moderate level of realized heritability.

The result of realized heritability for number of seeds per pod for lines of high group revealed that only two crosses, PS 1583 X Bragg (1.95) and RVS 200-1 X PS 1092(0.89) exhibited high heritability among the fourteen crosses while for low group, four crosses (JS 20-64 X JS 20-54, PS 1225 X PS 1347, JS 20-69 X JS 20-59 and RVS 200-1 X PS 1092) showed high value of realized heritability.

Realized heritability of high group for 100-seed weight ranged from -1.42 (PS 1583 X Pb1) to 2.02 (JS 20-29 X JS 20-55) and seven out of fourteen crosses exhibited high value of realized heritability while four crosses showed moderate value

of realized heritability. For low group, only two crosses showed high value of realized heritability, whereas seven crosses showed moderate value and five crosses showed low value of realized heritability.

The result of realized heritability of high group for harvest index revealed that only one cross, PS 1584 X JS 20-69 showed high value and four crosses showed moderate value of realized heritability and rest of all crosses showed negative value of realized heritability, while for low group the value of realized heritability was found to be high for ten crosses and four crosses showed negative value of realized heritability. Maximum ten crosses had showed high value of realized heritability in low group of harvest index ranging from 1.46 (PS 1583 X Pb1) to 11.87 (PS 1584X JS 20-69), while four crosses had displayed negative value of realized heritability.

The range of realized heritability for high group for seed yield per plant was from 0.33(JS 20-64 X JS 20-54) to 3.76 (RVS 200-1 XPS 1092) and ten crosses had showed high value of realized heritability, while four crosses had showed moderate value of realized heritability. For low group, five crosses showed high value of realized heritability, seven crosses showed moderate value of realized heritability and two crosses had showed negative value of realized heritability

The study on realized heritability for other characters had showed that few crosses showed high value of realized heritability while major number of crosses displayed low value of realized heritability.

Cober (1997) reported the range of realized heritability for seed shape was from 0.59 to 0.79 in soybean. Similarly, **Wiggins (2012)** reported range of realized heritability for seed yield to be from 0.90 to 1.33 in RIL population of soybean. Likewise researchers in other crops had also estimated the value of realized heritability for different characters. In wheat, **Bhatt (1977)** obtained high value of realized heritability for harvest index in two wheat crosses. **Surek and Beser (2004)** reported realized heritability in four crosses of rice for different characters among which 1000 grain weight had the highest realized heritability, while moderate to low value of realized heritability had been estimated for other three characters. Similarly, **Govintharaj (2017)** in rice had also reported the high value of realized heritability for 1000 grain weight and moderate value for number of grains per panicle.

Table 4.2.5: Realized heritability for high and low group of fourteen crosses of twelve characters

Cross	Number of pods per plant		Seed yield per plant (g)		Harvest index (%)		Days to 50% flowering		Dry matter weight per plant (g)		Plant height (cm)	
	r_h	r_l	r_h	r_l	r_h	r_l	r_h	r_l	r_h	r_l	r_h	r_l
PS 1583 x Pb1	1.19	0.79	2.27	0.51	-0.21	1.46	12.37	1.41	4.76	-0.35	0.64	0.74
PS 1583 x JS 335	1.46	1.68	1.71	0.4	0.22	1.6	0.78	0.58	0.40	0.35	-0.06	1.11
PS 1583 x DS 12-5	0.61	4.84	0.7	0.23	0.26	4.21	0.33	0.78	0.12	-5.83	68.63	0.85
PS 1583 x JS 20-29	0.71	3.3	0.65	0.61	-0.13	-15.94	1.08	1.00	0.16	-0.30	1.21	0.47
PS 1583 x Bragg	2.91	1.7	0.63	0.85	-0.36	3.05	1.09	1.22	-0.25	0.15	0.28	0.28
PS 1584 x JS 20-69	0.86	-1.61	0.5	-5.67	1.34	11.87	3.80	1.76	0.36	0.04	0.52	0.32
PS 1584 x JS 20-41	0.68	-5.01	0.53	1.32	-1.93	-1.04	3.00	1.72	0.48	0.70	0.27	0.41
PS 1042 x PS 1347	2.45	1.56	1.92	0.22	-0.14	6.2	1.23	1.19	0.22	0.72	-0.77	0.54
RVS 200-1 x PS 1092	4.68	0.59	3.76	0.51	-0.01	1.77	1.20	1.46	0.94	0.59	0.91	0.93
JS 20-63 x JS 97-52	2.41	1.23	1.07	0.56	-0.46	-3.53	1.11	1.09	-0.28	-0.74	0.37	0.29
JS 20-69 x JS 20-59	1.21	-3.47	0.82	0.53	0.1	2.36	1.07	1.05	-0.07	-0.40	0.56	0.50
JS 20-64 x JS 20-54	0.42	-0.56	0.33	1.09	-1.04	-0.71	1.11	1.06	-0.04	0.33	11.11	0.39
JS 20-29 x JS 20-55	0.51	1.5	0.45	0.73	-0.14	2.42	0.63	0.73	0.13	0.47	0.30	0.77
PS 1225 x PS 1347	3.79	0.89	1.99	-0.08	0.5	2.46	0.78	0.90	0.50	-1.76	0.70	-0.23

Cross	Basal node height (cm)		Basal pod height (cm)		Number of nodes per plant		Number of primary branches per plant		Number of seeds per pod		100-seed weight(g)	
	r_h	r_l	r_h	r_l	r_h	r_l	r_h	r_l	r_h	r_l	r_h	r_l
PS 1583 x Pb1	1.15	1.06	0.03	0.46	-0.12	0.04	0.26	-0.07	-0.14	-0.20	-1.42	-1.79
PS 1583 x JS 335	-0.17	0.48	-0.21	0.41	-0.07	0.43	0.04	0.01	-0.25	0.41	0.43	-0.12
PS 1583 x DS 12-5	-0.28	-0.34	0.16	-0.24	-0.18	-0.81	0.06	-0.07	0.03	0.12	-0.70	-0.16
PS 1583 x JS 20-29	0.31	1.22	-0.04	0.24	0.11	-0.16	-0.09	0.17	-0.20	0.08	0.79	0.54
PS 1583 x Bragg	0.04	0.17	1.13	-13.29	-0.35	-0.01	-2.08	0.18	1.95	-1.04	0.72	0.35
PS 1584 x JS 20-69	-1.19	0.11	-0.69	1.51	-0.61	-0.07	-0.07	0.12	0.08	0.06	0.59	0.55
PS 1584 x JS 20-41	1.44	0.72	0.63	-0.38	0.85	1.12	0.04	0.18	-0.43	0.43	0.48	-0.07
PS 1042 x PS 1347	0.29	-0.20	0.15	0.28	0.32	1.67	0.49	-1.50	-0.83	-0.13	-0.09	0.25
RVS 200-1 x PS 1092	-0.09	0.79	0.58	0.72	0.33	0.35	2.53	1.82	0.89	0.85	0.97	0.51
JS 20-63 x JS 97-52	-0.22	0.34	0.17	0.13	1.17	-0.58	-0.13	0.29	-0.62	-3.83	1.20	0.52
JS 20-69 x JS 20-59	0.53	-0.51	0.76	0.01	0.53	0.39	-0.55	0.20	-0.53	1.93	0.84	0.95
JS 20-64 x JS 20-54	1.10	0.72	0.36	-0.37	0.89	0.96	-0.67	0.23	0.03	3.45	0.71	0.36
JS 20-29 x JS 20-55	-0.12	0.04	-0.15	0.03	-4.37	1.96	0.14	-0.09	-0.70	-0.27	2.02	5.75
PS 1225 x PS 1347	-0.29	0.75	-0.60	0.75	-16.41	2.69	0.59	0.01	-0.46	2.02	0.28	0.05

4.2.6 On the basis of mean performance of the crosses

In the present study, the selection performed in F_2 generation was on the basis of the *per se* performance of individual lines of all the crosses for seed yield per plant. The lines exhibiting higher seed yield were grouped into high yielding group and the lines which displayed poor seed yield among all the lines of individual cross were forwarded into next generation as low yielding group. In order to evaluate the efficiency of selection performed in early generation, the mean performance of crosses in F_2 generation, in F_3 generation (high value group, low value group and bulk are compared to identify the best and the poor cross combinations giving consistent performance in both generation and in bulk progeny as well (**Table 4.2.6a and 4.2.6b**).

The best cross which exhibited highest mean performance for dry matter weight per plant in F_2 generation was PS 1042 X PS 1347 (85 g), PS 1583 X Bragg (77.50 g) followed by PS 1225 X PS 1347 (57.50 g) and). Likewise, in F_3 high value group the cross which showed high value of the character was PS 1584 X JS 20-69 (106.61 g) followed by JS 20-29 X JS 20-55 (96.43 g) and PS 1584 X JS 20-41 (94.12 g). The three cross combinations which were found highest for dry matter weight per plant among all the crosses in F_3 bulk were JS 20-29 X JS 20-55 (129 g), PS 1583 X Bragg (122.50 g) and JS 20-64 X JS 20-54 (113.67 g).

The lowest three crosses for the character dry matter weight per plant were JS 20-69 X JS 20-59 (42.50 g) PS 1583 X DS 12-5 (45 g) and PS 1583 X JS 20-29 (47.50 g), whereas in low value group of F_3 the poor performers were RVS 200-1X PS 1092 (31.82 g), PS 1583 X Pb1 (37.27 g) and PS 1042 X PS 1347 (43.27 g). Similarly, in bulk F_3 the lowest dry matter weight per plant were of crosses PS 1584 X JS 20-41 (52 g), PS 1042 X PS 1347 (64.33g) and PS 1583 X DS 12-5 (67.33 g).

For the number of pods per plant, the top three crosses in F_2 generation were PS 1225 X PS 1347 (77.96), PS 1583 X Bragg (68.18) and JS 20-29 X JS 20-55 (60.72 g). In F_3 high value group maximum number of pods per plant were showed by cross PS 1584 X JS 20-69 (123.86) followed by PS 1583 X JS 20-29 (109.41) and PS 1584 X JS 20-41 (105.22). In bulk group, the best cross combinations were JS 20-29 X JS 20-55 (184.50), JS 20-64 X JS 20-54 (145.25) and PS 1584 X JS 20-69 (142.61).

Table 4.2.6a: Top cross combinations showing highest mean performance of seed yield in F₂ generation, high group of F₃ generation and F₃ bulk

Sl.No.	Character	Crosses with higher mean performance in F ₂ generation
1.	Dry matter weight per plant (g)	PS 1042 X PS1347, PS 1583 X Bragg, PS 1225 X PS 1347
2.	Number of pods per plant	PS 1225 X PS 1347, PS 1583 X Bragg, JS 20-29 X JS 20-55
3.	Seed yield per plant (g)	PS 1584 X JS 20-69, PS 1583 X JS 20-29, PS 1225 X PS 1347
4.	Harvest index (%)	PS 1583 X JS 20-29, PS 1584 X JS 20-69, JS 20-69 X JS 20-59

Sl.No	Character	Crosses with higher mean performance in F ₃ generation(High group)
1.	Dry matter weight per plant (g)	PS 1584 X JS 20-69, JS 20-29 X JS 20-55, PS 1584 X JS 20-41
2.	Number of pods per plant	PS 1584 X JS 20-69, PS 1583 X JS 20-29, PS 1584 X JS 20-41
3.	Seed yield per plant (g)	PS 1584 X JS 20-69, PS 1583 X JS 20-29, JS 20-69 X JS 20-59
4.	Harvest Index (%)	PS 1583 X JS 20-29, PS 1584 X JS 20-69, JS 20-63 X JS 97-52

Sl.No	Character	Crosses with higher mean performance in F ₃ bulk generation
1.	Dry matter weight per plant (g)	JS 20-29 X JS 20-55, PS 1583 X Bragg, JS 20-64 X JS 20-54
2.	Number of pods per plant	JS 20-29 X JS 20-55, JS 20-64 X JS 20-54, PS 1584 X JS 20-69
3.	Seed yield per plant (g)	PS 1584 X JS 20-69, JS 20-29 X JS 20-55, JS 20-69 X JS 20-59
4.	Harvest index (%)	PS 1584 X JS 20-69, JS 20-69 X JS 20-59, PS 1584 X JS 20-41

Table 4.2.6.b: Cross combinations showing lowest mean performance of seed yield in F₂ generation, low group of F₃ generation and F₃ bulk

Sl.No	Character	Crosses with lower mean performance in F₂ generation
1.	Dry matter weight per plant (g)	JS 20-69 x JS 20-59, PS 1583 x DS 12.-5, PS 1583 X JS 20-29
2.	Number of pods per plant	RVS 200-1 x PS 1092, JS 20-64 x JS 20-54, PS 1583 x Pb1
3.	Seed yield per plant (g)	RVS 200-1 x PS 1092, JS 20-64 x JS 20-54, PS 1583 x DS 12-5
4.	Harvest index (%)	RVS 200-1 x PS 1092, JS 20-64 x JS 20-54, PS 1042 x PS 1347

Sl.No	Character	Crosses with lower mean performance in F₃ generation(low)
1.	Dry matter weight per plant (g)	RVS 200-1 x PS 1092, PS 1583 x Pb 1, PS 1042 x PS 1347
2.	Number of pods per plant	RVS 200-1 x PS 1092, PS 1583 x Pb 1, PS 1042 x PS 1347
3.	Seed yield per plant (g)	RVS 200-1 x PS 1092, PS 1583 x Pb 1, JS 20-29 x JS 20-55
4.	Harvest index (%)	RVS 200-1 x PS 1092, JS 20-29 x JS 20-55, JS 20-69 x JS 20-59

Sl.No	Character	Crosses with lower mean performance in F₃ bulk generation
1.	Dry matter weight per plant (g)	PS 1584 x JS 20-41, PS 1042 x PS 1347, PS 1583 x DS 12-5
2.	Number of pods per plant	PS 1584 x JS 20-41, PS 1225 x PS 1347, PS 1042 x PS 1347
3.	Seed yield per plant (g)	PS 1584 x JS 20-41, RVS 200-1 x PS 1092, PS 1042 x PS 1347
4.	Harvest index (%)	PS 1583 x Pb 1, RVS 200-1 x PS 1092, PS 1583 x Bragg

In F₂ generation, the lowest value of number of pods per plant was exhibited by cross RVS 200-1 X PS 1092 (42.40) followed by JS 20-64 X JS 20-54 (42.60) and PS 1583 X Pb1 (43.96) while among the low group of F₃ the crosses which had the lowest value for this character were RVS 200-1 X PS 1092(25.68), PS 1583 X Pb1 (35.96) and PS 1042 X PS 1347 (44.07). In F₃ bulk, the lowermost mean performance for the character was of PS 1584 X JS 20-41 (50.50), PS 1225 X PS 1347 (65.96) and PS 1042 X PS 1347 (76.50).

The study of mean performance of character harvest index revealed that crosses PS 1583 X JS 20-29 (42.27%), PS 1584 X JS 20-69 (41.40%) and JS 20-69 X JS 20-59 (37.79%) had the highest mean performance in F₂ generation while crosses PS 1583 X JS 20-29 (40.96%), PS 1584 X JS 20-69 (39.60%) and JS 20-63 X JS 97-52 (35.37%) exhibited the highest value in high value group of F₃ generation. Among the F₃ bulk, PS 1584 X JS 20-69 (48.76%), PS 1584 x JS 20-41 (32%) and JS 20-69 X JS 20-59 (31.88%) displayed the highest mean performance in F₃ bulk. Whereas, the crosses RVS 200-1 X PS 1092 (16.71%), JS 20-64 X JS 20-54 (17%) and PS 1042 X PS 1347 (18.42%) had lowest mean performance among the F₂ crosses. The crosses RVS 200-1 X PS 1092 (19.02%), JS 20-29 X JS 20-55 (21.91%) and JS 20-69 X JS 20-59 (22.88%) showed lowest mean performance among the F₃ low value group and PS 1583 X Pb1 (18.9%), RVS 200-1 X PS 1092 (23.32%) and PS 1583 X Bragg (24.33%) had lowest mean performance among the crosses in F₃ bulk for harvest index.

The cross combinations which exhibited the highest mean performance among the fourteen crosses in F₂ generation for seed yield per plant were PS 1584X JS 20-69 (20.70 g), PS 1583 X JS 20-29(20.08 g) and PS 1225 X PS 1347(19.58 g). In the high value progeny group of F₃ generation, the top three best cross combinations were PS 1584 X JS 20-69(42.63 g), PS 1583 X JS 20-29 (33.4 g) and JS 20-69 X JS 20-59 (29.79 g). Similarly in F₃ bulk, the highest value of seed yield was displayed by PS 1584 X JS 20-69 (50.12 g), JS 20-29 x JS 20-55 (39.76 g) and JS 20-69 X JS 20-59 (35.63 g). Both PS 1584 X JS 20-69 and PS 1583 X JS 20-29 were consistent in displaying the high value of seed yield per plant in all the groups, while PS 1225 X PS 1347 performed well in F₂ generation and F₃ bulk population.

Among all the crosses, the cross combination which had the lowest seed yield per plant was RVS 200-1 X PS 1092 (9.19 g) followed by JS 20-64 X JS 20-54 (9.35 g) and PS 1583 X DS 12-5 (11.51 g) in F₂ generation. In the low value progeny group of F₃ generation the lowest three cross combinations were RVS 200-1 X PS 1092 (6.17 g), PS 1583 X Pb1 (8.28 g) and JS 20-29 X JS 20-55 (9.8 g). Similarly, in bulk progeny the lowest performance was of crosses PS 1584 X JS 20-41 (16.65 g), RVS 200-1 X PS 1092 (17.42 g) and PS 1042 X PS 1347 (19.62 g).

The crosses which performed consistently better than the other crosses in both the generation could be selected in earlier generation and the crosses which had given poor performance consistently can be rejected in earlier generation rather than advancing into further generation.

The early generation selection becomes fruitful in any breeding programme only in the presence of additive gene effects. The preponderance of non-additive effects, complexity of character, effect of environment and also genotype x environment interaction lead to the inefficiency of selection in early generation of segregating population. Therefore, different parameters need to be taken into consideration for the study of efficiency of selection in early generation. In above study on the basis of all the genetic parameters, characters *viz.*, days to 50% flowering, plant height, number of pods per plant and seed yield per plant emerged as those characters which can be selected in early generation. Although, other characters were also found to be effective in some parameters but not in all, inferring that these characters may or may not be effective for selection due to presence of non-additive effects. Different studies led by different researchers in different crops revealed that sometime early generation is effective as reported by **Mahmud and Kramer (1951)** in soybean, **Frey (1954)** in barley, **Ntare and Aken'ova (1985)** in cowpea, **Sharma (1994)** in wheat, **St Martin and Geraldi (2002)**, **Surek (2004)**, **Govintharaj (2017)** and **Hittalmani (2016)** in rice. However, some researchers also reported it to be ineffective; **Weis *et al.* (1947)**, **Singh and Sharma (2015)** in soybean, **Briggs and Shebeski (1971)**, **Knott and Kumar (1975)**, **Seitzer and Evans (1978)** in wheat.

From the above study and the results obtained, it can be inferred that early generation selection can be described as a reliable indicator of the later generation performance for characters like days to 50% flowering, plant height, number of pods

per plant and seed yield per plant. Of which, seed yield per plant was found effective for selection in early generation through all the genetic parameters studied. But the prediction for other characters like dry matter weight per plant, basal node height, basal pod height, number of nodes per plant, number of primary branches per plant, number of seeds per pod, 100-seed weight and harvest index cannot be made in early generation and the selection would be effective in later generation only. From the study of mean performance of various crosses in F_2 and F_3 generations it can be recommended that the crosses which exhibit low yield in the early generation can be rejected without having doubt of losing the potential genotypes. As far as the breeding method is concerned, bulk method is proved to be more effective than the pedigree method for the soybean improvement programme.

4.3 Residual Heterosis

The results pertaining to residual heterosis in F_2 and F_3 for all the quantitative characters in the present investigation are presented in **Table 4.3.1a to 4.3.12b**. The character wise description of residual heterosis character wise in present study is detailed below:

4.3.1 Days to 50% flowering

The range of residual heterosis over mid parent was -8.65 (PS 1583 X DS 12-5) to 5.58 percent (JS20-63 X JS 97-52) in F_2 generation. Four crosses, JS20-29 X JS 20-55 (-3.48%), PS 1225 X PS 1347 (-5.47%), PS 1584 X JS 20-69 (5.47%) and PS 1583 X DS 12-5 (-8.65%) showed maximum and significant negative heterosis over mid parent. However, the range of heterosis over better parent was -4.04 (PS 1583 X DS 12-5 and PS 1225 X PS 1347) to 5.05 per cent (PS 183 X Bragg and JS 20-63 X JS 97-52). Out of 14 F_2 crosses, only three crosses showed significant and negative heterosis over better parent. Maximum and significantly negative better parent heterosis was exhibited equally by all the three crosses (PS 1583 X DS 12-5, PS 1584 X JS 20-69 and PS 1225 X PS 1347) *i.e.*, -4.04 per cent. None of the crosses exhibited significant negative heterosis over both the standard checks (**Table 4.3.1a**).

In F_3 , the range of residual heterosis over mid parent was -19.41 to 7.09 per cent. Out of 14 crosses, seven crosses showed significant negative residual heterosis

over mid parent. Maximum significant and negative residual heterosis was found in JS 20-69 X JS 20-59 (-19.41%) followed by JS 20-64 X JS 20-54 (-14.71%) and PS 1042 X PS 1347 (11.96%), PS 1584 X JS 20-69 (-7.09%), PS 1584 X JS 20-41 (-1.97%), PS 1583 X DS12-5 (-1.62) and RVS 200-1 X PS 1092 (-0.83%). Whereas, the range of residual heterosis over better parent was from -19.41(JS 20-69 X JS 20-59) to 8.54 (PS 1583 X Pb 1) per cent. Five crosses, JS 20-69 X JS 20-59 (-19.41%), JS 20-63 X JS 97-52 (-13.94%), JS 20-64 X JS 20-54 (-13.3%), PS 1042 X PS 1347 (-11.12%) and PS 1584 X JS 20-69 (-5.19%) exhibited significant negative heterobeltiosis. Residual heterosis over standard check, PS 19 was observed significantly negative in all the crosses, ranging from -26.61(JS 20-69 X JS 20-59) to -8.90(PS 1583 X Pb1) per cent. Likewise residual heterosis over standard check, SL 688 was observed as significant and in negative direction in all the crosses ranging from -223.89% (JS 20-69 X JS 20-59) to -2.32 (PS 1225 X PS 1347) per cent in F₃, indicating that these fourteen crosses were early than both the standard check for days to 50% flowering as given in **Table 4.3.1b**.

4.3.2 Dry matter weight per plant

In F₂ crosses, the residual heterosis over mid parent varied from -37.34 (PS 1584 X JS 20-69) to 20.20 per cent (JS 20-69 X JS 20-59), whereas residual heterosis over better parent ranged from -27.23 (PS 1583 X JS 335) to 33.46 per cent (JS 20-69 X JS 20-59) as given in Table 4.3.2a. Out of 14 F₂s, three and four crosses showed significant positive heterosis over mid parent and better parent. None of the crosses showed positive significant residual heterosis with standard checks, PS 19 and SL -688 (**Table 4.3.2a**).

In F₃, the range of residual heterosis varied from -34.93 (RVS 200-1 X PS 1092) to 23.36 per cent (PS 1584 X JS 20-41) and nine crosses displayed significant positive residual heterosis over mid parent. For better parent, the range was observed from -49.75(RVS 200-1 X PS 1092) to 3.27(PS 1584 X JS 20-41) per cent, while four crosses, PS 1584 X JS 20-41 (3.27), JS 20-29 X JS 20-55 (2.24), PS 1583 X Bragg (1.41) and PS 1225 X PS 1347 (1.12) displayed significant positive residual heterobeltiosis. None of the cross showed positive and significant residual heterosis over both the standard checks as presented in **Table 4.3.2b**.

Table 4.3.1a: Residual heterosis in percentage for days to 50% flowering in F₂ generation of soybean

Sn no	Cross	MP	BP	SP1	SP2
1	PS 1583 x Pb1	0.98	4.04*	6.19**	8.42**
2	PS 1583 x JS 335	2.06	0.00	2.06	4.21*
3	PS 1583 x DS 12-5	-8.65**	-4.04*	-2.06	0.00
4	PS 1583 x JS 20-29	-0.99	1.01	3.09	5.26**
5	PS 1583 x Bragg	2.46	5.05**	7.22**	9.47**
6	PS 1584 x JS 20-69	-5.47**	-4.04*	-2.06	0.00
7	PS 1584 x JS 20-41	0.00	0.00	2.06	4.21*
8	PS 1042 x PS 1347	-0.49	2.02	4.12*	6.32**
9	RVS 200-1 x PS 1092	-1.01	-1.01	1.03	3.16
10	JS 20-63 x JS 97-52	5.58**	5.05**	7.22**	9.47**
11	JS 20-69 x JS 20-59	-0.98	2.02	4.12*	6.32**
12	JS 20-64 x JS 20-54	-2.39	3.03	5.16**	7.37**
13	JS 20-29 x JS 20-55	-3.48*	-2.02	0.00	2.11
14	PS 1225 x PS 1347	-5.47**	-4.04*	-2.06	0.00

MP=Mid-parent, BP=Better parent, SP1= Check variety PS 19, SP2= Check variety SL 688

**Significant at 1% level of probability, *Significant at 5% level of probability

Table 4.3.1b: Residual heterosis in percentage for days to 50% flowering in F₃ generation of soybean

Sn no	Cross	MP	BP	SP1	SP2
1	PS 1583 x Pb1	5.19**	8.54**	-8.90**	-5.53**
2	PS 1583 x JS 335	3.64**	6.95**	-10.24**	-6.92**
3	PS 1583 x DS 12-5	-1.62**	3.62**	-13.04**	-9.81**
4	PS 1583 x JS 20-29	6.82**	7.96**	-9.39**	-6.04**
5	PS 1583 x Bragg	2.26**	3.35**	-13.26**	-10.05**
6	PS 1584 x JS 20-69	-7.09**	-5.19**	-17.04**	-13.97**
7	PS 1584 x JS 20-41	-1.97**	-0.97	-13.35**	-10.14**
8	PS 1042 x PS 1347	-11.96**	-11.12**	-17.46**	-14.41**
9	RVS 200-1 x PS 1092	-0.83**	-0.83	-18.54**	-15.52**
10	JS 20-63 x JS 97-52	-16.50**	-13.94**	-24.70**	-21.91**
11	JS 20-69 x JS 20-59	-19.41**	-19.41**	-26.61**	-23.89**
12	JS 20-64 x JS 20-54	-14.77**	-13.13**	-19.34**	-16.35**
13	JS 20-29 x JS 20-55	0.85**	6.10**	-9.05**	-5.69**
14	PS 1225 x PS 1347	2.42**	3.42**	-5.81**	-2.32**

MP=Mid-parent, BP=Better parent, SP1= Check variety PS 19, SP2= Check variety SL 688

**Significant at 1% level of probability, *Significant at 5% level of probability

Table 4.3.2a: Residual heterosis in percentage for dry matter weight per plant in F₂ generation of soybean

Sn no	Cross	MP	BP	SP1	SP2
1	PS 1583 x Pb1	-2.71	29.45**	-38.05**	-35.26**
2	PS 1583 x JS 335	-29.50**	-27.23**	-42.15**	-42.15**
3	PS 1583 x DS 12-5	-31.86**	-9.34	-56.62**	-56.62**
4	PS 1583 x JS 20-29	-22.73**	-19.11**	-41.23**	-41.23**
5	PS 1583 x Bragg	15.80**	55.79**	-26.77**	-26.77**
6	PS 1584 x JS 20-69	-37.34**	-30.17**	-57.74**	-57.74**
7	PS 1584 x JS 20-41	8.92**	36.15**	-32.51**	-32.51**
8	PS 1042 x PS 1347	-24.74**	-22.35**	-49.83**	-49.83**
9	RVS 200-1 x PS 1092	-18.46**	17.98	-52.62**	-52.62**
10	JS 20-63 x JS 97-52	-16.36**	-8.93	-43.18**	-43.18**
11	JS 20-69 x JS 20-59	20.20**	33.46**	-33.85**	-33.85**
12	JS 20-64 x JS 20-54	-27.51**	-14.29*	-53.85**	-53.85**
13	JS 20-29 x JS 20-55	-10.96*	4.57	-43.69**	-43.69**
14	PS 1225 x PS 1347	-12.21**	-11.44*	-40.21**	-40.21**

MP=Mid-parent, BP=Better parent, SP1= Check variety PS 19, SP2= Check variety SL 688

**Significant at 1% level of probability, *Significant at 5% level of probability

Table 4.3.2b: Residual heterosis in percentage for dry matter weight per plant in F₃ generation of soybean

Sn no	Cross	MP	BP	SP1	SP2
1	PS 1583 x Pb1	-9.11**	-22.75*	-46.72**	-45.78**
2	PS 1583 x JS 335	-24.51**	-32.07**	-41.43**	-40.41**
3	PS 1583 x DS 12-5	10.33**	-4.84**	-34.37**	-33.22**
4	PS 1583 x JS 20-29	0.18**	-3.31**	-28.32**	-27.06**
5	PS 1583 x Bragg	17.58**	1.41**	-30.06**	-28.83**
6	PS 1584 x JS 20-69	8.07**	-3.72**	-8.70**	-7.09**
7	PS 1584 x JS 20-41	23.36**	3.27**	-23.44**	-22.09**
8	PS 1042 x PS 1347	-18.82**	-23.78**	-46.12**	-45.17**
9	RVS 200-1 x PS 1092	-34.96**	-49.75**	-61.87**	-61.20**
10	JS 20-63 x JS 97-52	-9.74**	-17.09**	-38.53**	-37.45**
11	JS 20-69 x JS 20-59	2.87**	-20.52**	-24.63**	-23.31**
12	JS 20-64 x JS 20-54	3.08**	-10.98**	-32.46**	-31.27**
13	JS 20-29 x JS 20-55	18.82**	2.24**	-24.20**	-22.87**
14	PS 1225 x PS 1347	3.65**	1.12**	-28.51**	-27.26**

MP=Mid-parent, BP=Better parent, SP1= Check variety PS 19, SP2= Check variety SL 688

**Significant at 1% level of probability, *Significant at 5% level of probability

4.3.3 Plant height

In F_2 , only one cross, PS 1583 X DS 12-5 (-14.11) showed significant residual heterosis over mid parent while none of the crosses showed significant residual heterosis over better parent. Similarly, none of the cross showed significant residual heterosis over standard check, PS 19 whereas three crosses, PS 1583 X Bragg (-17.32%), PS 1583 X Pb1 (-9.49%) and JS 20-63 X JS 97-52 (-6.33%) showed significant negative residual heterosis over standard check SL 688 (**Table 4.3.3a**). In F_3 Out of fourteen, no cross showed positive significant mid parent heterotic effect for plant height, while four crosses, JS 20-64 X JS 20-54 (-19.16), PS 1042 X PS 1347 (-31.82%), JS 20-69 X JS 20-59 (-8.27%) and JS 20-3 X JS 97-52 (-1%) showed significant negative heterosis over mid parent. Three crosses, JS 20-64 X JS 20-54 (-22.05%), JS 20-63 X JS 97-52 (-15.01%) and JS 20-69 X JS 20-59 (-10.75%) showed significant negative heterobeltiosis and one of the cross had positive significant value. In case of standard check PS 19, no cross showed significant positive residual heterosis, while nine crosses showed negative significant residual heterosis ranging from -57.48 (RVS 200-1 X PS 1092) to -21.61(PS 1583 X Bragg) per cent. Over standard check SL 688, four crosses, RVS 200-1 X PS 1092 (-38.94%), PS 1042 X PS 1347 (-21.20%), JS 20-64 X JS 20-54 (-11.18%) and JS 20-69 X JS 20-59 (-4.01%), showed significant negative residual heterosis while only one cross JS 20-63 X JS 97-52 (4.75%) was found significantly heterotic in positive direction as given in **Table 4.3.3b**.

4.3.4 Basal node height

In F_2 , the range of residual heterosis over mid parent varied from -23.20(RVS 200-1 X PS1092) to 81.88(PS 1583 X JS 335). Out of 14 crosses, only one cross, RVS 200-1 X PS 1092 (-23.20) showed significant negative residual heterosis over mid parent, while four crosses, JS 20-29 X JS 20-55 (17.51), PS 1584 X JS 20-69 (35.19), JS 20-69 X JS 20-59 (77.43) and PS 1583 X JS335 (81.88) showed significant positive residual heterosis (**Table 4.3.4a**). Out of 14 F_2 crosses, none of the cross showed significant negative residual heterosis over better parent and over both the standard checks, (PS 19 and SL 688) while thirteen crosses over better parent and fourteen crosses over both the standard checks (PS 19 and SL 688) showed significant positive residual heterosis.

Table 4.3.3a: Residual heterosis in percentage for plant height in F₂ generation of soybean

Sn no	Cross	MP	BP	SP1	SP2
1	PS 1583 x Pb1	-21.69	-29.22	-32.26	-9.49*
2	PS 1583 x JS 335	-19.72	-27.69	-30.80	-7.54
3	PS 1583 x DS 12-5	-14.11**	-25.86	-29.04	-5.20
4	PS 1583 x JS 20-29	-23.47	-36.47	-39.20	-18.77
5	PS 1583 x Bragg	-30.43	-35.34	-38.12	-17.32**
6	PS 1584 x JS 20-69	-21.18	-36.82	-36.90	-15.69
7	PS 1584 x JS 20-41	-22.41	-35.18	-35.26	-13.51
8	PS 1042 x PS 1347	-32.43	-33.35	-39.89	-19.69
9	RVS 200-1 x PS 1092	-35.54	-48.18	-51.36	-35.02
10	JS 20-63 x JS 97-52	-5.55	-18.37	-29.89	-6.33**
11	JS 20-69 x JS 20-59	-3.37	-9.79	-37.46	-16.44
12	JS 20-64 x JS 20-54	-15.70	-21.54	-36.31	-14.90
13	JS 20-29 x JS 20-55	-13.19	-17.72	-41.95	-22.44
14	PS 1225 x PS 1347	-16.91	-18.01	-24.05	1.48

MP=Mid-parent, BP=Better parent, SP1= Check variety PS 19, SP2= Check variety SL 688

**Significant at 1% level of probability, *Significant at 5% level of probability

Table 4.3.3b: Residual heterosis in percentage for plant height in F₃ generation of soybean

Sn no	Cross	MP	BP	SP1	SP2
1	PS 1583 x Pb1	-11.87	-14.25	-22.94	10.66
2	PS 1583 x JS 335	-24.52	-28.26	-35.53	-7.42
3	PS 1583 x DS 12-5	-19.36	-27.89	-35.20*	-6.94
4	PS 1583 x JS 20-29	-20.51	-33.58	-40.31	-14.28
5	PS 1583 x Bragg	-7.56	-12.77	-21.61*	12.57
6	PS 1584 x JS 20-69	-14.95	-21.88	-30.11**	0.37*
7	PS 1584 x JS 20-41	-8.50	-18.03	-26.66**	5.32
8	PS 1042 x PS 1347	-31.82*	-36.06	-45.12**	-21.20*
9	RVS 200-1 x PS 1092	-41.33	-52.48	-57.48**	-38.94*
10	JS 20-63 x JS 97-52	-1.00**	-15.01*	-27.05**	4.75**
11	JS 20-69 x JS 20-59	-8.27**	-10.75**	-33.16**	-4.01**
12	JS 20-64 x JS 20-54	-19.16*	-22.05*	-38.15**	-11.18*
13	JS 20-29 x JS 20-55	-5.64	-15.43	-35.63	-7.57
14	PS 1225 x PS 1347	-27.97	-25.66	-34.10	-5.36

MP=Mid-parent, BP=Better parent, SP1= Check variety PS 19, SP2= Check variety SL 688

**Significant at 1% level of probability, *Significant at 5% level of probability

Table 4.3.4a: Residual heterosis in percentage for basal node height in F₂ generation of soybean

Sn no	Cross	MP	BP	SP1	SP2
1	PS 1583 x Pb1	-5.48	-1.85	29.67**	30.74**
2	PS 1583 x JS 335	81.88**	109.64**	112.20**	113.93**
3	PS 1583 x DS 12-5	10.57	48.00**	95.53**	97.13**
4	PS 1583 x JS 20-29	12.50	14.29**	46.34**	47.54**
5	PS 1583 x Bragg	11.99	30.77**	72.76**	74.18**
6	PS 1584 x JS 20-69	35.19**	101.21**	75.85**	77.30**
7	PS 1584 x JS 20-41	3.52	31.38**	73.58**	75.00**
8	PS 1042 x PS 1347	-8.37	6.18*	78.05**	79.51**
9	RVS 200-1 x PS 1092	-23.20**	10.65**	52.03**	53.28**
10	JS 20-63 x JS 97-52	15.49*	16.81**	66.67**	68.03**
11	JS 20-69 x JS 20-59	77.43**	112.09**	85.37**	86.89**
12	JS 20-64 x JS 20-54	8.02	29.15**	42.28**	43.44**
13	JS 20-29 x JS 20-55	17.51**	70.48**	118.29**	120.08**
14	PS 1225 x PS 1347	14.21	33.99**	66.67**	68.03**

MP=Mid-parent, BP=Better parent, SP1= Check variety PS 19, SP2= Check variety SL 688

**Significant at 1% level of probability, *Significant at 5% level of probability

Table 4.3.4b: Residual heterosis in percentage for basal node height in F₃ generation of soybean

Sn no	Cross	MP	BP	SP1	SP2
1	PS 1583 x Pb1	-10.33*	-4.22	-21.89**	-36.09
2	PS 1583 x JS 335	-5.29*	3.00*	-4.56	-21.91
3	PS 1583 x DS 12-5	-13.16	-11.39	-17.89	-32.82
4	PS 1583 x JS 20-29	-11.61	-5.59	-23.00*	-37.00**
5	PS 1583 x Bragg	0.26	9.86	-14.56	-30.09**
6	PS 1584 x JS 20-69	-25.70*	-25.70	-17.44	-32.45**
7	PS 1584 x JS 20-41	-10.87*	-9.40	-2.56	-20.27**
8	PS 1042 x PS 1347	-0.92**	7.33**	-28.44	-41.45**
9	RVS 200-1 x PS 1092	6.16*	36.32**	-29.11*	-42.00**
10	JS 20-63 x JS 97-52	-12.52	5.84*	-25.44	-39.00**
11	JS 20-69 x JS 20-59	-33.74*	-23.80	-15.33	-30.73*
12	JS 20-64 x JS 20-54	-32.87*	0.60	-25.33*	-38.91**
13	JS 20-29 x JS 20-55	12.78*	15.40**	-5.89*	-23.00
14	PS 1225 x PS 1347	19.94	22.86	-4.44	-21.82**

MP=Mid-parent, BP=Better parent, SP1= Check variety PS 19, SP2= Check variety SL 688

**Significant at 1% level of probability, *Significant at 5% level of probability

In F₃ generation, the range of mid parent residual heterosis was observed from -33.74 (JS 20-69 X JS 20-59) to 19.94 (PS 1225 X PS 1347) per cent and seven crosses had showed negative significant residual relative heterosis with maximum value in JS 20-69 X JS 20-59 (-33.74%) and minimum in PS1042 X PS 1347 (-0.92%). However for better parent, none of the crosses were found heterotic in negative direction. Significant and negative residual heterosis over standard check, PS19 was observed in five crosses, RVS 200-1 X PS 1092 (-29.11%), JS 20-64 X JS 20-54 (-25.33%), PS 1583 X JS 20-29 (-23%), PS 1583 X Pb1 (-21.89%) and JS 20-29 X JS 20-55 (-5.89%) whereas over standard check, SL 688 nine crosses showed negative and significant residual heterosis with maximum value in RVS 200-1 X PS1092 (-42%) and minimum in (-20.27%) as presented in **Table 4.3.4b**.

4.3.5 Basal pod height

In F₂, the residual heterosis range over mid parent was -36.91 (PS 1583 X Bragg) to 82.68 (JS 20-29 X JS 20-55) per cent and eight crosses out of fourteen crosses had showed significant negative residual heterosis over mid parent Eleven crosses had showed negative significant residual heterosis over better parent and the range was from -42.86 (PS 1583 X Bragg) to 58.67 (JS 20-29 X JS 20-55) per cent while over standard check PS 19 nine crosses were found to be negatively significant heterotic, ranging from -29.44 (PS 1583 X Bragg) to -15.14 (PS 1583 X Pb1) per cent. However, none of the crosses had showed significant negative residual heterosis over standard check SL 688, as given in **Table 4.3.5a**.

In F₃, the range of residual heterosis over mid parent was -28 (PS 1583 X JS 335) to 49.89 (JS 20-63 X JS 97-52) per cent and seven crosses i.e. PS 1583 X JS 335 (-28%), PS 1042 X PS 1347 (-26.50%), JS 20-64 X JS 20-54 (-14.10%), PS 1583 X DS 12-5 (-12.79%), PS 1225 X PS 1347 (-10.45%), PS 1583 X Bragg (-9.47%) and PS 1583 X Pb1 (-2.86%) had shown significant negative residual heterosis over mid parent. Out of fourteen crosses, six crosses PS 1042 X PS 1347 (-31.29%), PS 1225 X PS 1347 (-24.05%), PS 1583 X Bragg (-21.69%), PS 1583 X DS 12-5 (-17.31%), PS 1583 X Pb1 (-12.94%) and RVS 200-1 X PS 1092 (-3.64%) were found to be significantly negative heterotic over better parent and the range was from -31.29 to 32.50 per cent. Range of residual heterosis over standard check PS 19 varied from 0 to 69.11 per cent and all the crosses had displayed significant positive residual heterosis, whereas over standard check, SL 688 eight crosses showed negative significant heterosis ranging from -18.92 (PS 1042 X PS 1347) to -10.38 (PS 1225 X PS 1347) per cent, as given in **Table 4.3.5b**.

Table 4.3.5a: Residual heterosis in percentage for basal pod height in F₂ generation of soybean

Sn no	Cross	MP	BP	SP1	SP2
1	PS 1583 x Pb1	-36.54**	-41.05**	-15.14*	32.20**
2	PS 1583 x JS 335	-34.85**	-35.04**	-19.31**	25.69*
3	PS 1583 x DS 12-5	-10.52*	-14.12**	6.05	65.20**
4	PS 1583 x JS 20-29	-0.70	-28.32**	-11.48	37.89**
5	PS 1583 x Bragg	-36.91**	-42.86**	-29.44**	9.92
6	PS 1584 x JS 20-69	-37.16**	-38.47**	-22.92**	20.07
7	PS 1584 x JS 20-41	-32.98**	-34.78**	-21.71**	21.95
8	PS 1042 x PS 1347	-28.44**	-32.15**	-4.38	48.94**
9	RVS 200-1 x PS 1092	11.59	-21.61**	-21.61**	22.11*
10	JS 20-63 x JS 97-52	14.11*	-1.57	4.70	63.09**
11	JS 20-69 x JS 20-59	-7.12	-27.75**	-9.50	40.98**
12	JS 20-64 x JS 20-54	27.04**	15.43	-23.49**	19.19
13	JS 20-29 x JS 20-55	82.68**	58.67**	-13.05	35.45**
14	PS 1225 x PS 1347	-21.04**	-36.90**	-19.31**	25.69*

MP=Mid-parent, BP=Better parent, SP1= Check variety PS 19, SP2= Check variety SL 688

**Significant at 1% level of probability, *Significant at 5% level of probability

Table 4.3.5b: Residual heterosis in percentage for basal pod height in F₃ generation of soybean

Sn no	Cross	MP	BP	SP1	SP2
1	PS 1583 x Pb1	-2.86*	-12.94*	54.78**	7.15**
2	PS 1583 x JS 335	-28.00**	-33.31	18.56**	-17.92*
3	PS 1583 x DS 12-5	-12.79**	-17.31**	47.00**	1.77**
4	PS 1583 x JS 20-29	-6.51	-31.81	21.22**	-16.08**
5	PS 1583 x Bragg	-9.47**	-21.69*	39.22**	-3.62
6	PS 1584 x JS 20-69	16.00**	16.00**	28.89**	-10.77
7	PS 1584 x JS 20-41	14.53**	7.76**	35.78**	-6.00*
8	PS 1042 x PS 1347	-26.50**	-31.29**	17.11**	-18.92**
9	RVS 200-1 x PS 1092	7.91**	-3.64**	0.00**	-30.77*
10	JS 20-63 x JS 97-52	49.89**	32.50**	47.22**	1.92**
11	JS 20-69 x JS 20-59	32.35**	17.08**	69.11**	17.08**
12	JS 20-64 x JS 20-54	-14.10**	-23.76	13.00**	-21.77
13	JS 20-29 x JS 20-55	38.58**	27.88**	23.33**	-14.62**
14	PS 1225 x PS 1347	-10.45**	-24.05*	29.44**	-10.38*

MP=Mid-parent, BP=Better parent, SP1= Check variety PS 19, SP2= Check variety SL 688

**Significant at 1% level of probability, *Significant at 5% level of probability

4.3.6 Number of nodes per plant

Out of 14 F_2 crosses, eight, two, three and one cross showed significant positive heterosis over mid parent, better parent, standard check (PS 19) and standard check (SL 688), respectively. Highest significant positive mid parent heterosis for number of nodes per plant was shown by cross PS 1225 X PS 1347 (32.54%) followed by PS 1042 X PS 1347 (28.52%), JS 20-29 X JS 20-55 (25.61%), PS 1583 X Bragg (15.84), PS 1583 X JS 335 (15.48), PS 1583 X Pb1(15.13) and PS 1583 X JS 20-29 (13.98). The range varied from -27.82 (JS 20-64 X JS 20-54) to 32.54 (PS 1225 X PS 1347) per cent. In case of better parent heterosis, the range was -28.33 (JS 20-64 X JS 20-54) to 23.03 per cent (PS 1042 X PS 1347). Two crosses, PS 1042 X PS 1347 (23.03%) and PS 1225 X PS 1347 (20.60%) showed significant positive heterosis over better parent. The range of residual heterosis over standard check, PS 19 was -28.30 (JS 20-64 X JS 20-54) to 26.89 (PS 1583 X Pb 1) per cent and for standard check, SL 688 range was from -32.67(RVS 200-1 X PS 1092) to 2.74 (JS 20-69 X JS 20-59). One cross, PS 1225 X PS 1347 exhibited significant and positive heterosis over mid parent, better parent and standard check, PS 19 in F_2 , as given in **Table 4.3.6a**.

In F_3 generation, the range of mid parent residual heterosis was -25.83 to 26.31 per cent. Three crosses had showed positive significant residual heterosis over mid parent which were JS 20-69 X JS 20-59 (26.31%), RVS 200-1 X PS 1092 (23.95%) and PS 1584X JS 20-41 (15.47%). The range of residual heterobeltiosis was -32.78 to 15.56 per cent and only two crosses, RVS 200-1 X PS 1092 (15.56%) and JS 20-69 X JS 20-59 (4.29%)were found positively significant heterotic. However, only one cross, JS 20-69 X JS 20-59 (9.40) was observed significant over standard check, PS 19 and none of the crosses was positive heterotic over SL 688. The range of residual standard heterosis over, PS 19 and SL 688 was -23.23 to 9.4% and -26.81 to 4.29 per cent, respectively, as given in **Table 4.3.6b**.

4.3.7 Number of primary branches per plant

In F_2 , only two crosses, PS 1583 X Bragg (24.92) and PS 1583 X Pb1 (38.34) exhibited significant positive mid parent residual heterosis. For better parent and standard check (PS 19 and SL 688), none of the crosses showed positive significant residual heterosis (**Table 4.3.7a**).

Table 4.3.6a: Residual heterosis in percentage for number of nodes per plant in F₂ generation of soybean

Sn no	Cross	MP	BP	SP1	SP2
1	PS 1583 x Pb1	15.13**	5.40	26.89**	11.38
2	PS 1583 x JS 335	15.48**	10.67	10.71	-2.82
3	PS 1583 x DS 12-5	7.94	4.17	4.21	-8.53
4	PS 1583 x JS 20-29	13.98*	6.00	6.04	-6.92
5	PS 1583 x Bragg	15.84**	8.50	8.55	-4.72
6	PS 1584 x JS 20-69	3.67	-11.95*	4.71	-8.09
7	PS 1584 x JS 20-41	10.66	-0.25	-17.13**	-27.26**
8	PS 1042 x PS 1347	28.52**	23.03**	0.88	-11.45
9	RVS 200-1 x PS 1092	-7.91	-22.23**	-23.30**	-32.67**
10	JS 20-63 x JS 97-52	6.09	0.72	10.55	-2.96
11	JS 20-69 x JS 20-59	12.64*	-1.58	17.05**	2.74**
12	JS 20-64 x JS 20-54	-27.82**	-28.33**	-28.30**	-37.07**
13	JS 20-29 x JS 20-55	25.61**	10.41	-4.92	-16.54**
14	PS 1225 x PS 1347	32.54**	20.60**	20.55**	5.82

MP=Mid-parent, BP=Better parent, SP1= Check variety PS 19, SP2= Check variety SL 688

**Significant at 1% level of probability, *Significant at 5% level of probability

Table 4.3.6b: Residual heterosis in percentage for number of nodes per plant in F₃ generation of soybean

Sn no	Cross	MP	BP	SP1	SP2
1	PS 1583 x Pb1	-25.83**	-32.78**	-21.32**	-25.00**
2	PS 1583 x JS 335	-12.69**	-17.15**	-21.21**	-24.90**
3	PS 1583 x DS 12-5	-12.39**	-14.62**	-18.80**	-22.59**
4	PS 1583 x JS 20-29	-3.57	-8.50**	-12.98**	-17.05**
5	PS 1583 x Bragg	-12.54**	-19.27**	-23.23**	-26.81**
6	PS 1584 x JS 20-69	-23.99**	-23.99**	-20.26**	-23.99**
7	PS 1584 x JS 20-41	15.47**	-6.03*	-1.43	-6.03*
8	PS 1042 x PS 1347	-5.52*	-15.81**	-5.52*	-9.94**
9	RVS 200-1 x PS 1092	23.95**	15.56**	4.32	-0.56
10	JS 20-63 x JS 97-52	-8.73**	-21.64**	-12.07**	-16.18**
11	JS 20-69 x JS 20-59	26.31**	4.29	9.40**	4.29
12	JS 20-64 x JS 20-54	-17.24**	-18.17**	-12.18**	-16.28**
13	JS 20-29 x JS 20-55	-13.48**	-23.83**	-14.52**	-18.51**
14	PS 1225 x PS 1347	-8.84**	-9.80**	3.40	-1.43

MP=Mid-parent, BP=Better parent, SP1= Check variety PS 19, SP2= Check variety SL 688

**Significant at 1% level of probability, *Significant at 5% level of probability

Table 4.3.7a: Residual heterosis in percentage for number of primary branches per plant in F₂ generation of soybean

Sn no	Cross	MP	BP	SP1	SP2
1	PS 1583 x Pb1	38.34**	14.24	-2.62	8.43
2	PS 1583 x JS 335	4.56	-15.75**	-23.52**	-14.84
3	PS 1583 x DS 12-5	1.85	-17.44**	-26.63**	-18.30**
4	PS 1583 x JS 20-29	2.46	-17.56**	-24.86**	-16.32**
5	PS 1583 x Bragg	24.92**	-0.17**	-7.51	2.99
6	PS 1584 x JS 20-69	-34.40	-44.55**	-27.08**	-18.80**
7	PS 1584 x JS 20-41	-3.91	-9.43**	-7.07	3.48
8	PS 1042 x PS 1347	-11.12	-18.08**	-30.19**	-22.27**
9	RVS 200-1 x PS 1092	-14.23	-17.65	-23.74**	-15.09
10	JS 20-63 x JS 97-52	-16.93**	-35.08**	-23.08**	-14.34
11	JS 20-69 x JS 20-59	-15.55**	-31.70**	-10.18	0.01
12	JS 20-64 x JS 20-54	-10.92	-23.45**	-9.29	1.01
13	JS 20-29 x JS 20-55	-21.82**	-24.39**	-31.08**	-23.26**
14	PS 1225 x PS 1347	-4.35	-6.50	-16.85**	-7.41

MP=Mid-parent, BP=Better parent, SP1= Check variety PS 19, SP2= Check variety SL 688

**Significant at 1% level of probability, *Significant at 5% level of probability

Table 4.3.7b: Residual heterosis in percentage for number of primary branches per plant in F₃ generation of soybean

Sn no	Cross	MP	BP	SP1	SP2
1	PS 1583 x Pb1	28.14*	12.13	-3.96	22.21
2	PS 1583 x JS 335	39.28**	26.57**	-0.54	26.57*
3	PS 1583 x DS 12-5	20.03	1.50	-5.67	20.03
4	PS 1583 x JS 20-29	29.29*	9.33*	1.61	29.29*
5	PS 1583 x Bragg	33.73**	21.53**	-4.50	21.53
6	PS 1584 x JS 20-69	-2.72	-15.54**	14.67	45.91**
7	PS 1584 x JS 20-41	12.35	0.32**	0.32	27.66*
8	PS 1042 x PS 1347	12.65	-7.77**	-27.52**	-7.77
9	RVS 200-1 x PS 1092	-13.88	-13.88**	-26.23*	-6.13
10	JS 20-63 x JS 97-52	-20.24*	-20.24**	-20.24*	1.50
11	JS 20-69 x JS 20-59	0.60	-20.58	7.82	37.19**
12	JS 20-64 x JS 20-54	14.97	-11.52**	-17.77	4.63
13	JS 20-29 x JS 20-55	3.25	-4.72*	-11.46	12.67
14	PS 1225 x PS 1347	6.83	-4.60	-4.60	21.39

MP=Mid-parent, BP=Better parent, SP1= Check variety PS 19, SP2= Check variety SL 688

**Significant at 1% level of probability, *Significant at 5% level of probability

In F_3 , out of 14 cross only four crosses, PS 1583 X JS 335 (39.28%), PS 1583 X Bragg (33.73%), PS 1583X JS 20-29 (29.29%) and PS 1583 X Pb1 (28.14%) showed significant positive residual heterosis over mid parent. For better parent, the range of residual heterosis was -20.58 to 26.57 per cent and three crosses displayed positive significant heterobeltiosis which were PS 1583 X JS 335 (26.57%), PS 1583 X Bragg (21.53%) and PS 1583 X JS 20-29 (9.33%). None of the crosses were found to be significant for positive residual heterosis over standard check PS 19 while five crosses, PS 1584X JS 20-69 (45.91%), JS20-69 X JS 20-59 (37.1%), PS 1583 X JS 20-29 (29.29%), PS 1584 X JS 20-41 (27.66%) and PS 1583 X JS 335 (26.57%) exhibited positive significant residual heterosis over standard check SL 688 as given in **Table 4.3.7b**.

4.3.8 Number of pods per plant

Out of 14 F_2 s four crosses showed significant positive heterosis over mid parent. The range of heterosis over mid parent for number of pods per plant was -42.10 (RVS 200-1 X PS 1092) to 17.10 per cent (PS 1583 X Bragg). Higher values of mid parent heterosis signified that these crosses were superior for number of pods per plant. The range of better parent heterosis was -51.63 (RVS 200-1 PS 1092) to 16.28 per cent (PS 1583 X Bragg) and four crosses showed significant positive residual heterosis over better parent. None of the crosses showed positive significant residual heterosis over both the standard checks as shown in **Table 4.3.8a**.

In F_3 generation, six crosses, PS 1584 X JS 20-41(59.23%), PS 1583 X JS 20-29 (24.85%), JS 20-29 X JS 20-55 (15.13%), PS 1584X JS 20-69 (13.04%), PS 1583 X DS 12-5 (9.31%) and JS 20-69 X JS 20-59 (4.35%) showed significant positive residual heterosis for mid parent and three crosses, PS 1584 X JS 20-41 (16.73%), PS 1584 X JS 20-69 (12.83%) and PS 1583 X JS 20-29 (3.63%) showed significant and positive residual heterosis over better parent. The range of mid parent heterosis was -34.22 to 59.23 per cent while for better parent the range was -45.78 to 31.13 per cent as shown in **Table 4.3.8b**. None of the crosses had shown significant positive residual heterosis against the standard check; PS 19 while two crosses PS 1584 X JS 20-41(.97%) and PS 1584 X JS 20-69 (2.44%) had showed positive residual heterosis over standard check SL 688.

Table 4.3.8a : Residual heterosis in percentage for number of pods per plant in F₂ generation of soybean

Sn no	Cross	MP	BP	SP1	SP2
1	PS 1583 x Pb1	-19.65**	-28.92**	-49.98**	-36.39**
2	PS 1583 x JS 335	-28.43**	-42.38**	-48.88**	-34.99**
3	PS 1583 x DS 12-5	-25.31**	-34.24**	-53.23**	-40.52
4	PS 1583 x JS 20-29	13.25**	12.97**	-38.54**	-21.84**
5	PS 1583 x Bragg	17.10**	16.28**	-37.05**	-19.95**
6	PS 1584 x JS 20-69	-16.67**	-25.49**	-47.56**	-33.32**
7	PS 1584 x JS 20-41	-10.46**	-25.67**	-47.69**	-33.48**
8	PS 1042 x PS 1347	-15.35**	-18.22**	-52.77**	-39.95**
9	RVS 200-1 x PS 1092	-42.10**	-51.63**	-59.56**	-48.58**
10	JS 20-63 x JS 97-52	13.70*	5.33**	-46.15**	-31.53*
11	JS 20-69 x JS 20-59	-6.80	-11.35**	-50.81**	-37.45**
12	JS 20-64 x JS 20-54	-30.09**	-39.29**	-58.37**	-47.06**
13	JS 20-29 x JS 20-55	11.87**	2.16**	-44.42**	-29.33**
14	PS 1225 x PS 1347	-13.48**	-30.74**	-33.45**	-15.37

MP=Mid-parent, BP=Better parent, SP1= Check variety PS 19, SP2= Check variety SL 688

**Significant at 1% level of probability, *Significant at 5% level of probability

Table 4.3.8b: Residual heterosis in percentage for number of pods per plant in F₃ generation of soybean

Sn no	Cross	MP	BP	SP1	SP2
1	PS 1583 x Pb1	-10.80**	-25.23**	-42.24**	-38.50**
2	PS 1583 x JS 335	-12.15**	-30.59**	-37.49**	-33.43**
3	PS 1583 x DS 12-5	9.31**	-11.85**	-24.84**	-19.97**
4	PS 1583 x JS 20-29	24.85**	3.63**	-17.96**	-12.64**
5	PS 1583 x Bragg	43.46	31.13	-31.49**	-27.05**
6	PS 1584 x JS 20-69	13.04**	12.83**	-3.80**	2.44**
7	PS 1584 x JS 20-41	59.23**	16.73**	-0.48**	5.97**
8	PS 1042 x PS 1347	-11.28**	-19.37**	-47.53**	-44.13**
9	RVS 200-1 x PS 1092	-34.22**	-45.78**	-61.42**	-58.92**
10	JS 20-63 x JS 97-52	-17.13**	-21.34**	-40.50**	-36.64**
11	JS 20-69 x JS 20-59	4.35**	-15.73**	-28.42**	-23.78**
12	JS 20-64 x JS 20-54	-11.09**	-33.02**	-19.92**	-14.73**
13	JS 20-29 x JS 20-55	15.13**	-1.89**	-22.32**	-17.29**
14	PS 1225 x PS 1347	-10.99**	-19.79**	-34.95**	-30.74**

MP=Mid-parent, BP=Better parent, SP1= Check variety PS 19, SP2= Check variety SL 688

**Significant at 1% level of probability, *Significant at 5% level of probability

4.3.9 Number of seeds per pod

In F₂ generation, out of 14 crosses no cross had exhibited positive significant residual heterosis over mid parent, better parent and standard checks (PS 19 and SL 688). Mostly the significant values were in negative direction and therefore, are not suitable for the further research purpose, as shown in **Table 4.3.9a**.

In F₂ generation, four crosses, JS 20-69 X JS 20-59 (4.18%), PS 1583 X Bragg (3.84%), PS 1042 X PS 1347(2.18%) and PS 1583X DS 12-5 (0.82%) had showed positive residual heterosis over mid parent. None of the crosses showed significant values for residual heterosis over better parent, while for standard check PS 19 eleven crosses showed positive residual heterosis, maximum in PS 1584 X JS 20-69 (18.39%) and minimum in JS 20-64 X JS 20-54 (4.93%). However, for standard check, SL 688 only one cross, PS 1584 X JS 20-69 (7.32%) showed positive residual heterosis as presented in **Table 4.3.9b**.

4.3.10 Seed yield per plant

In F₂ generation, the range of residual heterosis was from -63.58 (JS 20-64 X JS 20-54) to -3.91 (PS 1583 X Bragg) for mid parent heterosis, from -67.87 (JS 20-64 X JS 20-54) to -5.78 (PS 1042 X PS 1347) for heterobeltiosis, from -66.59 (JS 20-64 x JS 20-54) for residual heterosis over standard check PS 19 and from -66.59 (JS 20-64 x JS 20-54) for residual heterosis over standard check SL 688. Out of fourteen crosses, no cross had shown significant positive residual heterosis value over mid parent, better parent and standard checks (PS 19 and SL 688), as presented in **Table 4.3.10a**.

However in F₃, four crosses (PS 1584 X JS 20-41, PS 1583 X Bragg, PS 1584 X JS 20-69 and PS 1583 X JS 202-9) and two crosses (PS 1584 X JS 20-41 and PS 1583 X Bragg) exhibited significant positive residual heterosis value over mid parent and better parent, respectively. Apart from these, only one cross, PS 1584 X JS 20-69 had shown significant positive residual heterosis value over standard checks PS 19 and SL 688 which had value of residual heterosis over PS 19 as 6.03 per cent and for SL 688 as 8.88 per cent, as presented in **Table 4.3.10b**.

Table 4.3.9a: Residual heterosis in percentage for number of seeds per pod in F₂ generation of soybean

Sn no	Cross	MP	BP	SP1	SP2
1	PS 1583 x Pb1	-10.87*	-14.11*	5.92	-4.18
2	PS 1583 x JS 335	-23.89**	-25.87**	-10.58	-19.11**
3	PS 1583 x DS 12-5	-17.55**	-20.78**	-9.42	-18.05**
4	PS 1583 x JS 20-29	-17.51	-18.15**	-4.93	-14.00*
5	PS 1583 x Bragg	-3.20**	-7.37	5.92	-4.18
6	PS 1584 x JS 20-69	-20.66**	-23.46**	-2.87	-12.13
7	PS 1584 x JS 20-41	-7.34**	-16.50**	-1.52	-10.91
8	PS 1042 x PS 1347	-8.38**	-11.50	-0.99	-10.43
9	RVS 200-1 x PS 1092	-15.49**	-19.57**	0.81	-8.80
10	JS 20-63 x JS 97-52	-11.50**	-15.93**	1.79	-7.91
11	JS 20-69 x JS 20-59	-12.69	-17.31**	4.93	-5.07
12	JS 20-64 x JS 20-54	-5.41	-12.89*	-1.17	-10.59
13	JS 20-29 x JS 20-55	-10.75	-12.29	2.06	-7.67
14	PS 1225 x PS 1347	-6.42	-8.67	1.97	-7.75

MP=Mid-parent, BP=Better parent, SP1= Check variety PS 19, SP2= Check variety SL 688

**Significant at 1% level of probability, *Significant at 5% level of probability

Table 4.3.9b: Residual heterosis in percentage for number of seeds per pod in F₃ generation of soybean

Sn no	Cross	MP	BP	SP1	SP2
1	PS 1583 x Pb1	-11.59**	-14.45**	0.90	-8.54
2	PS 1583 x JS 335	-12.88**	-13.21**	3.14	-6.50**
3	PS 1583 x DS 12-5	0.82**	-6.27**	10.54**	0.20
4	PS 1583 x JS 20-29	-12.80**	-14.86**	5.38*	-4.47*
5	PS 1583 x Bragg	3.84**	-7.41**	9.19**	-1.02
6	PS 1584 x JS 20-69	-6.71**	-9.90**	18.39**	7.32**
7	PS 1584 x JS 20-41	-5.62**	-8.46**	9.19**	-1.02
8	PS 1042 x PS 1347	2.18	-11.84**	5.16*	-4.67*
9	RVS 200-1 x PS 1092	-16.73**	-9.96**	-0.67	-9.96**
10	JS 20-63 x JS 97-52	-1.46**	-4.07	5.83*	-4.07*
11	JS 20-69 x JS 20-59	4.18**	-8.79**	11.66**	1.22
12	JS 20-64 x JS 20-54	-12.20	-22.00**	4.93*	-4.88*
13	JS 20-29 x JS 20-55	-3.66	-14.13**	6.28**	-3.66
14	PS 1225 x PS 1347	-8.53	-11.28**	5.83*	-4.07*

MP=Mid-parent, BP=Better parent, SP1= Check variety PS 19, SP2= Check variety SL 688

**Significant at 1% level of probability, *Significant at 5% level of probability

Table 4.3.10a: Residual heterosis in percentage for seed yield per plant in F₂ generation of soybean

Sn no	Cross	MP	BP	SP1	SP2
1	PS 1583 x Pb1	-46.46**	-52.41**	-51.92**	-50.58**
2	PS 1583 x JS 335	-41.15**	-49.43**	-44.73**	-44.73**
3	PS 1583 x DS 12-5	-16.31**	-38.60**	-51.75**	-51.75**
4	PS 1583 x JS 20-29	-24.10**	-29.45**	-35.48**	-35.48**
5	PS 1583 x Bragg	-3.91	-10.84*	-29.94**	-29.94**
6	PS 1584 x JS 20-69	-15.51**	-34.93**	-25.92**	-25.92**
7	PS 1584 x JS 20-41	-19.61**	-25.31**	-54.02**	-54.02**
8	PS 1042 x PS 1347	-4.02	-5.78	-50.87**	-50.87**
9	RVS 200-1 x PS 1092	-47.16**	-59.67**	-66.45**	-66.45**
10	JS 20-63 x JS 97-52	-48.76**	-52.11**	-52.39**	-52.39**
11	JS 20-69 x JS 20-59	-37.52**	-48.35**	-41.20**	-41.20**
12	JS 20-64 x JS 20-54	-63.58**	-67.87**	-66.59**	-66.59**
13	JS 20-29 x JS 20-55	-26.68**	-51.54**	-55.68**	-55.68**
14	PS 1225 x PS 1347	-4.46	-27.74**	-26.58**	-26.58**

MP=Mid-parent, BP=Better parent, SP1= Check variety PS 19, SP2= Check variety SL 688

**Significant at 1% level of probability, *Significant at 5% level of probability

Table 4.3.10b: Residual heterosis in percentage for number of seeds yield per plant in F₃ generation of soybean

Sn no	Cross	MP	BP	SP1	SP2
1	PS 1583 x Pb1	-42.50**	-47.01**	-56.12**	-54.94**
2	PS 1583 x JS 335	-43.16**	-54.80**	-46.53**	-45.1**
3	PS 1583 x DS 12-5	-21.20*	-32.62**	-33.73**	-31.95**
4	PS 1583 x JS 20-29	5.63**	-7.94**	-13.49**	-11.17**
5	PS 1583 x Bragg	12.41**	4.32*	-27.14**	-25.19**
6	PS 1584 x JS 20-69	9.80**	-17.41**	6.03**	8.88**
7	PS 1584 x JS 20-41	49.06**	44.87**	-0.62**	2.05
8	PS 1042 x PS 1347	-21.17**	-22.69**	-49.01**	-47.64**
9	RVS 200-1 x PS 1092	-59.25**	-69.61**	-71.18**	-70.41**
10	JS 20-63 x JS 97-52	-23.92**	-29.08**	-37.01**	-35.32**
11	JS 20-69 x JS 20-59	-18.67**	-43.19**	-27.06**	-25.10**
12	JS 20-64 x JS 20-54	-17.20**	-37.70**	-29.98**	-28.10**
13	JS 20-29 x JS 20-55	-12.96**	-28.05**	-32.39**	-30.57**
14	PS 1225 x PS 1347	-18.68**	-33.33**	-33.91**	-32.14**

MP=Mid-parent, BP=Better parent, SP1= Check variety PS 19, SP2= Check variety SL 688

**Significant at 1% level of probability, *Significant at 5% level of probability

4.3.11 100-seed weight

Out of 14 crosses, none of the crosses showed significant positive residual heterosis over mid parent, better parent and standard check PS19. Only one cross, PS 1584 X JS 20-69 (2.90%) showed positive residual heterosis over standard check, SL 688, as presented in **Table 4.3.11a**.

Similarly, in F₃ generation only three crosses, RVS 200-1 X PS 1092 (21.61%), JS 20-64 X JS 20-54 (10.14%) and PS 1584 X JS 20-41 (0.91%) exhibited positive residual heterosis over mid parent, while none of the cross displayed positive significant residual heterosis over better parent and standard check SL 688. However, for standard checks PS 19 two crosses were found significantly heterotic in positive direction which were JS 20-64 X JS 20-54 (23.94%) and PS 1584 X JS 20-41 (5.22%), as given in **Table 4.3.11b**.

4.3.12 Harvest index

In F₂ generation, the range of residual heterosis over mid parent was -50.03 (JS 20-64 X JS 20-54) to 29.58 (PS 1584 X JS 20-69) per cent. Three crosses, PS 1584 X JS 20-69 (29.58%), PS 1583 X DS 12-5 (26.92%) and PS 1042 X PS 1347 (27.50%) showed positive residual heterosis over mid parent for harvest index as depicted in **Table 4.3.12a**. The range of residual heterosis over better parents was -52.48 (JS 20-69 X JS 20-59) to 25.99 (PS 1042 X PS 1347) per cent and only one cross, PS 1042 X PS 1347 had shown significant positive residual heterosis over better parent. For standard check PS 19, the range of residual heterosis was -28.45 (PS 1584 X JS 20-41) to 85.25 (PS 1584 X JS 20-69) per cent. Out of 14 crosses only three crosses, PS 1584 X JS 20-69 (85.25%), PS 1225 X PS 1347 (31.29%) and PS 1583 X JS 20-29 (24.83%) had shown significant positive residual heterosis over PS 19. Over standard check SL 688, two crosses PS 1584 X JS 20-69 (85.25%) and PS 1225 X PS 1347 (31.29%) exhibited significant positive residual heterosis.

In F₃ generation, none of the crosses displayed significant positive residual heterosis over mid parent and better parent. However, two crosses and three crosses in standard check, PS 19 and SL 688, showed significant positive residual heterosis. For PS 19, the two crosses were PS 1583 X JS 20-29 (20.67%) and PS 1584 X JS 20-69 (12.08%) while for SL 688, significant residual heterosis in positive direction again displayed by PS 1583 X JS 20-29 (21.77%), PS 1584 X JS 20-69 (3.11%) and PS 1583 X Bragg (4.41%), as shown in **Table 4.3.12b**.

Table 4.3.11a: Residual heterosis in percentage for 100 seed weight in F₂ generation of soybean

Sn no	Cross	MP	BP	SP1	SP2
1	PS 1583 x Pb1	-26.82**	-31.07**	-26.35**	-29.66**
2	PS 1583 x JS 335	-18.70**	-19.29**	-13.75**	-13.75**
3	PS 1583 x DS 12-5	-15.92**	-26.71**	-21.69**	-21.69**
4	PS 1583 x JS 20-29	-4.87	-5.71	0.75	0.75
5	PS 1583 x Bragg	2.28	-5.84	0.62	0.62
6	PS 1584 x JS 20-69	2.9	2.47	2.9	2.90**
7	PS 1584 x JS 20-41	-5.16	-6.14	-6.46**	-6.46**
8	PS 1042 x PS 1347	-4.55	-6.03	-9.49**	-9.49**
9	RVS 200-1 x PS 1092	-9.78**	-16.26**	-19.78	-19.78*
10	JS 20-63 x JS 97-52	-0.73	-1.12	-2.52	-2.52
11	JS 20-69 x JS 20-59	-2.49	-14.79**	4.16	4.16
12	JS 20-64 x JS 20-54	-14.28**	-19.72**	-10.57**	-10.57**
13	JS 20-29 x JS 20-55	-8.50**	-18.43**	-14.27**	-14.27**
14	PS 1225 x PS 1347	-2.46	-6.28	-9.73**	-9.73**

MP=Mid-parent, BP=Better parent, SP1= Check variety PS 19, SP2= Check variety SL 688

**Significant at 1% level of probability, *Significant at 5% level of probability

Table 4.3.11b: Residual heterosis in percentage for number of 100-seed weight in F₃ generation of soybean

Sn no	Cross	MP	BP	SP1	SP2
1	PS 1583 x Pb1	-24.82**	-26.57**	-9.11	-29.60**
2	PS 1583 x JS 335	-26.47	-29.17*	-12.33*	-32.10**
3	PS 1583 x DS 12-5	-38.02**	-39.58**	-25.22	-42.08**
4	PS 1583 x JS 20-29	-16.87**	-24.78	-6.89**	-27.88
5	PS 1583 x Bragg	-17.25**	-26.80	-9.39**	-29.82
6	PS 1584 x JS 20-69	-1.62**	-5.88**	-5.67**	-26.94
7	PS 1584 x JS 20-41	0.91**	-10.07	5.22**	-18.50
8	PS 1042 x PS 1347	-11.65*	-16.27	-5.67**	-26.94*
9	RVS 200-1 x PS 1092	21.61**	-0.81	8.78	-15.75**
10	JS 20-63 x JS 97-52	-12.69**	-16.00**	-11.33**	-31.33
11	JS 20-69 x JS 20-59	-4.23**	-10.81**	-10.61**	-30.77
12	JS 20-64 x JS 20-54	6.14	5.53	23.94*	-4.00*
13	JS 20-29 x JS 20-55	10.14*	8.43	8.67	-15.83**
14	PS 1225 x PS 1347	-19.73	-22.98	-13.22**	-32.79*

MP=Mid-parent, BP=Better parent, SP1= Check variety PS 19, SP2= Check variety SL 688

**Significant at 1% level of probability, *Significant at 5% level of probability

Table 4.3.12a: Residual heterosis in percentage for harvest index in F₂ generation of soybean

Sn no	Cross	MP	BP	SP1	SP2
1	PS 1583 x Pb1	-49.71**	-63.21**	-17.54	-24.52**
2	PS 1583 x JS 335	-26.47**	-16.50*	0.90	0.90
3	PS 1583 x DS 12-5	26.92**	12.63	17.59	17.59
4	PS 1583 x JS 20-29	4.62	-7.01	24.83**	24.83
5	PS 1583 x Bragg	-20.59**	-32.90**	1.51	1.51
6	PS 1584 x JS 20-69	29.58**	-6.62**	85.25**	85.25**
7	PS 1584 x JS 20-41	-28.45**	-36.39**	-28.45**	-28.45**
8	PS 1042 x PS 1347	27.50**	25.99*	3.29	3.29
9	RVS 200-1 x PS 1092	-35.29**	-35.30**	-25.36**	-25.36**
10	JS 20-63 x JS 97-52	-38.70**	-39.42**	-11.58	-11.58*
11	JS 20-69 x JS 20-59	-47.91**	-52.48**	-5.73	-5.73
12	JS 20-64 x JS 20-54	-50.03**	-50.66**	-23.11**	-23.11**
13	JS 20-29 x JS 20-55	-13.80	-38.16**	-16.99	-16.99**
14	PS 1225 x PS 1347	10.01	-17.24**	31.29**	31.29*

MP=Mid-parent, BP=Better parent, SP1= Check variety PS 19, SP2= Check variety SL 688

**Significant at 1% level of probability, *Significant at 5% level of probability

Table 4.3.12b: Residual heterosis in percentage for number of harvest index in F₃ generation of soybean

Sn no	Cross	MP	BP	SP1	SP2
1	PS 1583 x Pb1	-36.40**	-53.02**	-13.25**	-12.46**
2	PS 1583 x JS 335	-23.93**	-33.90**	-9.30**	-8.47**
3	PS 1583 x DS 12-5	-34.01**	-50.02**	-1.68	-0.78
4	PS 1583 x JS 20-29	5.84**	-4.80**	20.67**	21.77**
5	PS 1583 x Bragg	-6.31**	-13.49**	3.47	4.41*
6	PS 1584 x JS 20-69	0.64	-17.22**	12.08**	13.11**
7	PS 1584 x JS 20-41	-10.56**	-26.82**	0.42	1.34
8	PS 1042 x PS 1347	-3.12*	-10.67**	-5.09*	-4.22*
9	RVS 200-1 x PS 1092	-36.82**	-39.95**	-24.91**	-24.22**
10	JS 20-63 x JS 97-52	-17.17**	-18.49**	0.84	1.77
11	JS 20-69 x JS 20-59	-20.02**	-30.91**	-6.45**	-5.59**
12	JS 20-64 x JS 20-54	-17.33**	-29.97**	3.76	4.71*
13	JS 20-29 x JS 20-55	-30.77**	-34.01**	-16.36**	-15.59**
14	PS 1225 x PS 1347	-23.06**	-38.12**	-8.78**	-7.94**

MP=Mid-parent, BP=Better parent, SP1= Check variety PS 19, SP2= Check variety SL 688

**Significant at 1% level of probability, *Significant at 5% level of probability

Table 4.3a : Summary of residual heterosis for various quantitative characters over mid parent in F₂ and F₃ generation of soybean

SI. No	Character	Generation	No. of crosses significantly superior	Cross combination showing significant residual heterosis over mid parent in desired direction in F ₂ and F ₃
1	Days to 50% flowering	F ₂	4	PS 1583 X DS 12-5, PS 1584 X JS 20-69, PS 1225 X PS 1347 and JS 20-29 X JS 20-55
		F ₃	8	JS 20-69 X JS 20-59, JS 20-63 X JS 97-52, JS 20-64 X JS 20-54 , PS 1042 X PS 1347, PS 1584 X JS 20-69, PS 1584 X JS 20-41, PS 1583X DS 12-5 and RVS 200-1 X PS 1092
2	Dry matter weight per plant (g)	F ₂	3	JS 20-69 X JS 20-59, PS 1583 X Bragg and PS 1584 X JS 20-41
		F ₃	9	PS 1583 X DS 12-5, PS 1584 X JS 20-69, JS 20-64 X JS 20-54 and JS 20-69 X JS 20-59
3	Basal node height (cm)	F ₂	1	RVS 200-1 X PS 1092
4	Basal Pod Height (cm)	F ₂	7	JS 20-29 X JS 20-55, JS 20-64 X JS 20-54 and JS 20-63 X JS 97-52
		F ₃	6	JS 20-63 X JS 97-52, JS 20-29 X JS 20-55, JS 20-69 X JS20-59, PS 1584 X JS 20-69, PS 2584 X JS 20-41 and RVS 200-1 X PS 1092
5	Number of nodes per plant	F ₂	8	PS 1225 X PS 1347, PS 1042 X PS 1347, JS 20-29 X JS 20-55, Ps 1593 X Bragg, PS 1583 X JS 335, PS 1583 X Pb1, PS 1583 X JS 20-29 and JS 20-69 x JS 20-59
		F ₃	3	JS 20-9 X JS 20-59, RVS 200-1 X PS 1092 and PS 1584 X JS 20-41
6	Number of primary branches per plant	F ₂	2	PS 1583 X Pb1 and PS 1583 X Bragg
		F ₃	4	PS 1583 X JS 335, PS 1583 X Bragg, PS 1583 X JS 20-29 and PS 1583 X Pb1
7	Number of pods per plant	F ₂	4	PS 1583 X Bragg, JS 20-63 X JS 97-52, PS 1583 X JS 20-29 and JS 20-29 X JS 20-55
		F ₃	6	PS 1584 X JS 20-41, PS 1583 X JS 20-29, JS 20-29 X JS 20-55, PS 1584 X JS 20-69, PS 1583 X DS12-5 and JS 20-69 X JS20-59
8	Number of seeds per pod	F ₃	4	JS 20-69 X JS 20-59, PS 1583 X Bragg, PS 1042 X PS 1347 and PS 1583 X DS12-5
9	Seed yield per plant (g)	F ₃	4	PS 1584 X JS 20-41, PS 1584 X JS 20-69, PS 1583 X Bragg and PS 1583 X JS 20-29
10	100-seed weight (g)	F ₃	3	RVS 200-1 X PS 1092, JS 20-64 X JS 20-54 and PS 1584 X JS 20-41
11	Harvest index (%)	F ₂	3	PS 1584 X JS 20-69, PS 1042 X PS 1347 and PS 1583 X DS 12-5
		F ₃	1	PS 1583 X JS 20-29

Table 4.3b: Summary of residual heterosis for various quantitative characters over better parent in F₂ and F₃ generation of soybean

Sl. No	Character	Generation	No. of crosses significantly superior	Cross combination showing significant residual heterosis over better parent in desired direction in F ₂ and F ₃
1	Days to 50% Flowering	F ₂	3	PS 1583 X DS 12-5, PS 1584 X JS 20-69 and PS 1225 X PS 1347
		F ₃	5	JS 20-69 X JS 20-59, JS 20-63 X JS 97-52 , JS 20-64 X JS 20-54, PS 1042 X PS 1347 and PS 1584 X JS 20-69
2	Dry matter weight per plant (g)	F ₂	4	PS 1583 X Bragg, PS 1584 X JS 21-41, JS 20-69 X JS 20-59 and PS 1582 X PB 1
		F ₃	4	PS 1584 X JS 20-41, JS 20-29 X JS 20-55, PS 1583X Bragg and PS 1225 X PS 137
3	Basal pod height (cm)	F ₂	1	JS 20-29 X JS 20-55
		F ₃	5	JS 20-63 X JS 97-52, S 20-29 X JS 20-55, PS 1584 X JS 20-69, JS 20-69 X JS 20-59 and PS 1584 X JS 20-41.
4	Number of nodes per plant	F ₂	2	PS 1042 X PS 1347 and PS 1225 X PS 1347
		F ₃	2	RVS 200-1 X PS 1092and JS 20-69 X JS 20-59
5	Number of primary branches per plant	F ₃	3	PS 1583 X JS 335, PS 1583 X Bragg and PS 1583 X JS 20-29
6	Number of pods per plant	F ₂	4	PS 1583 x Bragg, PS 1583 X JS 20-29, JS 20-63 X JS 97-52 and JS 20-29 X JS 20-55
		F ₃	3	PS 1584 X JS 20-41, PS 1584 X JS 20-69 and pS 1583 X JS 20-29
7	Seed yield per plant(g)	F ₃	2	PS 1584 X JS 20-41 and PS 1583 X Bragg
8	Harvest index (%)	F ₂	1	PS 1042 X PS 1347

Table 4.3c: Summary of residual heterosis for various quantitative characters over standard check PS 19 in F₂ and F₃ generation of soybean

SI No	Character	Generation	No. of crosses significantly superior	Cross combination showing significant residual heterosis over standard check PS 19 in desired direction in F ₂ and F ₃
1	Days to 50% flowering	F ₃	14	JS 20-69 X JS 20-59, JS 20-63 X JS 97-52, JS 20-64 X JS 20-54, RVS 200-1 X PS 1092, PS 1042 X PS 1347, PS 1584 X JS 20-69, PS 1584 X JS 20-41, PS 1583 X Bragg and PS 1583 X DS 12-5
2	Basal node height (cm)	F ₃	5	RVS 200-1 X PS 1092, JS 20-64 X JS 20-54, PS 1583 X JS 20-29, PS 1583 X Pb1 and JS 20-29 X JS20-55
3	Number of nodes per plant	F ₂	3	PS 1583 X Pb1, PS 1225 X PS 1347 and JS 20-69 X JS 20-59
		F ₃	1	JS 20-69 X JS 20-59
4	Number of seeds per pod	F ₃	11	PS 1583 X DS 12-5, PS 1583 X JS 20-29, PS 1583 X Bragg, PS 1584 X JS 20-69, PS 1584 X JS 20-41, PS 1042 X PS 1347, JS 20-63 X JS 97-52, JS 20-69 X JS 20-59, JS 20-64 X JS 20-54, JS 20-29 X JS 20-55 and PS 1225 X PS 1347
5	Seed yield per plant (g)	F ₃	1	PS 1584X JS 20-69
6	100-seed weight (g)	F ₃	2	JS 20-64 X JS 20-54 and PS 1584 X JS 20-41
7	Harvest index (%)	F ₂	3	PS 1584 X JS 20-69, PS 1225 X PS 1347 and PS 1584 X JS 20-41
		F ₃	2	PS 1583 X JS 20-29 and PS 1584 X JS 20-69

Table 4.3d: Summary of residual heterosis for various quantitative characters over standard check SL 688 in F₂ and F₃ generation of soybean

SI No	Character	Generation	No. of crosses significantly superior	Cross combination showing significant residual heterosis over standard check SL688 in desired direction in F ₂ and F ₃
1	Days to 50% flowering	F ₃	14	JS 20-69 X JS 20-59, JS 20-63 X JS 97-52, JS 20-64 X JS 20-54, RVS 200-1 X PS 1092, PS 1042 X PS 1347, PS 1584 X JS 20-69, PS 1584 X JS 20-41, PS 1583 X Bragg and PS 1583 X DS 12-5
2	Basal node height (cm)	F ₃	9	RVS 200-1 X PS 1092, PS 1042 X PS 1347, JS 20-63 X JS 97-52, JS 20-64 X JS 20-54, PS 1583 X JS 20-29, PS 1584 X JS 20-69, JS 20-69 X JS 20-59, PS 1583 X Bragg, PS 1584 X JS 20-41
3	Basal pod height (cm)	F ₃	4	JS 20-69 X JS 20-59, PS 1583 X Pb1, JS 20-63 X JS 97-52 and PS 1583 X DS12-5
4	Number of nodes per plant	F ₂	1	JS 20-64 X JS 20-54
5	Number of primary branches per plant	F ₃	5	PS 1584 X JS 20-69, JS 20-69 X JS 20-59, PS 1583 X JS 20-29, PS 1584 X JS 20-41 and PS 1583 X JS 335
6	Number of pods per plant	F ₃	2	PS 1584 X JS20-41 and PS 1584X JS 20-69
7	Number of seeds per pod	F ₃	1	PS 1584 X JS 20-69
8	Seed yield per plant (g)	F ₃	1	PS 1584 X JS 20-69
9	100-seed weight (g)	F ₂	1	PS 1584 X JS 20-69
10	Harvest index (%)	F ₂	2	PS 1584 X JS 20-69 and PS 1225 X PS 1347
		F ₃	3	PS 1583 X JS 20-29, PS 1584X JS 20-69 and PS 1583 X Bragg

Heterosis is the phenomenon of the superiority of F_1 over their parents. The magnitude as well as the direction of the heterosis is of profound importance in the improvement of self-pollinated crops through various breeding procedures. Heterosis had also been suggested as an aid in developing pure line varieties (**Powers, 1952**) where considerable additive gene effects are present and the crosses with such effects, most likely give better segregants in later generations. In the present study, estimates of heterobeltiotic response as well as responses relative to standard variety (PS 19 and SL 688) were computed for all the characters in different cross combinations.

The present investigation on the magnitude of residual heterosis over mid, better and standard checks had been studied for twelve yield and yield related characters in 14 F_2 and F_3 crosses. Among the 14 F_2 and F_3 crosses studied for days to 50% flowering, maximum significant negative residual heterosis over mid parent in crosses was observed in four crosses and eight crosses respectively. The number of crosses which showed negative heterobeltiosis for this character in F_2 is three and in F_3 are five, while fourteen crosses had showed negative residual standard heterosis over both PS 19 and SL688 in F_3 generation. The results inferred that the parents involved in these crosses contributed earliness genes responsible for reducing number of days to 50% flowering. **Dogney *et al.* (1998)** reported negative residual heterosis over mid parent and positive residual heterosis over better parent for days to 50% flowering in soybean. **Guleria *et al.* (2000)**, **Patil *et al.* (2008)**, **Aditya *et al.* (2014)**, **Kaushar (2014)**, **Joshi (2015)** and **Sharma and Maloo (2017)** obtained similar results for days to 50% flowering.

Three and four F_2 crosses showed positive heterosis over mid parent and better parent for dry matter weight per plant, respectively. In F_3 , nine and four crosses exhibited significant positive residual heterosis over mid parent and better parent, respectively. **Aditya (2003)**, **Bhartiya (2004)**, **Massey (2005)**, **Ramana *et al.* (2006)**, **Arya (2007)**, **Samant *et al.* (2014)** and **Kaushar (2014)** reported similar results for dry matter weight per plant in soybean.

It was apparent from the results that none of the crosses exhibited positive residual heterosis over mid parent, better parent and over both standard checks in both the generation, while many crosses had given significant negative residual heterosis for plant height. Thus it appeared as in these crosses the combination of parents produced reduced gene effects for decreased plant height. **Leffel and Weiss (1958)** studied 45

hybrids in soybean and reported significant positive residual heterosis in ten hybrids over better parent for plant height. **Brim and Cockerham (1961), Caviness and Vathana (1968), Mjakusko (1969), Dorney *et al.* (1998), Guleria *et al.* (2000), Zhang and Yang (2000), Massey (2005, 2007), Arya (2007), Perez *et al.* (2009), Samant *et al.* (2014) Bhartiya *et al.* (2014) and Kaushar (2014)** also reported significant positive residual heterosis for plant height in soybean crosses. **Joshi (2015)** also reported negative residual heterosis for plant height.

Among the fourteen F₂ crosses, eight, two, three and one cross showed significant positive heterosis over mid parent, better parent and standard checks respectively for number of nodes per plant, while three, two and one cross showed positive significant residual heterosis over mid- parent, better parent and standard check PS 19. **Caviness and Vathana (1968)** reported residual heterosis for number of nodes per plant of hybrid between Lee and strain R 61 900. **Sood *et al.* (1996), Dorney *et al.* (1998), Zhang and Yang (2000), Arya (2007), Bhartiya *et al.* (2014) and Kaushar (2014)** reported similar results for number of nodes per plant.

Two F₂ crosses expressed significant positive heterosis for number of primary branches per plant over mid parent. Four F₃ crosses exhibited significant positive heterosis over mid parent, three crosses over better parent and five crosses over standard check SL 688. **Woodworth (1933), Guleria *et al.* (2000), Massey (2005), Ramana *et al.* (2006), Arya (2007), Samant *et al.* (2014) and Kaushar (2014)** also reported similar findings on residual heterosis for increased number of primary branches in soybean.

Number of pods per plant is one of the most important yield components in soybean. Four crosses exhibited significant positive heterosis over mid parent and better parent, respectively, for number of pods per plant in F₂. Whereas, six F₃ crosses showed significant positive residual heterosis over mid parent, three crosses over better parent and two crosses over standard check SL 688. This could be most probably due to non-additive type of gene action. Similar findings were also reported by **Woodworth (1933), Bastawisy *et al.* (1997), Dorney *et al.* (1998) Ponnusamy and Harer (1998), Guleria *et al.* (2000), Massey (2005, 2007), Ramana *et al.* (2006), Arya (2007), Sudaric *et al.* (2009), Bhartiya *et al.* (2014) and Kaushar (2014)** for number of pods per plant in soybean.

For number of seeds per pod, four, eleven and one crosses exhibited significant positive heterosis over mid parent, over standard check PS 19 and over standard check SL 688 in F₂. **Dogney *et al.* (1998)** reported positive and significant heterosis over better parent for seeds per pod. **Pandini *et al.* (2002)**, **Massey (2005, 2007)**, **Sudaric *et al.* (2009)** and **Joshi (2015)** also reported positive residual heterosis for number of seeds per pod.

100-seed weight is an important yield contributing character and directly influences seed yield per plant. Only one F₂ cross showed significant positive residual heterosis over standard check SL 688. Whereas three and two F₃ crosses had showed significant residual heterosis over mid parent and over standard check PS 19, respectively. **Sood (1999)**, **Dogney *et al.* (1998)**, **Zhang and Yang (2000)**, **Aditya (2003)**, **Patil *et al.* (2003)**, **Arya (2007)**, **Massey (2007)**, **Sudaric *et al.* (2009)** and **Kaushar (2014)** also reported similar results for 100- seed weight.

In general, heterosis for harvest index was observed in both the directions. In F₂ generation, three, one, three and two crosses had displayed positive significant residual heterosis over mid parent, better parent, standard check PS 19 and standard check SL 688, respectively. Similarly, In F₃ generation only one cross exhibited positive residual heterosis over mid parent and three crosses showed positive residual heterosis over standard check SL 688. Similar results were obtained by **Massey (2005, 2007)**, **Ramana *et al.* (2006)**, **Arya (2007)**, **Sudaric *et al.* (2009)** **Bhartiya (2004)**, **Kaushar (2014)** and **Joshi (2015)** observed low positive residual heterosis and negative heterobeltiosis for harvest index.

4.4 Transgressive segregation analysis

The proportion of individuals that surpasses the parental phenotypic limit either in positive or negative direction in a segregating generation gives the phenomenon of transgressive segregation and the individuals are known as transgressive segregants. The breeder can get an insight into the role of hybridization in the evolution relating to the frequency of transgressive segregation. The percentage of transgressive segregation observed in F₂ generation for each character in the present investigation had been presented in **Table 4.4.1**.

Table 4.4.1 Percentage of transgressive segregation in F₂ generation of soybean

Sn No	Crosses	Days to 50 % flowering		Dry matter weight per plant (g)		Plant height (cm)		Basal node height (cm)		Basal pod height (cm)		Number of nodes per plant	
		+ve	-ve	+ve	-ve	+ve	-ve	+ve	-ve	+ve	-ve	+ve	-ve
1	PS 1583 x Pb1	62	34	18	32	14	62	18	82	6	86	58	6
2	PS 1583 x JS 335	70	18	6	90	8	86	74	6	14	84	68	12
3	PS 1583 x DS 12-5	72	10	-	70	12	52	52	34	32	64	62	14
4	PS 1583 x JS 20-29	56	38	12	74	14	28	34	48	20	24	52	14
5	PS 1583 x Bragg	62	32	28	24	20	80	46	46	12	80	48	4
6	PS 1584 x JS 20-69	48	28	10	86	4	24	26	28	12	84	58	4
7	PS 1584 x JS 20-41	74	27	28	20	-	40	52	24	14	82	72	2
8	PS 1042 x PS 1347	36	78	10	80	42	58	78	22	6	88	62	18
9	RVS 200-1 x PS 1092	0	96	4	30	0	98	28	68	20	56	12	8
10	JS 20-63 x JS 97-52	88	4	18	64	2	12	22	74	38	10	76	18
11	JS 20-69 x JS 20-59	66	10	26	38	6	70	12	68	10	38	96	2
12	JS 20-64 x JS 20-54	44	40	2	70	4	34	-	58	52	34	78	22
13	JS 20-29 x JS20-55	18	15	10	56	18	60	92	8	84	6	64	10
14	PS 1225 x PS 1347	82	14	26	58	20	80	22	42	12	48	70	8

Sn No	Crosses	Number of primary branches per Plant		Number of pods per plant		Number of seeds per plant		Seed yield per plant (g)		100-seed weight (g)		Harvest index (%)	
		+ve	-ve	+ve	-ve	+ve	-ve	+ve	-ve	+ve	-ve	+ve	-ve
1	PS 1583 x Pb1	84	4	12	54	12	72	8	90	32	42	24	46
2	PS 1583 x JS 335	10	8	6	60	0	96	6	94	58	38	45	40
3	PS 1583 x DS 12-5	14	26	14	68	2	90	4	54	24	42	26	34
4	PS 1583 x JS 20-29	14	22	26	30	8	72	14	76	18	26	26	18
5	PS 1583 x Bragg	34	4	62	48	38	38	34	58	22	20	38	18
6	PS 1584 x JS 20-69	2	60	32	64	12	84	10	50	74	2	60	26
7	PS 1584 x JS 20-41	38	24	12	46	10	32	22	62	24	2	32	40
8	PS 1042 x PS 1347	38	30	30	60	4	86	44	52	72	22	48	40
9	RVS 200-1 x PS 1092	36	30	-	82	-	76	-	68	60	26	35	45
10	JS 20-63 x JS 97-52	6	20	64	30	4	76	4	94	0	80	54	30
11	JS 20-69 x JS 20-59	0	30	36	52	12	68	6	76	2	68	30	25

4.4.1 Days to 50% flowering

For days to 50% flowering, ten out of fourteen crosses exhibited positive transgressive segregation and all fourteen crosses showed negative transgressive segregation, Maximum number of transgressive segregants for delayed flowering were obtained in crosses JS 20-63 x JS 97-52 (88%) followed by PS 1225 x PS 1347 (82%), PS 1584 x JS 20-41 (74%), PS 1583 x DS 12-5 (72%), PS 1583 x JS 335 (70%), JS 20-69 x JS 20-59 (66%), PS 1583 x Bragg (62%), PS 1583 x JS 20-29 (56%), PS 1584 x JS 20-69 (48%) and PS JS 20-64 x JS 20-54 (44%).

Maximum number of transgressive segregants for early flowering was obtained in the crosses, RVS 200-1 x PS 1092 (96%) followed by PS 1042 x PS 1347 (78%), JS 20-64 x JS 20-54 (40%), PS 1583 x JS 20-29 (38%), PS 1583 x Pb1 (34%), PS 1583 x Bragg (32%), PS 1584 x JS 20-69 (28%), PS 1584 x JS 20-41 (27%), PS 1583 x JS 335 (18%) in F₂ crosses.

4.4.2 Dry matter weight per plant

Out of fourteen crosses, thirteen of the crosses exhibited positive transgressive segregants ranging from 28 (PS 1583 x Bragg, PS 1584 x JS 20-41) to 2 (JS 20-64 x JS 20-54) per cent and all fourteen of the crosses exhibited negative transgressive segregants from 90 (PS 1583 x JS 335) to 20 (PS 1584 x JS 20-41) per cent for dry matter weight per plant. Maximum number of transgressive segregants for high dry matter weight was obtained in the crosses, PS 1583 x Bragg, PS 1584 x JS 20-41 (28%) followed by JS 20-69 x JS 20-59, PS 1225 x PS 1347 (26%), PS 1583 x Pb1, JS 20-63 x JS 97-52 (18%) and PS 1584 x JS 20-69, PS 1042 x PS 1347, JS 20-29 x JS 20-55 (10%) in F₂ crosses.

4.4.3 Plant height

For plant height eleven of the crosses exhibited positive transgressive segregants ranging from 42 (PS 1042 x PS 1347) to 2 (JS 20-63 x JS 97-52) per cent and thirteen of the crosses exhibited negative transgressive segregants ranging from 98 (P RVS 200-1 x PS 1092) to 12 (JS 20-63 x JS 97-52) per cent. Maximum number of transgressive segregants for higher plant height was obtained in cross, PS 1042 x PS 1347 (42%) followed by PS 1583 X Bragg (20%), PS 1225 X PS 1347(20%), JS 20-29 x JS 20-55 (18%), PS 1583 X Pb1 (14%) and PS 1583 X JS 20-29 (14%). Maximum

number of negative transgressive segregants for higher plant was obtained in cross, RVS 200-1 x PS 1092 (98%) followed by PS 1583 x JS 335 (86%), PS 1225 x PS 1347 (80%), PS 1583 x Bragg (80%), JS 20-69 x JS 20-59 (70%), PS 1583 x Pb1 (62%) and JS 20-29 x JS 20-55 (60%).

4.4.4 Basal node height

Among fourteen F₂ crosses, thirteen crosses were transgressive segregants in positive direction ranging from 92 (JS 20-29 x JS 20-55) to 12 (JS 20-69 x JS 20-59) per cent for basal node height per plant. All fourteen crosses exhibited negative transgressive segregants ranging from 82 (PS 1583 x Pb1) to 6 (PS 1583 x JS 335) per cent. The highest per cent of transgressive segregants for shorter basal node height per plant was obtained in the cross, PS 1583 x Pb1 (82%) followed by JS 20-63 x JS 97-52 (74%), JS 20-69 x JS 20-59 (68%), RVS 200-1 x PS 1092 (68%), JS 20-64 x JS 20-54 (58%) and PS 1583 x JS 20-29 (48%). The crosses exhibiting transgressive segregants for longer basal node height were obtained in JS 20-29 x JS 20-55 (92%) followed by PS 1042 x PS 1347 (78%), PS 1583 x JS 335 (74%), PS 1583 x DS 12-5 (52%) and PS 1584 x JS 20-41 (52%).

4.4.5 Basal pod height

All the fourteen F₂ crosses exhibited transgressive segregation in both the direction for basal pod height per plant. The range for positive direction transgressive segregants was 86.7% (JS 20-29 x JS 20-55) to 6% (PS 1583 x Pb1, and PS 1042 x PS 1347) and for negative direction ranging from 88% (PS 1042 x PS 1347) to 6% (JS 20-29 x JS 20-55). The highest percentage of transgressive segregants for shorter basal pod height per plant was obtained in the cross, PS 1042 x PS 1347 (88%) followed by PS 1583 x Pb1 (86%), PS 1583 x JS 335 (84%), PS 1584 x JS 20-69 (84%), PS 1584 x JS 20-41 (82%), PS 1583 x Bragg (80%), PS 1583 x DS 12-5 (64%) and RVS 200-1 x PS 1092 (56%). The crosses exhibiting transgressive segregants for longer basal node height were obtained in JS 20-29 x JS 20-55 (84%) followed by JS 20-64 x JS 20-54 (52%), JS 20-63 x JS 97-52 (38%), PS 1583 x DS 12-5 (32%) and RVS 200-1 x PS 1092 (20%).

4.4.6 Number of nodes per plant

Among the fourteen F₂ crosses, all crosses were transgressive segregants in positive direction ranging from 96 (JS 20-69 x JS 20-59) to 12 (RVS 200-1 x PS 1092)

per cent for number of nodes per plant. All the crosses also exhibited negative transgressive segregants ranging from 22 (JS 20-64 x JS 20-54) to 2 (JS 20-69 x JS 20-59) per cent. The highest percentage of transgressive segregants for more number of nodes per plant was obtained in the cross, JS 20-69 x JS 20-59 (96%) followed by JS 20-64 x JS 20-54 (78%), JS 20-63 x JS 97-52 (76%), PS 1584 x JS 20-41 (72%), and PS 1583 x JS 335 (68%). The crosses exhibiting maximum negative transgressive segregants were obtained in JS 20-64 x JS 20-54 (22%) followed by PS 1042 x PS 1347 (18%), PS JS 20-63 x JS 97-52 (18%), PS 1583 x DS 12-5 (14%) and PS 1583 x JS 20-29 (14%).

4.4.7 Number of primary branches per plant

Out of fourteen crosses, thirteen crosses and all fourteen crosses exhibited transgressive segregants in positive and negative direction, respectively. The highest frequency of transgressive segregants for high number of primary branches per plant was found in cross, PS 1583 x Pb1 (84%) followed by PS 1584 x JS 20-41 (38%), PS 1042 x PS 1347 (38%) and RVS 200-1 x PS 1092 (36%). The range for positive transgressive segregants was 84% (PS 1583 x Pb1) to 2 (PS 1584 x JS 20-69) per cent. The lowest per cent of transgressive segregants for high number of primary branches per plant was obtained in crosses, JS 20-29 x JS 20-55 (78%), PS 1584 x JS 20-69 (60%), PS 1225 x PS 1347 (42%), PS 1042 x PS 1347 (30%) and RVS 200-1 x PS 1092 (30%) in F₂. The range for negative transgressive segregants was 78% (JS 20-29 x JS 20-55) to 3.3 (PS 1583 x Pb1 and PS 1583 x Bragg) per cent.

4.4.8 Number of pods per plant

Among the fourteen F₂ crosses, thirteen crosses showed positive transgressive segregants ranging from 64 (JS 20-63 x JS 97-52) to 6 (PS 1583 x JS 335) per cent for this character. The maximum transgressive segregants in positive direction were obtained in cross, JS 20-63 x JS 97-52 (64%) followed by PS 1583 x Bragg (62%), JS 20-29 x JS 20-55 (52%), JS 20-69 x JS 20-59 (36%) and PS 1584 x JS 20-69. The negative transgressive segregants showed a range from 82 (RVS 200-1 x PS 1092) to 30 (PS 1583 x JS 20-29, JS 20-63 x JS 97-52 and JS 20-29 x JS 20-55) per cent. The maximum transgressive segregants in negative direction were obtained in crosses, RVS 200-1 x PS 1092 (82%), JS 20-64 x JS 20-54 (74%), PS 1583 x DS 12-5 (68%), PS 1583 x JS 335 (60%) and PS 1042 x PS 1347 (60%).

4.4.9 Number of seeds per pod

Among fourteen F_2 crosses, only two crosses did not show transgressive segregation in any of the direction and were within parental limits. Twelve crosses showed positive transgressive segregants ranging from 38 (PS 1583 x Bragg) to 2 (PS 1583 x DS 12-5) per cent for this character. The maximum number of transgressive segregants in positive direction was obtained in cross, PS 1583 x Bragg (38%) followed by PS 1225 x PS 1347 (22%), JS 20-64 x JS 20-54 (14%), PS 1583 x Pb1, PS 1584 x JS 20-69, JS 20-69 x JS 20-59, JS 20-29 x JS 20-55 (12%) and PS 1584 x JS 20-41 (10%). The negative transgressive segregants ranged from 96 (PS 1583 x JS 335) to 32 (PS 1584 x JS 20-41) per cent.

4.4.10 Seed yield per plant

For seed yield per plant, eleven crosses out of fourteen F_2 crosses showed positive and all fourteen crosses showed negative transgressive segregants. The highest percentage of transgressive segregants in positive direction for this character were found in cross, PS 1042 x PS 1347 (44%) followed by PS 1583 x Bragg (34%), PS 1584 x JS 20-41 (22%), PS 1225 x PS 1347 (16%), PS 1583 x JS 20-29 (14%), PS 1584 x JS 20-69 (10%), PS 1583 x Pb1 (8%), PS 1583 x JS 335 (6%), JS 20-69 x JS 20-59 (6%), PS 1583 x DS 12-5 (4%) and JS 20-63 x JS 97-52 (4%) The range of percentage of transgressive segregants in negative direction was 100 (JS 20-64 x JS 20-54 to 28 (JS 20-29 x JS 20-55) per cent.

4.4.11 100-seed weight

For 100- seed weight, thirteen of the F_2 crosses showed positive transgressive segregants ranging from 74 (PS 1584 x JS 20-69) to 2 (JS 20-69 x JS 20-59) per cent. The highest percentage of transgressive segregants in positive direction in F_2 for this character was found in PS 1042 x PS 1347 (74%) followed by RVS 200-1 x PS 1092 (60%), PS 1583 x JS 335 (58%), PS 1225 x PS 1347 (56%) and JS 20-64 x JS 20-54 (40%). Minimum percentage of transgressive segregants was noted in JS 20-69 x JS 20-59 (2%) and negative transgressive segregants revealed a range from 90 (JS 20-29 x JS 20-55) to 2 (PS 1584 x JS 20-69 and PS 1584 x JS 20-41) per cent.

Table 4.4.2 : Best cross combinations showing highest frequency of transgressive segregation in desired direction

SI. No.	Character	Crosses with desired transgressive segregation
1	Days to 50% flowering	RVS 200-1 X PS 1092 (96%), PS 1042 X PS 1347 (78%), JS 20-64 X JS 20-54 (40%), PS 1583 X JS 20-29 (38 %), PS 1583 X Pb1 (34%)
2	Dry matter weight per plant (g)	PS 1584 X JS 20-41 (28%), PS 1583 X Bragg (28%), JS 20-69 X JS 20-59 (26 %), PS 1225 X PS 1347 (26%)
3	Plant height (cm)	PS 1583 X JS 335 (86%), RVS 200-1 X PS 1092 (98%), PS 1225 X PS 1347 (80%), PS 1583 X Bragg (80%), JS 20-69 X JS 20-59 (70 %)
4	Basal node height (cm)	PS 1583 X Pb1 (82%), JS 20-63 X JS 97-52 (74%), JS 20-69 X JS 20-59 (68%), RVS 200-1 X PS 1092 (68%), JS 20-64 X JS 20-54 (58%)
5	Basal pod height (cm)	PS 1042 X PS 1347(88%), PS 1583 X Pb1(86%), PS 1583 X JS 335 (84%), PS 1584 X JS 20-69 (84%), PS 1584 X JS 20-41 (82%)
6	Number of nodes per plant	JS 20-69 X JS 20-59 (96%), JS 20-64 X JS 20-54 (78%), PS 1584 X JS 20-41 (72%), PS 1225 X PS 1347 (70%), PS 1583 X JS 335 (68%)
7	Number of primary branches per plant	PS 1583 X Pb1 (84%), PS 1584 X JS 20-41 (38%), PS 1042 X PS 1347 (38%), RVS 200-1 X PS 1092 (36%), PS 1583 X Bragg (34%)
8	Number of pods per plant	JS 20-63 X JS 97-52 (64%), PS 1583 X Bragg (62%), JS 20-29 X JS 20-55 (52%), JS 20-69 X JS 20-59 (36%), PS 1584 X JS 20-69 (32%)
9	Number of seeds per pod	PS 1583 X Bragg (38%), PS 1225 X PS 1347 (22%), JS 20-64 X JS 20-54 (14%)
10	Seed yield per plant (g)	PS 1042 X PS 1347 (44%), PS 1583 X Bragg (34%), PS 1584 X JS 20-41 (22%), PS 1225 X PS 1347 (16%), PS 1583 X JS 20-29 (14%)
11	100-seed weight (g)	PS 1584 X JS 20-69 (74%), PS 1042 X PS 1347 (72%), RVS 200-1 X PS 1092 (60%), PS 1583 X JS 335 (58%), PS 1225 X PS 1347 (56%)
12	Harvest index (%)	PS 1584 X JS 20-69 (60%), JS 20-63 X JS 97-52(54%), JS 20-29 X JS 20-55 (52%), PS 1225 X PS 1347 (52%), PS 1042 X PS 1347 (48%)

4.4.12 Harvest index

The highest frequency of transgressive segregants in positive direction was shown by cross, PS 1584 x JS 20-69 (60%) followed by JS 20-63 x JS 97-52 (54%), JS 20-29 x JS 20-55 (52%), PS 1225 x PS 1347 (52%) and PS 1225 x PS 1347 (48%). The lowest frequency for highest index in positive direction was noticed in the crosses, PS 1583 x Pb1 (24%) and JS 20-64 x JS 20-54 (24%). Transgressive segregants in negative direction had a range from 60 (JS 20-64 x JS 20-54) to 18 (PS 1583 x JS 20-29) per cent.

In a segregating generation, there are chances of getting individuals which exceeds their parental limits and such individuals are referred to as transgressive segregant and the phenomenon of obtaining such individuals is known as Transgressive segregation.

Such plants are appeared by accumulation of favourable genes from the parents as a consequence of recombination (**DeVicente and Tanksley, 1993; Rieseberg and Ellstrand, 1993; Cosse *et al.*, 1995**). Best cross combination showing highest frequency of transgressive segregation in desired direction is presented in **Table 4.4.2**.

In F₂, both positive and negative transgressive segregants for days to 50% flowering were observed in several crosses. Maximum frequency of transgressive segregation with early flowering was exhibited in cross, RVS 200-1 x PS 1092 (96%) followed by PS 1042 x PS 1347, JS 20-64 x JS 20-54, PS 1583 x JS 20-29, PS 1583 x Pb1, PS 1583 x Bragg, PS 1584 x JS 20-69, PS 1584 x JS 20-41, PS 1583 x JS 335. **Miller (1976), Coyne and Steadman (1977), Kalaidzhieva and Kalaidjieva (1978), Reddy and Singh (1990), Mansur *et al.* (1996), Kaushar (2014), Aditya *et al.* (2014) and Joshi (2015)** also reported transgressive segregation for days to 50% flowering.

Consistent appearance of highest percentage of transgressive segregants for increased plant height in positive direction was observed in cross, PS 1042 x PS 1347 (42) followed by PS 1583 X Bragg (20%),

PS 1225 x PS 1347 (20%), JS 20-29 x JS 20-55 (18%), PS 1583 x Pb1 (14%) and PS 1583 x JS 20-29 (14%) in F₂, indicated the accumulation of such genes contributed by both the parents, as a consequence of recombination, which led to the increased plant height. However, in cross, RVS 200-1 x PS 1092 (98%) followed by PS 1583 x JS 335 (86%), PS 1225 x PS 1347 (80%), PS 1583 x Bragg (80%), JS 20-69 x

JS 20-59 (70%), PS 1583 x Pb1 (62%) and JS 20-29 x JS 20-55 (60%) highest percentage of negative transgressive segregants for plant height showed the accumulation of such genes contributed by both the parents, as a consequence of recombination, which led to the decrease in plant height. **Miller (1976)** found transgressive segregation for plant height in soybean. **Srivastava *et al.* (1976), Malik and Singh (1987)** reported transgressive segregation for plant height in soybean. **Kant and Singh (1998)** reported higher number of significantly superior transgressive segregants for plant height in the F₂ generation of E-153 X Pant L-23433.

The highest number of transgressive segregants for dry matter weight per plant was shown by the crosses, PS 1583 x Bragg, PS 1584 x JS 20-41 (28%) followed by JS 20-69 x JS 20-59, PS 1225 x PS 1347 (26%), PS 1583 x Pb1, JS 20-63 x JS 97-52 (18%) and PS 1584 x JS 20-69, PS 1042 x PS 1347, JS 20-29 x JS 20-55 (10%). **Kaushar (2014)** also reported the crosses showing maximum frequency of transgressive segregants for dry matter weight per plant in F₂ generation of soybean

Presence of both positive and negative transgressive segregants for number of nodes per plant was observed in F₂. The maximum frequency of transgressive segregants with higher number of node per plant was exhibited in cross, JS 20-69 x JS 20-59. **Kaushar (2014) and Joshi (2015)** reported transgressive segregants for number of nodes per plant in both F₂ and F₃ generations of soybean.

For number of primary branches per plant, higher percentage of positive transgressive segregants was noticed in cross, PS 1347 X DS 9814, PS 1347 X PS 1241, PS 1347 X PS 1042 and UPSM 534 X PS 1042. **Kaushar (2014), Aditya *et al.* (2014) and Joshi (2015)** also reported transgressive segregation for number of primary branches per plant in soybean.

The maximum frequency of transgressive segregants with higher number of pods per plant was exhibited in cross, JS 20-63 x JS 97-52 followed by PS 1583 x Bragg, JS 20-29 x JS 20-55, JS 20-69 x JS 20-59 and PS 1584 x JS 20-69. Similar results were also reported by **Miku and Damaskin (1984), Malik and Singh (1987), Kaushar (2014), Aditya *et al.* (2014) and Joshi (2015).**

Moderate to high frequency of transgressive segregants in positive direction was recorded for number of seeds per pod by most of the crosses. PS 1583 x Bragg,

PS 1225 x PS 1347, JS 20-64 x JS 20-54, PS 1583 x Pb1, PS 1584 x JS 20-69, JS 20-69 x JS 20-59, JS 20-29 x JS 20-55 and PS 1584 x JS 20-41 (10%) displayed higher percentage of transgressive segregants in F₂. **Zhang *et al.* (1987)**, **Malik and Singh (1987)**, **Mansur *et al.* (1996)**, **Aditya *et al.* (2014)** and **Joshi (2015)** also reported transgressive segregants for number of seeds per pod in soybean.

Presence of both positive and negative transgressive segregants for 100- seed weight was observed in all the F₂ crosses. The highest percentage of transgressive segregants in positive direction in F₂ for the character was found in PS 1042 x PS 1347 followed by RVS 200-1 x PS 1092, PS 1583 x JS 335, PS 1225 x PS 1347 and JS 20-64 x JS 20-54 indicating the possibility of selecting better types, which might have resulted due to accumulation of favourable genes from the concerned parents and also because of favourable epistatic effects. The negligible appearance of positive transgressive segregants for this trait in crosses, PS 1421 X NRC 90, PS 1347 X TGX 1681-3F and PS 1347 X PS 1241 may be due to the presence of certain inhibitory genes in the parent involved in the cross which did not allow the genes from other parent to express in segregating generation. **Kaushar (2014)** and **Joshi (2015)** had also reported transgressive segregants for 100- seed weight in F₂ generations of soybean.

For harvest index, highest percentage of transgressive segregants was observed in cross, PS 1584 x JS 20-69 followed by JS 20-63 x JS 97-52, JS 20-29 x JS 20-55, PS 1225 x PS 1347 and PS 1225 x PS 1347 indicating the presence of complementary effects of favourable alleles for this trait in these crosses. **Kaushar (2014)** and **Joshi (2015)** also reported similar results for harvest index in soybean.

The highest frequency of positive transgressive segregants for yield per plant was recorded in most of the crosses. The maximum frequency of transgressive segregation was exhibited by PS 1042 x PS 1347 followed by PS 1583 x Bragg, PS 1584 x JS 20-41, PS 1225 x PS 1347, PS 1583 x JS 20-29, PS 1584 x JS 20-69, PS 1583 x Pb1, PS 1583 x JS 335, JS 20-69 x JS 20-59, PS 1583 x DS 12-5 and JS 20-63 x JS 97-52. According to **Robinson and Cockerham (1961)** and **Marani (1968)**, significant F₂/F₃ deviations in the form of transgressive segregants indicated the presence of epistatic effects even though linkage may present precise estimates of the type of epistasis operating. 90 per cent appearance of transgressive segregants in F₂ cross, PS 1347 X DS 9814 indicated the involvement of additive and additive X additive epistatic effects along with the

dominance effect in the control of seed yield in this cross. **Mansur *et al.* (1996)** indicated that transgressive behavior is most pronounced for yield and the related traits and the range of the recombinant inbred lines (RILs) of soybean had been shown to be due to genotypic differences. **Miku and Damaskin (1984), Kapila and Gupta (1991), Bhatnagar and Karmakar (1995), Massey *et al.* (2008) and Lee *et al.* (2010)** reported higher number of transgressive segregants for yield in soybean. Similar results were also reported by **Kaushar (2014), Aditya *et al.* (2014) and Joshi (2015)** for higher seed yield in soybean crosses.

4.5 Estimates of inter-character correlation

The seed yield is a complex and highly variable character and a result of cumulative effect of its component characters and therefore, direct selection for yield may not be very effective. The yield components may not always be independent in their action but may be inter-linked. The selection practiced for one character may simultaneously bring change in the other related character. Thus, the information on the magnitudes and direction of association between the component characters are essential for the improvement in the desirable direction. This information may be useful in the prediction of correlated response to directional selection in the construction of selection indices and in the detection of some characters having no values in themselves but being indication of the more important ones under consideration (**Johnson *et al.*, 1955**).

For selection purpose phenotypic correlation is of little practical value unless genetic and environmental correlations between pairs of characters are in the same direction when estimated separately. Genetic correlation provides a measure of genetic association between characters and is generally used in selection for one character as a mean of improving another one. Genetic correlation may be accounted by linkage or pleiotropy. Thus, the association between two traits that can be directly observed is the phenotypic correlation. The genotypic correlation in the true sense may be interpreted as the correlation of breeding value. The environmental correlation includes both environmental and non-additive genetic deviations.

In general, phenotypic correlations were smaller than genotypic correlations. This could occur when genes governing two traits are similar and the environmental condition

pertaining to the expression of these traits had small and similar effects. Phenotypic, genotypic and environmental correlations between character pairs for all the characters are presented in Tables 4.5.1 and 4.5.2 for F₂ and F₃ generation, respectively.

Genotypic correlations, in general, were higher than phenotypic correlations. Directions of phenotypic and genotypic correlations were almost same for all the character combinations. The environment correlations, in general, were lower in magnitude as compared to the phenotypic and genotypic correlations.

4.5.1 Days to 50% flowering

Days to 50% flowering showed significant positive correlation in both genotypic and phenotypic level with dry matter weight ($r_g = 0.518$, $r_p = 0.423$), number of pods per plant ($r_g = 0.345$, $r_p = 0.275$), whereas, with 100-seed weight ($r_g = 0.300$) showed significant positive correlation in only genotypic level. Negative significant genotypic and phenotypic correlation with this character was showed by basal node height ($r_g = -0.345$, $r_p = -0.269$), whereas in F₃, days to 50% flowering showed significant negative genotypic and phenotypic correlation with basal pod height ($r_g = -0.271$, $r_p = -0.212$), whereas rest all characters did not show significant correlation at any level.

4.5.2 Dry matter weight per plant

Dry matter weight per plant showed significant positive genotypic and phenotypic correlation with plant height ($r_g = 0.592$, $r_p = 0.549$), number of pods per plant ($r_g = 0.634$, $r_p = 0.611$), number of seeds per pod ($r_g = 0.313$, $r_p = 0.243$), seed yield per plant ($r_g = 0.580$, $r_p = 0.548$), 100-seed weight ($r_g = 0.627$, $r_p = 0.544$) and significant positive correlation only at genotypic level with number of primary branches per plant ($r_g = 0.273$) whereas, it showed significant negative correlation with basal node height ($r_g = -0.627$, $r_p = -0.523$). However, in F₃, dry matter weight per plant showed significant positive genotypic and phenotypic correlation with plant height ($r_g = 0.532$, $r_p = 0.500$), basal node height ($r_g = 0.627$, $r_p = 0.422$), number of primary branches per plant ($r_g = 0.860$, $r_p = 0.657$), number of pods per plant ($r_g = 0.899$, $r_p = 0.877$), number of seeds per pod ($r_g = 0.880$, $r_p = 0.827$), seed yield per plant ($r_g = 0.927$, $r_p = 0.923$) and harvest index ($r_g = 0.618$, $r_p = 0.600$).

Table 4.5.1 Inter-character correlation coefficient between different character at phenotypic, genotypic and environmental level in F₂ generation of soybean

		Days to 50 % flowering	Dry matter weight per plant (g)	Plant height (cm)	Basal node height (cm)	Basal pod height (cm)	Number of nodes per plant	Number of primary branches per plant	Number of pods per plant	Number of seeds per plant	Seed yield per plant(g)	100-seed weight (g)	Harvest index (%)
Days to 50 % flowering	rg		0.518**	0.189	-0.345**	-0.015	0.185	0.182	0.345**	-0.049	0.218	0.300*	-0.144
	rp		0.423**	0.190	-0.269*	0.011	0.105	0.176	0.275*	-0.191	0.167	0.201	-0.124
	re		-0.010	0.304**	0.071	0.133	-0.153	0.160	-0.073	-0.423**	-0.163	-0.146	-0.034
Dry matter weight per plant (g)	rg			0.592**	-0.627**	0.057	0.227	0.273*	0.634**	0.313**	0.580**	0.627**	-0.088
	rp			0.549**	-0.553**	0.031	0.228	0.225	0.611**	0.243*	0.548**	0.544**	-0.130
	re			-0.048	0.112	-0.186	0.257*	0.012	0.370**	0.212	0.131	0.048	-0.577**
Plant height (cm)	rg				-0.377**	0.442**	0.037	0.083	0.585**	0.315**	0.390**	0.269*	0.038
	rp				-0.359**	0.406**	0.011	0.071	0.563**	0.198	0.375**	0.216	0.039
	re				-0.141	-0.008	-0.225	0.008	0.240*	-0.018	0.010	-0.257*	0.056
Basal node height (cm)	rg					-0.081	-0.321**	-0.307**	-0.512**	-0.456**	-0.888**	-0.755**	-0.582**
	rp					-0.059	-0.301*	-0.295*	-0.502**	-0.262*	-0.860**	-0.692**	-0.574**
	re					0.109	-0.215	-0.275*	-0.407**	0.070	-0.576**	-0.346**	-0.502**
Basal pod height (cm)	rg						0.061	-0.008	0.136	0.318**	0.056	0.016	0.059
	rp						0.020	-0.045	0.116	0.182	0.048	-0.000	0.056
	re						-0.190	-0.217	-0.065	-0.044	-0.048	-0.094	0.034
Number of nodes per plant	rg							0.053	0.210	-0.097	0.469**	0.136	0.424**
	rp							0.123	0.210	0.046	0.458**	0.204	0.391**
	re							0.346**	0.242*	0.286*	0.550**	0.470**	0.239*
Number of primary branches per plant	rg							0.181	0.600**	0.451**	0.210	0.265*	
	rp							0.163	0.289*	0.395**	0.149	0.248*	
	re							0.098	-0.118	0.156	-0.061	0.204	
Number of pods per plant	rg								0.299*	0.572**	0.284*	0.203	
	rp								0.207	0.567**	0.267*	0.197	
	re								0.099	0.527**	0.173	0.120	
Number of seeds per plant	rg									0.607**	0.315**	0.470**	
	rp									0.414**	0.252*	0.272*	
	re									0.185	0.206	-0.094	
Seed yield per plant (g)	rg										0.647**	0.749**	
	rp										0.632**	0.742**	
	re										0.684**	0.668**	
100-seed weight (g)	rg											0.332**	
	rp											0.334**	
	re											0.384**	
Harvest index (%)	rg												
	rp												
	re												

**Significant at 1% level of probability, *Significant at 5% level of probability

Table4.5.2 Inter-character correlation coefficient between different characters at phenotypic, genotypic and environmental level in F₃ generation of soybean

		Days to 50 % flowering	Dry matter weight per plant (g)	Plant height (cm)	Basal node height (cm)	Basal pod height (cm)	Number of nodes per plant	Number of primary branches per plant	Number of pods per plant	Number of seeds per plant	Seed yield per plant(g)	100-seed weight (g)	Harvest index (%)
Days to 50 % flowering	rg		0.056	0.123	0.616**	-0.271	-0.369	0.224	0.113	-0.241	0.005	0.090	-0.057
	rp		0.050	0.120	0.436*	-0.212	-0.367	0.171	0.119	-0.232	0.008	0.091	-0.045
	re		-0.541**	0.157	0.128	0.393*	-0.416*	0.007	0.355	-0.261	0.390*	0.332	0.639**
Dry matter weight per plant (g)	rg			0.532**	0.627**	0.330	-0.141	0.860**	0.899**	0.880**	0.927**	0.364	0.618**
	rp			0.500**	0.422*	0.292	-0.123	0.657**	0.877**	0.827**	0.923**	0.251	0.600**
	re			0.289	-0.175	0.118	0.614**	0.058	0.190	0.673**	0.256	-0.113	-0.596**
Plant height (cm)	rg				0.629**	0.726**	-0.483**	0.676**	0.464*	0.424*	0.479**	-0.089	0.346
	rp				0.288	0.688**	-0.443*	0.426*	0.445*	0.397*	0.448*	-0.016	0.315
	re				-0.421*	0.551**	-0.105	-0.205	0.321	0.253	0.256	0.158	-0.021
Basal node height (cm)	rg					0.189	-0.030	0.640**	0.566**	0.349	0.465*	0.473*	-0.152
	rp					0.151	-0.008	0.468*	0.392*	0.195	0.335	0.069	-0.064
	re					0.104	0.071	0.277	0.055	-0.091	0.295	-0.326	0.376*
Basal pod height (cm)	rg						-0.016	0.594**	0.190	0.406*	0.226	-0.343	0.101
	rp						-0.042	0.391*	0.172	0.379*	0.200	-0.289	0.109
	re						-0.242	-0.011	0.093	0.277	0.118	-0.222	0.293
Number of nodes per plant	rg							-0.205	-0.196	-0.146	-0.125	0.036	-0.318
	rp							-0.195	-0.176	-0.097	-0.116	0.038	-0.323
	re							-0.278	0.179	0.336	0.367	0.079	-0.496**
Number of primary branches per plant	rg								0.810**	0.742**	0.807**	-0.005	0.526**
	rp								0.577**	0.609**	0.611**	-0.170	0.396*
	re								-0.183	0.348	-0.102	-0.369	-0.016
Number of pods per plant	rg									0.769**	0.952**	0.521**	0.662**
	rp									0.673**	0.938**	0.477*	0.645**
	re									-0.155	0.844**	0.744**	0.187
Number of seeds per plant	rg										0.853**	0.154	0.589**
	rp										0.778**	-0.001	0.522**
	re										-0.027	-0.359	-0.181
Seed yield per plant(g)	rg											0.382*	0.770**
	rp											0.295*	0.762**
	re											0.529**	0.178
100-seed weight (g)	rg												-0.035
	rp												-0.001
	re												0.222
Harvest index(%)	rg												
	rp												
	re												

**Significant at 1% level of probability, *Significant at 5% level of probability

4.5.3 Plant height

Plant height showed significant positive genotypic and phenotypic correlation with basal pod height ($r_g=0.442$, $r_p=0.406$), number of pods per plant ($r_g=0.585$, $r_p=0.563$), Seed yield per plant ($r_g=0.390$, $r_p=0.375$). However, plant height also showed significant positive correlation with number of seeds per pod ($r_g=0.3150$), 100-seed weight ($r_g=0.269$) at genotypic level. On the other hand plant height showed significant negative genotypic and phenotypic level with basal node height ($r_g=-0.377$, $r_p=-0.359$).

In F_3 , plant height showed significant positive correlation at genotypic as well as phenotypic level with basal pod height ($r_g=0.629$, $r_p=0.688$), number of primary branches per plant ($r_g=0.676$, $r_p=0.426$), number of pods per plant ($r_g=0.464$, $r_p=0.445$), number of seeds per pod ($r_g=0.424$, $r_p=0.397$), seed yield per plant ($r_g=0.479$, $r_p=0.448$). Whereas basal node height ($r_g=0.629$) showed significant positive correlation with plant height only genotypic level. Plant height was found significantly negative correlated with number of nodes per plant ($r_g=-0.483$, $r_p=-0.443$) at both genotypic and phenotypic level.

4.5.4 Basal node height

In F_2 , basal node height showed significant negative correlation at genotypic and phenotypic level with many other characters like days to 50% flowering ($r_g=-0.345$, $r_p=-0.269$), dry matter weight ($r_g=-0.627$, $r_p=-0.553$), Plant height ($r_g=-0.377$, $r_p=-0.539$) number of nodes per plant ($r_g=-0.321$, $r_p=-0.301$), number of primary branches ($r_g=-0.307$, $r_p=-0.295$), number of pods per plant ($r_g=-0.512$, $r_p=-0.502$), number of seeds per pod ($r_g=-0.456$, $r_p=-0.262$), seed yield per plant ($r_g=-0.888$, $r_p=-0.860$), 100-seed weight ($r_p=-0.755$, $r_g=-0.692$) and harvest index ($r_g=-0.582$, $r_p=-0.574$). However, in F_3 , basal node height showed significant positive correlation at genotypic phenotypic level with days to 50% flowering ($r_g=0.616$, $r_p=0.436$), dry matter weight ($r_g=0.627$, $r_p=0.422$), primary branches per plant ($r_g=0.640$, $r_p=0.468$) and number of pods per plant ($r_g=0.566$, $r_p=0.392$), whereas plant height ($r_g=0.629$), seed yield per plant ($r_g=0.465$) and 100-seed weight ($r_g=0.473$) were found genotypic significantly positive correlated with basal node height.

4.5.5 Basal pod height

Basal pod height showed positive significant correlation at genotypic and phenotypic level with plant height ($r_g=0.442$, $r_p=0.406$) and only at genotypic level with number of seeds per pod ($r_g=0.318$) and in F_3 , basal pod height showed positive significant correlation at genotypic and phenotypic level with plant height ($r_g=0.726$, $r_p=0.688$), number of primary branches per plant ($r_g=0.594$, $r_p=0.391$) and number of seeds per pod ($r_g=0.406$, $r_p=0.379$).

4.5.6 Number of nodes per plant

Number of nodes per plant showed positive significant correlation with seed yield per plant ($r_g=0.726$, $r_p=0.688$), harvest index ($r_g=0.594$, $r_p=0.391$) and negative significant correlation with basal node height ($r_g=0.406$, $r_p=0.379$) at both genotypic and phenotypic level. In F_3 , the character showed negative significant correlation with plant height ($r_g= -0.483$, $r_p= -0.443$), at both genotypic and phenotypic level.

4.5.7 Number of primary branches per plant

At genotypic level, in F_2 generation number of primary branches per plant showed significant positive correlation with dry matter weight per plant ($r_g=0.273$) at genotypic level only while with number of seeds per pod ($r_g=0.600$, $r_p=0.289$), seed yield per plant ($r_g=0.451$, $r_p=0.395$) and harvest index ($r_g=0.265$, $r_p=0.248$) at both genotypic as well as phenotypic level. Primary branches per plant also showed significant negative correlation with basal node height ($r_g= -0.307$, $r_p= -0.295$) at both genotypic and phenotypic levels. In F_3 generation, primary branches per plant showed significant positive genotypic and phenotypic correlation with dry matter weight ($r_g=0.860$, $r_p=0.657$), plant height ($r_g=0.676$, $r_p=0.426$), basal node height ($r_g=0.640$, $r_p=0.648$), basal pod height ($r_g=0.594$, $r_p=0.391$), number of pods per plant ($r_g=0.810$, $r_p=0.577$), number of seeds per pod ($r_g=0.472$, $r_p=0.609$), seed yield per plant ($r_g=0.807$, $r_p=0.611$) and harvest index ($r_g=0.526$, $r_p=0.396$).

4.5.8 Number of pods per plant

In F_2 , number of pods per plant showed significant positive genotypic and phenotypic correlation with days to 50% flowering ($r_g=0.345$, $r_p=0.275$) dry matter weight per plant ($r_g=0.634$, $r_p=0.611$), plant height ($r_g=0.585$, $r_p=0.563$), seed yield per

plant ($rg=0.572$, $rp=0.567$), 100-seed weight ($rg=0.284$, $rp=0.267$) and showed positive significant genotypic correlation with number of seeds per pod ($rg=0.299$) on the other hand it showed negative significant genotypic and phenotypic correlation with basal node height ($rg= -0.307$, $rp= -0.295$). Likewise in F_3 , number of pods per plant showed significant positive genotypic and phenotypic correlation with dry matter weight per plant ($rg=0.899$, $rp=0.877$), plant height ($rg=0.464$, $rp=0.445$), basal node height ($rg=0.566$, $rp=0.392$), number of primary branches per plant ($rg=0.810$, $rp=0.577$), seeds per pod ($rg=0.769$, $rp=0.673$), seed yield per plant ($rg=0.952$, $rp=0.938$), 100-seed weight ($rg=0.521$, $rp=0.477$) and harvest index ($rg=0.662$, $rp=0.645$).

4.5.9 Number of seeds per pod

In F_2 generation, number of seeds per pod showed significant positive genotypic and phenotypic correlation with dry matter weight per plant ($rg=0.313$, $rp=0.243$), number of primary branches per plant ($rg=0.600$, $rp=0.289$), seed yield per plant ($rg=0.607$, $rp=0.414$), 100-seed weight ($rg=0.315$, $rp=0.252$) and harvest index ($rg=0.470$, $rp=0.272$) whereas, it showed significant positive genotypic correlation with plant height ($rg=0.315$), basal pod height ($rg=0.318$), number of pods per plant ($rg=0.299$) and significant negative genotypic as well as phenotypic correlation with basal node height ($rg= -0.456$, $rp= -0.262$). In F_3 generation, number of seeds per pod showed significant positive genotypic and phenotypic correlation with dry matter weight per plant ($rg=0.880$, $rp=0.827$), plant height ($rg=0.424$, $rp=0.397$), basal pod height ($rg=0.406$, $rp=0.379$), number of primary branches per plant ($rg=0.742$, $rp=0.609$), number of pods per plant ($rg=0.769$, $rp=0.673$), seed yield per plant ($rg=0.853$, $rp=0.778$), and harvest index ($rg=0.589$, $rp=0.522$).

4.5.10 Seed yield per plant

In F_2 generation, seed yield per plant showed significant positive genotypic and phenotypic correlation with dry matter weight per plant ($rg=0.580$, $rp=0.548$), plant height ($rg=0.390$, $rp=0.375$), number of nodes per plant ($rg=0.469$, $rp=0.458$), number of primary branches per plant ($rg=0.451$, $rp=0.395$), number of pods per plant ($rg=0.572$, $rp=0.567$), number of seeds per pod ($rg=0.607$, $rp=0.414$), 100-seed weight ($rg=0.647$, $rp=0.632$) and harvest index ($rg=0.749$, $rp=0.742$) whereas, it showed significant negative genotypic and phenotypic correlation with basal node height ($rg= -0.888$, $rp= -0.860$). In F_3 generation, seed yield per plant showed significant

positive genotypic correlation with 100-seed weight ($r_g=0.382$) and significant positive correlation at genotypic as well phenotypic level with dry matter weight per plant ($r_g=0.927, r_p=0.923$), plant height ($r_g=0.479, r_p=0.448$), number of primary branches per plant ($r_g=0.807, r_p=0.611$), number of pods per plant ($r_g=0.952, r_p=0.938$), number of seeds per pod ($r_g=0.853, r_p=0.778$), and harvest index ($r_g=0.770, r_p=0.762$).

4.5.11 100-seed weight

100-seed weight showed significant positive genotypic and phenotypic correlation with dry matter weight per plant ($r_g=0.627, r_p=0.544$), number of pods per plant ($r_g=0.284, r_p=0.267$), number of seeds per pod ($r_g=0.315, r_p=0.252$), seed yield per plant ($r_g=0.647, r_p=0.632$) and harvest index ($r_g=0.332, r_p=0.334$) whereas, it showed significant negative genotypic and phenotypic correlation with basal node height ($r_g = -0.755, r_p = -0.692$). In F_3 generation, 100-seed weight showed significant positive genotypic and phenotypic correlation with dry number of pods per plant ($r_g=0.521, r_p=0.477$) and it also showed significant positive genotypic correlation with basal node height ($r_g=0.473$) and seed yield per plant ($r_g=0.382$).

4.5.12 Harvest index

In F_2 , harvest index showed significant positive genotypic and phenotypic correlation with number of nodes per plant ($r_g=0.424, r_p=0.391$), number of primary branches per plant ($r_g=0.265, r_p=0.248$), number of seeds per pod ($r_g=0.470, r_p=0.272$), seed yield per plant ($r_g=0.749, r_p=0.742$) and 100-seed weight ($r_g=0.332, r_p=0.334$). In F_3 generation, harvest index showed significant positive genotypic and phenotypic correlation with dry matter weight per plant ($r_g=0.618, r_p=0.600$), number of primary branches per plant ($r_g=0.526, r_p=0.396$), number of pods per plant ($r_g=0.662, r_p=0.645$), number of seeds per pod ($r_g=0.589, r_p=0.522$) and seed yield per plant ($r_g=0.770, r_p=0.762$).

In the present study, days to 50% flowering showed significant positive correlation with, number of pods per plant and dry matter weight per plant at phenotypic and genotypic levels in F_2 . In F_3 , days to 50% flowering had significant positive correlation with basal node height at phenotypic and genotypic levels. There were non-significant negative and positive phenotypic and genotypic correlations with other characters. Similar results were reported by Thorat *et al.* (2001), Kaushar (2014) and Joshi (2015).

Dry matter weight per plant showed highly significant and positive value of phenotypic and genotypic correlations with days to 50% flowering, plant height, number of pods per plant, number of seeds per pod, seed yield per plant and 100-seed weight. Negative and highly significant genotypic and phenotypic correlations were observed for basal node height in F_2 . In F_3 , dry matter weight per plant showed positive significant phenotypic and genotypic correlations with plant height, basal node height, number of primary branches per plant, number of pods per plant, number of seeds per pod, seed yield per plant and harvest index.

Basal node height showed negative significant value of phenotypic and genotypic correlation with days to 50% flowering, dry matter weight per plant, plant height, number of nodes per plant, number of primary branches per plant, number of pods per plant, number of seeds per pod, seed yield per plant, 100-seed weight and harvest index in F_2 , whereas it showed non-significant positive and negative values with other characters in F_3 generation.

Number of primary branches per plant showed significant positive values of phenotypic and genotypic correlations with number of seeds per pod, yield per plant and harvest index in F_2 while in F_3 it had positive significant correlation with dry matter weight plant per plant, plant height, basal node height, basal pod height number of pods per plant, number of seeds per pod, yield per plant and harvest index. Similar results were reported by **Rubaihaya (1973), Rajput *et al.*, (2000), Gaikwad *et al.*, (2007) Machikowa and Laosuwan (2011), Sarutayophat (2012), Arshad *et al.* (2014) Kaushar (2014) and Joshi (2015).**

Number of pods per plant showed significant positive values of phenotypic and genotypic correlations with days to 50% flowering, dry matter weight, plant height, 100-seed weight, and yield per plant in F_2 . Highly significant and positive value of phenotypic and genotypic correlations was observed with dry matter weight per plant, plant height, basal node height, number of primary branches per plant, number of seeds per pod, 100-seed weight, harvest index and yield per plant in F_3 . Number of nodes per plant showed non-significant negative values of phenotypic and genotypic correlations with number of pods per plant. **Karnwal and Singh (2009), Samant (2010), Sarutayophat (2012), Kaushar (2014) and Joshi (2015)** showed significant association between number of pods per plant and yield per plant.

Seed yield per plant showed highly significant positive phenotypic and genotypic correlations for plant height, basal node height, number of primary branches per plant, number of pods per plant, number of seeds per pod, 100-seed weight and harvest index in F₂. Whereas, in F₃ seed yield per plant showed significant and positive values of genotypic and phenotypic correlations with dry matter weight per plant, plant height, number of primary branches per plant, number of pods per plant, number of seeds per pod, 100-seed weight and harvest index. Similar results were obtained by **Chaudhary and Singh (1974)**, **Myakushko and Dudka (1986)**, **Singh and Yadava (2000)**, **Thorat *et al.* (2001)**, **Chettri *et al.* (2003)**, **Yadav (2005)**, **Bhairav *et al.* (2006)**, **Pandey *et al.* (2008)**, **Karnwal and Singh (2009)**, **Showkat and Tyagi (2010)**, **Zafar Iqbal *et al.* (2010)**, **Machikowa and Laosuwan (2011)**, **Sarutayophat (2012)**, **Kaushar (2014)** and **Joshi (2015)**.

Harvest Index showed highly significant and positive value of phenotypic and genotypic correlation with number of primary branches per plant, number of seeds per pod and seed yield per plant in both the generation.

Gohil *et al.* (2003) studied the character association between yield and its attributes in soybean and reported significant positive correlation of seed yield with plant height, branches per plant, pod clusters per plant, pods per plant and 100-seed weight. However, they reported a negative correlation of both oil and protein contents with seed yield in soybean which was contrary to the results obtained in the present study. **Chandel *et al.* (2005)** studied correlation among 15 characters by evaluating 24 genotypes of soybean and reported that plant height, 100-seed weight, biological yield, harvest index and oil content exhibited a significant and positive correlation with seed yield. **Chavan *et al.* (2016)** also reported correlation of number of pods, 100- seed weight with seed yield. **Sonwane *et al.* (2006)** observed a significant and positive correlated of grain yield with duration of seed filling period, pods per plant, seeds per pod, seed weight and harvest index. **Gaikwad *et al.* (2007)** also reported that harvest index and pods per plant were significantly and positively correlated with seed yield per plant in soybean. **Baig *et al.* (2017)** also indicated the correlation of days to 50% flowering, plant height, 100-grain weight, number of pods with seed yield in 35 cultivars of soybean. Similar findings were also reported by **Chaudhary and Singh, (1974)**; **Das *et al.* (1989)**; **Jadhav *et al.* (1995)**; **Rajput *et al.* (2000)**; **Iqbal *et al.***

(2010); Aditya *et al.* (2011); Chandel *et al.* (2014); Dubey *et al.* (2015), Nagarajan *et al.* (2015), Chavan *et al.* (2016), Baig *et al.* (2017), Bisinotto *et al.* (2017).

Environmental correlation

It includes both environmental and non-additive effects. Invariably, environmental correlation values were lower as compared to the genotypic and phenotypic ones. A perusal of environmental correlation in F_2 and F_3 is given in **Table 4.5.1 and 4.5.2**. Almost all the correlation values between different characters were non-significant. Whereas, highly significant positive correlation was found between days to 50% flowering and plant height ($r = 0.304^{**}$), dry matter weight per plant and number of nodes per plant ($r = 0.257^*$), dry matter weight per plant and number of pods per plant ($r = 0.370^{**}$), plant height and number of pods per plant ($r = 0.240^{**}$), number of nodes per plant and primary branches ($r = 0.346^{**}$), number of nodes per plant and number of pods per plant ($r = 0.242^*$), number of nodes per plant and number of seeds per pod ($r = 0.286^*$), number of nodes per plant and seed yield per plant ($r = 0.550^{**}$), number of nodes per plant and 100-seed weight ($r = 0.470^{**}$), number of nodes per plant and harvest index ($r = 0.239^*$), number of pods per plant and seed yield per plant ($r = 0.527^{**}$), seed yield per plant and 100-seed weight ($r = 0.684^{**}$), seed yield per plant and harvest index ($r = 0.668^{**}$), 100-seed weight with harvest index ($r = 0.384^{**}$) whereas, significant negative correlation was found between dry matter weight per plant and harvest index ($r = -0.577^{**}$), plant height and 100-seed weight ($r = -0.257^*$), basal node height and number of primary branches per plant ($r = -0.275^*$), basal node height and number of pods per plant ($r = -0.407^{**}$), basal node height and yield per plant ($r = -0.576^{**}$), basal node height and 100-seed weight ($r = -0.346^*$), basal node height and harvest index ($r = -0.502^*$).

In environmental correlation, some of the characters showed highly significant and significant correlation as described above and maximum characters showed non-significant negative and non-significant positive correlation to each other in F_2 (**Table 4.5.1**).

In F_3 , most of the correlation values between different characters were non-significant. Whereas, highly significant positive correlation was observed between days to 50% flowering and basal pod height ($r = 0.393^*$), days to 50% flowering and seed yield ($r = 0.390^*$), days to 50% flowering and harvest index ($r = 0.348^{**}$), days to

50% flowering and plant height, days to 50% flowering and number of pods per plant ($r = 0.639^{**}$), dry matter weight per plant and number of nodes per plant ($r = 0.614^{**}$), dry matter weight per plant and number of seeds ($r = 0.673^{**}$), dry matter weight per plant and plant height, dry matter weight per plant and basal pod height per plant ($r = 0.551^{**}$), number of pods per plant and seed yield ($r = 0.844^{**}$), number of pods per plant and 100-seed weight ($r = 0.744^{**}$), seed yield per plant and 100-seed weight ($r = 0.529^{**}$), whereas significant negative correlation was observed between days to 50% flowering and dry matter weight per plant ($r = -0.541^{**}$), days to 50% flowering and number of nodes per plant ($r = -0.416^{*}$), dry matter weight per plant and harvest index ($r = -0.596^{**}$), plant height and basal node height ($r = -0.421^{*}$), number of nodes per plant and harvest index ($r = -0.496^{**}$) as shown in **Table 4.5.2**. Similar results were also reported by **Showkat and Tyagi (2010)**, **Zafar Iqbal et al. (2010)**, **Machikowa and Laosuwan (2011)**, **Kaushar (2014)** and **Joshi (2015)**.

4.6 Path coefficient analysis

Path coefficients are standardized partial regression coefficients and they provide a means for estimating the direct and indirect effects of one variable upon another. Correlation coefficient does not provide a reliable estimate of relative direct and indirect contribution of different component characters towards the seed yield. Path coefficient analysis, therefore, helps in partitioning of correlation coefficients of all the component traits associated with seed yield into direct and indirect effects. Hence, the path coefficient analysis provides a clear insight into the contribution of individual component characters towards the total genetic architecture of yield. An extensive literature on yield analysis had now developed but the problem that the components of seed yield are to some extent inter-dependent, still exists (**Adams, 1967; Hardwick and Andrews, 1980**). Physiological and genetic aspects of this inter-dependence are still debatable (**Adams and Grafius, 1971**). Under these circumstances, the value of yield analysis in programmes of plant improvement must be called in question (**Langer, 1967; Kuhn and Stucker, 1976**).

However, a few plant breeders appear to turn to statistical procedures such as factor analysis or path-coefficient analysis (**Duarte and Adams, 1972; Bhatt, 1973; Denis and Adams, 1978**). The path of coefficient is free of unit, the concept of path correlation coefficient was originally developed by **Wright (1921)** but the technique

was used by **Dewey and Liu (1959)**. The path coefficient analysis was carried out by taking seed yield per plant as a dependent variable and rests all characters as independent variables. Genotypic and phenotypic direct effects in F_2 and F_3 generations of various characters on seed yield per plant are presented in **Tables 4.6.1a, 4.6.1b and 4.6.2a, 4.6.2b respectively**.

An overview of phenotypic path coefficient analysis of F_2 revealed that harvest index had highest positive direct effect (0.743) on seed yield per plant followed by dry matter weight per plant (0.589), number of primary branches per plant (0.042), number of seeds per pod (0.035) and number of pods per plant (0.019), whereas basal node height (-0.105), 100-seed weight (-0.022), plant height (-0.022), basal pod height (-0.016), days to 50% flowering (-0.016) and number of nodes per plant (-0.002) exhibited direct but negative effects on yield per plant (**Table 4.6.1b**). At genotypic level harvest index (0.935) was most important direct contributor to the yield per plant followed by dry matter weight per plant (0.865), number of primary branches per plant (0.075) and basal pod height (0.032), whereas 100-seed weight (-0.169), number of nodes per plant (-0.114), number of seeds per pod (-0.101), plant height (-0.079), number of pods per plant (-0.054), basal node height (-0.053) and days to 50% flowering (-0.027) exhibited direct but negative effects to yield per plant in F_2 as showed in **Table 4.6.1a**.

In F_3 generation, at phenotypic level number of pods per plant (0.400) was the most important positive direct contributor towards the seed yield per plant followed by harvest index (0.328), number of seeds per pod (0.175), number of nodes per plant (0.162), dry matter weight per plant (0.161), plant height (0.150), basal node height (0.065), number of primary branches (0.031) and 100-seed weight (0.028). The maximum negative direct effect at phenotypic level was that of basal pod height (-0.133) followed by days to 50% flowering (-0.017) as shown in **Table 4.6.2b**. The most important positive direct contributor towards the seed yield per plant in F_3 at genotypic level was number of pod per plant (0.828), followed by number of seeds per pod (0.275), harvest index (0.246), number of nodes per plant (0.177), dry matter weight per plant (0.139), days to 50% flowering (0.111), plant height (0.093), basal node height (0.091) and basal pod height (0.043), whereas two characters, number of primary branches (-0.452) and 100-seed weight (-0.172) showed negative direct effects on seed yield per plant (**Table 4.6.2a**).

In F₂, dry matter weight per plant, harvest index showed highly significant positive correlation as well as exhibits highly positive direct effect on seed yield per plant, while in F₃ number of pods per plant, displayed highly significant positive correlation and exhibits highly positive direct effect on seed yield. The positive and significant association of these traits with yield per plant and high direct effect of these traits towards the total yield revealed that there is true relationship between these characters and the direct selection for these component traits will bring an improvement in the yield per plant, the dependent variable.

On the other hand characters like 100-seed weight, number of nodes per plant, number of seeds per pod, number of pods per plant, plant height showed highly significant positive genotypic correlation but negative direct effects on seed yield per plant in F₂ and likewise in F₃, number of primary branches per plant and 100-seed weight displayed highly significant positive genotypic correlation but negative direct effects on seed yield per plant. This suggest that the effect of these characters on dependent variable i.e., yield may be due to highly positive indirect effects. For example in F₂, number of nodes per plant showed positive genotypic correlation (0.469) with seed yield and that was not because of negative direct effect (-0.114) on yield per plant but due to the high positive indirect effect *via* harvest index (0.396), similarly in F₃ number of primary branches per plant showed significant genotypic correlation (0.807) because of the high indirect effect through number of pods per plant (0.671) on seed yield per plant. This effect of an independent character on the dependent one *via* other independent character is called as indirect effect.

Ramanna *et al.* (2000) reported highest positive direct effect of number of pods per plant on seed yield followed by 100-seed weight and also observed a negative direct effect of days to 50% flowering on seed yield. Similar findings were reported for number of pods per plant (**Gaikwad *et al.*, 2007; Karnwal and Singh, 2009; Iqbal *et al.*, 2010 and Gireesh *et al.*, 2012**), 100-seed weight and seeds per pod (**Chandel *et al.*, 2014**), number of primary branches per plant, number of pods per plant, number of seeds per pod and 100-seed weight (**Thakur *et al.*, 2015**), number of primary branches per plant, pods per plant, seeds per pod, 100-seed weight and biological yield (**Jain *et al.*, 2015**).

Table 4.6.1a Path coefficient analysis showing the direct and indirect effects of various characters on yield per plant at genotypic level in F₂ generation of soybean

Sl. No	Character	Days to 50 % flowering	Dry matter weight per plant (g)	Plant height (cm)	Basal node height (cm)	Basal pod height (cm)	Number of nodes per plant	Number of primary branches per plant	Number of pods per plant	Number of seeds per pod	100-seed weight (g)	Harvest index (%)
1	Days to 50 % flowering	-0.027	-0.014	-0.005	0.009	0.000	-0.005	-0.005	-0.009	0.001	-0.008	0.004
2	Dry matter weight per plant (g)	0.448	0.865	0.512	-0.542	0.049	0.197	0.236	0.548	0.270	0.542	-0.076
3	Plant height (cm)	-0.015	-0.047	-0.079	0.030	-0.035	-0.003	-0.007	-0.046	-0.025	-0.021	-0.003
4	Basal node height (cm)	0.018	0.033	0.020	-0.053	0.004	0.017	0.016	0.027	0.024	0.040	0.031
5	Basal pod height (cm)	0.000	0.002	0.014	-0.003	0.032	0.002	0.000	0.004	0.010	0.001	0.002
6	Number of nodes per plant	-0.021	-0.026	-0.004	0.037	-0.007	-0.114	-0.006	-0.024	0.011	-0.016	-0.048
7	Number of primary branches per plant	0.014	0.021	0.006	-0.023	-0.001	0.004	0.075	0.014	0.045	0.016	0.020
8	Number of pods per plant	-0.019	-0.034	-0.032	0.028	-0.007	-0.011	-0.010	-0.054	-0.016	-0.015	-0.011
9	Number of seeds per pod	0.005	-0.032	-0.032	0.046	-0.032	0.010	-0.061	-0.030	-0.101	-0.032	-0.047
10	100-seed weight (g)	-0.051	-0.106	-0.046	0.128	-0.003	-0.023	-0.035	-0.048	-0.053	-0.169	-0.056
11	Harvest index (%)	-0.135	-0.082	0.036	-0.544	0.055	0.396	0.247	0.190	0.440	0.310	0.935
	Correlation with yield	0.218	0.58	0.39	-0.888	0.056	0.469	0.451	0.572	0.607	0.647	0.749

Residual 0.00732

Table 4.6.1b Path Coefficient analysis showing the direct and indirect effects of various characters on yield per plant at phenotypic level in F₂ generation of soybean

Sl. No	Character	Days to 50 % flowering	Dry matter weight per plant (g)	Plant height (cm)	Basal node height (cm)	Basal pod height (cm)	Number of nodes per plant	Number of primary branches per plant	Number of pods per plant	Number of seeds per pod	100-seed weight (g)	Harvest index (%)
1	Days to 50 % flowering	-0.016	-0.007	-0.003	0.004	0.000	-0.002	-0.003	-0.005	0.003	-0.003	0.002
2	Dry matter weight per plant (g)	0.250	0.589	0.324	-0.326	0.018	0.134	0.132	0.360	0.143	0.321	-0.077
3	Plant height (cm)	-0.004	-0.012	-0.022	0.008	-0.009	0.000	-0.002	-0.012	-0.004	-0.005	-0.001
4	Basal node height (cm)	0.028	0.058	0.038	-0.105	0.006	0.032	0.031	0.053	0.028	0.073	0.061
5	Basal pod height (cm)	0.000	0.000	-0.006	0.001	-0.016	0.000	0.001	-0.002	-0.003	0.000	-0.001
6	Number of nodes per plant	0.000	-0.001	0.000	0.001	0.000	-0.002	0.000	0.000	0.000	0.000	-0.001
7	Number of primary branches per plant	0.007	0.009	0.003	-0.012	-0.002	0.005	0.042	0.007	0.012	0.006	0.010
8	Number of pods per plant	0.005	0.012	0.011	-0.009	0.002	0.004	0.003	0.019	0.004	0.005	0.004
9	Number of seeds per pod	-0.007	0.009	0.007	-0.009	0.006	0.002	0.010	0.007	0.035	0.009	0.010
10	100-seed weight (g)	-0.004	-0.012	-0.005	0.015	0.000	-0.004	-0.003	-0.006	-0.006	-0.022	-0.007
11	Harvest index (%)	-0.092	-0.097	0.029	-0.426	0.042	0.290	0.184	0.146	0.202	0.248	0.743
	Correlation with yield	0.167	0.548	0.375	-0.86	0.048	0.458	0.395	0.567	0.414	0.632[*]	0.742

Residual 0.01972

Table 4.6.2a: Path coefficient analysis showing the direct and indirect effects of various characters on yield per plant at genotypic level in F₃ generation of soybean

Sl. No	Character	Days to 50 % flowering	Dry matter weight per plant (g)	Plant height (cm)	Basal node height (cm)	Basal pod height (cm)	Number of nodes per plant	Number of primary branches per plant	Number of pods per plant	Number of seeds per pod	100-seed weight (g)	Harvest index (%)
1	Days to 50 % flowering	0.111	0.006	0.014	0.068	-0.030	-0.041	0.025	0.013	-0.027	0.010	-0.006
2	Dry matter weight per plant (g)	0.008	0.139	0.074	0.087	0.046	-0.020	0.119	0.125	0.122	0.051	0.086
3	Plant height (cm)	0.012	0.050	0.093	0.059	0.068	-0.045	0.063	0.043	0.040	-0.008	0.032
4	Basal node height (cm)	0.056	0.057	0.057	0.091	0.017	-0.003	0.058	0.051	0.032	0.043	-0.014
5	Basal pod height (cm)	-0.012	0.014	0.031	0.008	0.043	-0.001	0.026	0.008	0.018	-0.015	0.004
6	Number of nodes per plant	-0.065	-0.025	-0.086	-0.005	-0.003	0.177	-0.036	-0.035	-0.026	0.006	-0.056
7	Number of primary branches per plant	-0.102	-0.389	-0.306	-0.289	-0.269	0.093	-0.452	-0.366	-0.336	0.002	-0.238
8	Number of pods per plant	0.094	0.744	0.384	0.469	0.158	-0.162	0.671	0.828	0.637	0.432	0.549
9	Number of seeds per pod	-0.066	0.242	0.117	0.096	0.112	-0.040	0.204	0.212	0.275	0.042	0.162
10	100-seed weight (g)	-0.016	-0.063	0.015	-0.081	0.059	-0.006	0.001	-0.090	-0.026	-0.172	0.006
11	Harvest index (%)	-0.014	0.152	0.085	-0.037	0.025	-0.078	0.129	0.163	0.145	-0.008	0.246
	Correlation with yield	0.005	0.927	0.479	0.465	0.226	-0.125	0.807	0.952	0.853	0.382	0.770

Residual 0.01510

Table 4.6.2b: Path coefficient analysis showing the direct and indirect effects of various characters on yield per plant at phenotypic level in F₃ generation of soybean

Sl. No	Character	Days to 50 % flowering	Dry matter weight per plant (g)	Plant height (cm)	Basal node height (cm)	Basal pod height (cm)	Number of nodes per plant	Number of primary branches per plant	Number of pods per plant	Number of seeds per pod	100-seed weight (g)	Harvest index (%)
1	Days to 50 % flowering	-0.017	-0.001	-0.002	-0.007	0.004	0.006	-0.003	-0.002	0.004	-0.002	0.001
2	Dry matter weight per plant (g)	0.008	0.161	0.081	0.068	0.047	-0.020	0.106	0.142	0.134	0.040	0.097
3	Plant height (cm)	0.018	0.075	0.150	0.043	0.103	-0.066	0.064	0.067	0.060	-0.002	0.047
4	Basal node height (cm)	0.028	0.027	0.019	0.065	0.010	0.000	0.030	0.025	0.013	0.004	-0.004
5	Basal pod height (cm)	0.028	-0.039	-0.092	-0.020	-0.133	0.004	-0.052	-0.023	-0.051	0.039	-0.015
6	Number of nodes per plant	-0.057	-0.020	-0.071	0.001	-0.005	0.162	-0.027	-0.030	-0.015	0.003	-0.054
7	Number of primary branches per plant	0.005	0.020	0.013	0.014	0.012	-0.005	0.031	0.018	0.019	-0.005	0.012
8	Number of pods per plant	0.048	0.351	0.178	0.157	0.069	-0.075	0.231	0.400	0.269	0.191	0.258
9	Number of seeds per pod	-0.041	0.145	0.070	0.034	0.066	-0.016	0.107	0.118	0.175	0.000	0.091
10	100-seed weight (g)	0.003	0.007	0.000	0.002	-0.008	0.000	-0.005	0.013	0.000	0.028	0.000
11	Harvest index (%)	-0.015	0.197	0.103	-0.021	0.036	-0.109	0.130	0.211	0.171	0.000	0.328
	Correlation with yield	0.008	0.923	0.448	0.335	0.200	-0.119	0.611	0.938	0.778	0.295	0.762

Residual 0.01988

In the present study, the estimates of the residual factor in F_2 were 0.0197 and 0.0073 at phenotypic and genotypic levels, respectively, while in F_3 there were 0.0198 and 0.0151 at phenotypic and genotypic levels respectively indicating that there are some other minor factors which had not been considered here and need to be included in this analysis to bring the desired improvement in yield. A residual value in the path analysis indicated the importance of other yield attributes not included in this study. **Dixit and Singh (1975), Bhattacharya (1999), Chakraborty and Haque (2000), Verma (2004), Singh *et al.* (2008), Singh *et al.* (2012), Arshad *et al.* (2014) and Kaushar (2014) and Joshi (2015)** also reported similar findings.

Ramanna *et al.* (2000) reported highest positive direct effect of number of pods per plant on seed yield followed by 100-seed weight and also observed a negative direct effect of days to 50% flowering on seed yield. Similar findings were reported for number of pods per plant (**Gaikwad *et al.*, 2007; Karnwal and Singh, 2009; Iqbal *et al.*, 2010 and Gireesh *et al.*, 2012**), 100-seed weight and seeds per pod (**Chandel *et al.*, 2014**), number of primary branches per plant, number of pods per plant, number of seeds per pod and 100-seed weight (**Thakur *et al.*, 2015**), number of primary branches per plant, pods per plant, seeds per pod, 100-seed weight and biological yield (**Jain *et al.*, 2015**).

On the basis of results obtained from the correlation and path coefficient analysis, the characters like number of primary branches per plant, number of nodes per plant, number of pods per plant, number of seeds per pod, dry matter weight per plant and harvest index were found to be the most important yield attributes contributing maximum towards higher yields in soybean. Hence, more emphasis laid on these characters during selection would be highly rewarding as it facilitates the identification of promising genotypes with superior yield in soybean.

4.7 Molecular marker analysis

Simple sequence repeat markers (SSR) are being extensively used in genome studies, marker assisted selection and cultivar identification and are well known for their versatility in providing a quick assay and for their highly informative data (**Joshi, 2015**). Twenty SSR markers were used out of which seventeen (Satt184, Satt187, Satt146, Satt197, Satt200, Satt228, Satt267, Satt268, Satt277, Satt281, Satt300, Satt433, Satt449, Satt508, Satt527, Satt565 and Satt586) gave amplification for assessing molecular diversity among twenty-two soybean lines (**Table 4.7.1**) in current study.

Table 4.7.1: List of genotypes used for molecular diversity analysis through SSR markers

Sl. No.	Genotypes
1	JS 20-59
2	JS 20-64
3	JS 20-69
4	JS 97-52
5	JS 20-54
6	JS 20-63
7	DS12-5
8	PS 1584
9	PS 1583
10	PS 1092
11	JS 20-41
12	Bragg
13	PS 1042
14	JS 335
15	PS 1225
16	RVS 200-1
17	PS 19
18	Pb-1
19	SL-688
20	PS 1347
21	JS 20-29
22	JS 20-55

The primer wise analysis of SSR markers have been described on pages along with amplification profiles (4.7.1 to 4.7.4).

Satt184

This primer detected two polymorphic loci across the twenty-two genotypes. The SSR amplicons varied from 150-175 bp. The PIC value of this primer was observed to be 0.301.

Satt187

The primer amplified three polymorphic bands which varied from 185-260 bp. The PIC value of this primer was 0.643.

Satt200

The primer amplified single polymorphic band across the twenty-two genotypes present at 200 bp. The PIC value of this primer was 0.339.

Satt228

The primer detected two polymorphic bands ranged from 200 to 215 bp with PIC value 0.640.

Satt267

The Satt267 generated two polymorphic bands that were ranged from 200-220 bp. Satt267 showed PIC value of 0.619.

Satt268

The primer pair resulted in two amplified SSR locus ranged from 195 to 225bp. The PIC value of this primer was 0.659.

Satt277

The primer pair resulted in four amplified SSR locus. The bands ranged from 160 to 300 bp. The PIC value of this primer was found to be 0.883.

Satt281

Five polymorphic loci were generated and ranged from 160 to 800 bp. The PIC value displayed by the primer was 0.836.

Satt300

This primer pair generated two polymorphic loci and displayed a range from 200 to 230 bp. The PIC value of this primer was 0.640.

Satt433

The Satt433 generated only one polymorphic band at 180 bp. The primer had PIC value of 0.207.

Satt508

One polymorphic locus was generated at 265 bp by this primer. The PIC value of Satt508 primer was 0.372.

Satt527

The primer pair generated two polymorphic loci and ranged from 190 to 215bp. The PIC value of this primer was 0.431.

Satt586

The primer pair generated only one polymorphic locus at 185 bp. The PIC value of this primer was 0.339.

4.7.1 Genetic diversity/DNA Polymorphism analysis of soybean genotypes using SSR markers

Seventeen markers were initially screened on twenty-two genotypes. Out of seventeen, thirteen polymorphic and four monomorphic markers were used to generate SSR profiles of genotypes. The number of bands generated by seventeen markers for all the twenty-two genotypes was 32, which gave an average of 1.88 alleles per marker. Gel electrophoresis photographs of SSR marker profile of parental lines are given in figure 4.7.1 to 4.7.4. The photographs revealed minimum of one allele to five alleles. However, maximum number of five polymorphic bands was identified in Satt281. Average percentage of all bands that were polymorphic is of 100% for all primers. Amplified alleles varied in size from 150 to 800 bp. The total number of bands, number of polymorphic bands, percentage of polymorphic bands and PIC (Polymorphic Information Content) value obtained from each marker are shown in Table 4.7.2. The applicability of genetic markers to analyse a trait depends on the extent of

polymorphism detectable with the given markers. It is thus necessary to establish the polymorphic information content (PIC), which express the ability of a locus to discriminate between the lines. The PIC values of SSR primers ranged from 0.301 (Satt184) to 0.883 (Satt277) with mean value of 0.53. This indicated that SSR markers could be efficiently applied to detect polymorphism even with relatively low number of alleles. The markers namely, Satt187, Satt228, Satt267, Satt268, Satt277, Satt281 and Satt300 had PIC values more than average whereas, Satt184, Satt200, Satt433, Satt508, Satt527 and Satt586 had PIC values less than the average. Marker Satt146, satt197, Satt449 and Satt565 were monomorphic, hence resulted in no PIC.

The Jaccard's similarity coefficient estimates between pair of different genotypes varied from 0.286 (JS 20-59 and Pb1, JS 20-54 and Pb1, PS 1584 and PS 1347, JS 20-41 and PS 1347) to 0.82 (JS 97-52 and JS 20-29, PS 1583 and RVS 200-1, PS 1583 and JS 20-29 and PS 1042 and Pb1) genetic similarity, as displayed in **Table 4.7.4**.

4.7.2 Genotype clustering based on molecular data

The UPGMA (un-weighted pair group method with arithmetic mean) dendrogram was constructed using Jaccard's similarity coefficient of SSR marker data generated on twenty-two genotypes employing the programme NTSYS 2.11 and Powermarker v3.25 (**Fig 4.7.5**).

UPGMA ordered the twenty-two genotypes into two main groups namely Group A and Group B. Group A further divided into two subgroups *i.e.*, Subgroup A1 and A2. Subgroup A1 comprises of PS 1225 forming Cluster I while subgroup A2 consists of two clusters (Cluster II and III). Cluster II consisted of only one genotype *i.e.* JS 335 and Cluster III consisted of JS 20-41, PS 19, PS 1042, Pb1 and SL 688. Group B further divided into two subgroups, B1 and B2. Subgroup B1 comprises of three clusters (Cluster IV, V and cluster VI), of which cluster IV comprised of PS 1584 and JS 20-55, cluster V consisted of only one genotype JS 20-69 and cluster VI consisted of JS 20-64, JS 20-63, DS 12-5, PS 1092 and Bragg. Cluster VII of subgroup B2 comprises of maximum genotypes *viz.*, JS 20-59, JS 97-52, JS 20-29, PS 1583, RVS 200-1, JS 20-54 and PS 1347.

The parents of all the crosses taken up for the experiment were in different clusters except PS 1583 and JS 20-29. Both of which were in same cluster VII. Genetic

diversity is critical to crop breeding in cultivar development, germplasm enhancement and end-product commercialization. The genetic structure and genetic diversity of regular grain-type soybean have been well analysed (**Brown-Guedira *et al.*, 2000; Cui *et al.*, 2001; Ude *et al.*, 2003; Li *et al.*, 2008, Kaushar, 2014 and Rani *et al.*, 2016**). Breeding for food-grade soybean is a fairly new challenge and information on genetic structure and diversity of food grade soybean is very limited. Exploring the genetic diversity of soybeans from different places will help breeders to utilize available germplasm for breeding specialty soybeans and for broadening genetic pool.

In the present study, molecular diversity was assessed by seventeen SSR markers: thirteen of them showed polymorphism and produced 32 polymorphic alleles (100 per cent polymorphism) among twenty-two parental genotypes with an average of 1.88 alleles per locus. Similar results were reported by **Dayaman *et al.* (2009)** who observed 4.45 alleles per locus and 97.95% polymorphism among 45 soybean accessions at 11SSR loci. The SSR diversity observed in the present study is comparable to those reported by **Joshi (2015)** who reported the average number of alleles per primer was 1.9, while polymorphism percentage was 100%. Similar findings were also reported by **Zhang *et al.* (2013)** who detected 3.23 alleles per locus among the forty-eight soybean accessions at 22 EST-SSR loci. **Kausar (2014)** observed 1.85 alleles per primer, whereas polymorphism percentage in the bands was 100. **Gupta and Manjaya (2016)** also reported total of 54 alleles at 12 polymorphic SSR loci with an average of 4.5 alleles per locus in 23 soybean genotypes. **Ristova *et al.* (2010)** detected four alleles per locus and an average marker diversity of 0.585 among 23 soybean genotypes from South-eastern Europe and five plant introductions at 20 SSR loci. They also characterized allele frequency distribution with a high proportion of alleles at very low frequencies with 11% of unique alleles. **Tavud-Pirra *et al.* (2009)** observed five alleles per locus and an average marker diversity of 0.65 among 32 breeding lines. Various researchers have reported high number of alleles per locus, **Fu *et al.* (2007)**, who detected 6.3 alleles per locus (included null alleles) and an average value of polymorphic information content of 0.63 among forty five Canadian soybean cultivars and thirty-seven exotic germplasm accessions, analysed at 37 SSR loci. Similarly, **Diwan and Cregan (1997)** reported 10.1 alleles per locus thirty-five North American cultivars examined at twenty SSR loci. Similar findings on high average number of

alleles per locus (over 10) have also been reported by various workers (**Abe *et al.*, 2003; Wang *et al.*, 2006; Wang and Takahata, 2007; Wang *et al.*, 2008; Tavaud *et al.*, 2009; Yoon *et al.*, 2009**), but in these studies, the workers have analysed higher numbers of genotypes compared to the present study. In contrast, the average genetic distance (similarity) among a set of genotypes measures genetic diversity at the population level (**Lu and Bernardo, 2001**). Compared to results reported by **Fu *et al.* (2007)** we found a higher level of genetic diversity among twenty soybean genotypes expressed in terms of genetic similarities. Cluster analysis separated all genotypes from each other based on mean genetic similarity coefficient (an arbitrarily line for clustering of genotypes suggested by **Bhatt (1969)** and assigned them into groups, which largely corresponded to their origin and pedigree. Grouping of genotypes have revealed the congruency of the respective clusters with the known pedigrees. For example (JS 20-59, JS 97-52, JS 20-29 and JS 20-54) were clustered together in cluster VII. Similar results were also reported by **Ristova *et al.* (2010) Kaushar (2014), Joshi (2015) and Rani *et al.* (2016)**. **Dayaman *et al.* (2009)** also clustered 45 soybean accessions according to their place of origin. The molecular analysis proves to be an aid in plant breeding to identify the diverse materials in the early step of the breeding programme. In the research performed, the relatively low average number of alleles per locus observed in the genotypes indicated that the genetic base of the research material was relatively narrow. To ensure sustaining breeding progress in the future, the introduction of new germplasms in breeding programmes seems to be essential.

Table 4.7.2 Summary of SSR amplified products in twenty-two genotypes of soybean

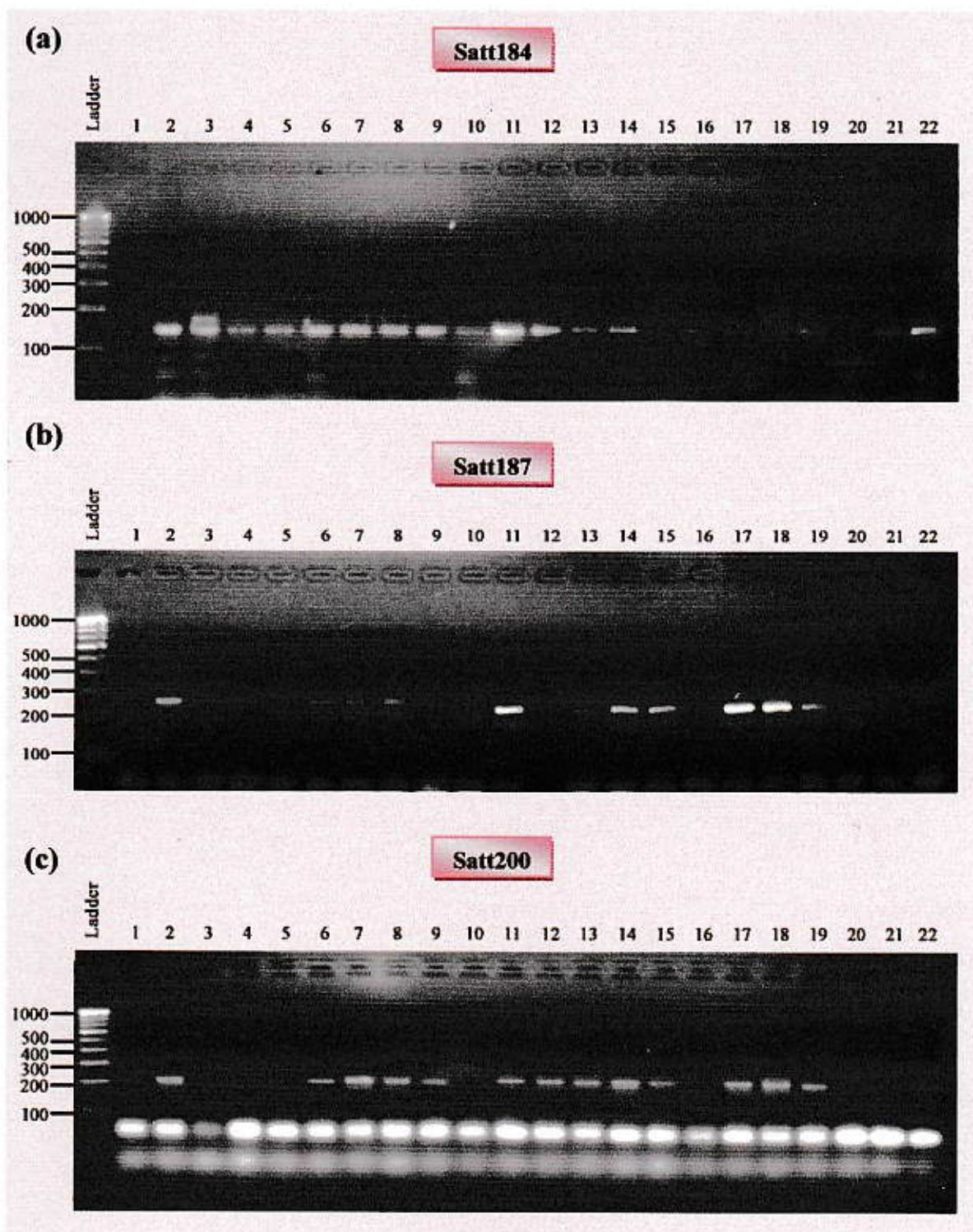
Specification	Particular
Total number of markers tested	17
Number of polymorphic markers	13
Total number of monomorphic markers	4
Total number of alleles amplified	32
Size range of amplified alleles (in bp)	150-800
Average number of alleles per primer	1.88
Total number of polymorphic bands identified	28
Total number of monomorphic bands identified	4
Percentage of all bands that were polymorphic	100

Table 4.7.3 Amplified alleles, polymorphism and PIC values obtained with SSR primers

S. No.	Primer Code	No. of Allele Amplified	No. of Polymorphic Allele	Percentage Polymorphism	Range of Amplified Allele (bp)	Major Allele Frequency	Gene Diversity	PIC Value
1	Satt184	2	2	100	150-175	0.818	0.318	0.301
2	Satt187	3	3	100	185-260	0.409	0.665	0.643
3	Satt200	1	1	100	200	0.636	0.463	0.339
4	Satt228	2	2	100	200-215	0.500	0.665	0.640
5	Satt267	2	2	100	200-220	0.409	0.678	0.619
6	Satt268	2	2	100	195-225	0.318	0.715	0.659
7	Satt277	4	4	100	160-300	0.591	0.603	0.883
8	Satt281	5	5	100	160-800	0.318	0.826	0.836
9	Satt300	2	2	100	200-230	0.409	0.698	0.640
10	Satt433	1	1	100	180	0.818	0.298	0.207
11	Satt508	1	1	100	265	0.545	0.496	0.372
12	Satt527	2	2	100	190-215	0.591	0.483	0.431
13	Satt586	1	1	100	185	0.682	0.434	0.339

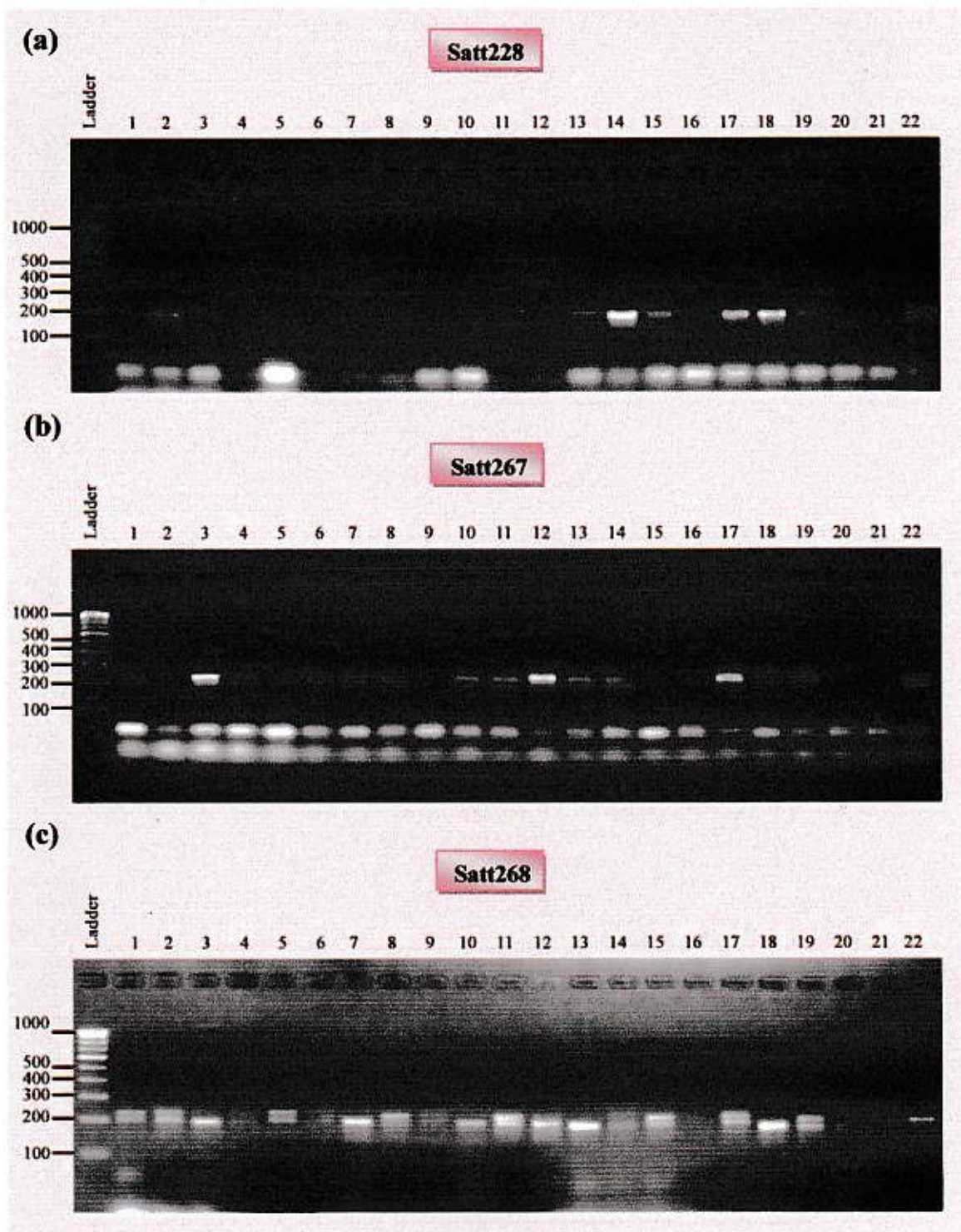
Table 4.7.4: Similarity coefficient between genotypes using thirteen SSR profiles

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22
1	1.00																					
2	0.58	1.00																				
3	0.65	0.50	1.00																			
4	0.79	0.50	0.72	1.00																		
5	0.75	0.61	0.61	0.61	1.00																	
6	0.65	0.72	0.65	0.72	0.54	1.00																
7	0.61	0.61	0.68	0.68	0.58	0.75	1.00															
8	0.50	0.65	0.58	0.65	0.54	0.65	0.75	1.00														
9	0.79	0.65	0.58	0.79	0.68	0.72	0.54	0.50	1.00													
10	0.58	0.65	0.58	0.58	0.61	0.72	0.75	0.58	0.58	1.00												
11	0.36	0.65	0.50	0.36	0.54	0.50	0.54	0.58	0.43	0.50	1.00											
12	0.65	0.58	0.65	0.58	0.61	0.72	0.75	0.50	0.58	0.65	0.58	1.00										
13	0.47	0.40	0.61	0.54	0.50	0.40	0.50	0.47	0.54	0.40	0.75	0.47	1.00									
14	0.54	0.54	0.54	0.61	0.36	0.47	0.58	0.47	0.54	0.54	0.54	0.68	0.65	1.00								
15	0.36	0.58	0.50	0.36	0.47	0.43	0.33	0.43	0.43	0.36	0.58	0.36	0.47	0.40	1.00							
16	0.68	0.68	0.61	0.75	0.72	0.68	0.58	0.54	0.83	0.68	0.47	0.54	0.43	0.50	0.54	1.00						
17	0.36	0.58	0.43	0.36	0.47	0.36	0.40	0.58	0.36	0.36	0.79	0.43	0.75	0.61	0.58	0.33	1.00					
18	0.29	0.43	0.50	0.36	0.40	0.29	0.40	0.43	0.43	0.36	0.72	0.43	0.83	0.61	0.50	0.33	0.72	1.00				
19	0.54	0.47	0.61	0.54	0.50	0.40	0.58	0.61	0.47	0.33	0.68	0.54	0.79	0.65	0.54	0.36	0.68	0.75	1.00			
20	0.65	0.43	0.43	0.65	0.47	0.50	0.40	0.29	0.72	0.50	0.29	0.36	0.47	0.54	0.58	0.75	0.36	0.36	0.40	1.00		
21	0.75	0.54	0.61	0.83	0.65	0.75	0.65	0.54	0.83	0.54	0.47	0.61	0.65	0.50	0.33	0.65	0.47	0.47	0.50	0.61	1.00	
22	0.47	0.47	0.61	0.54	0.50	0.54	0.65	0.68	0.40	0.47	0.54	0.68	0.50	0.58	0.40	0.43	0.54	0.54	0.58	0.33	0.58	1.00



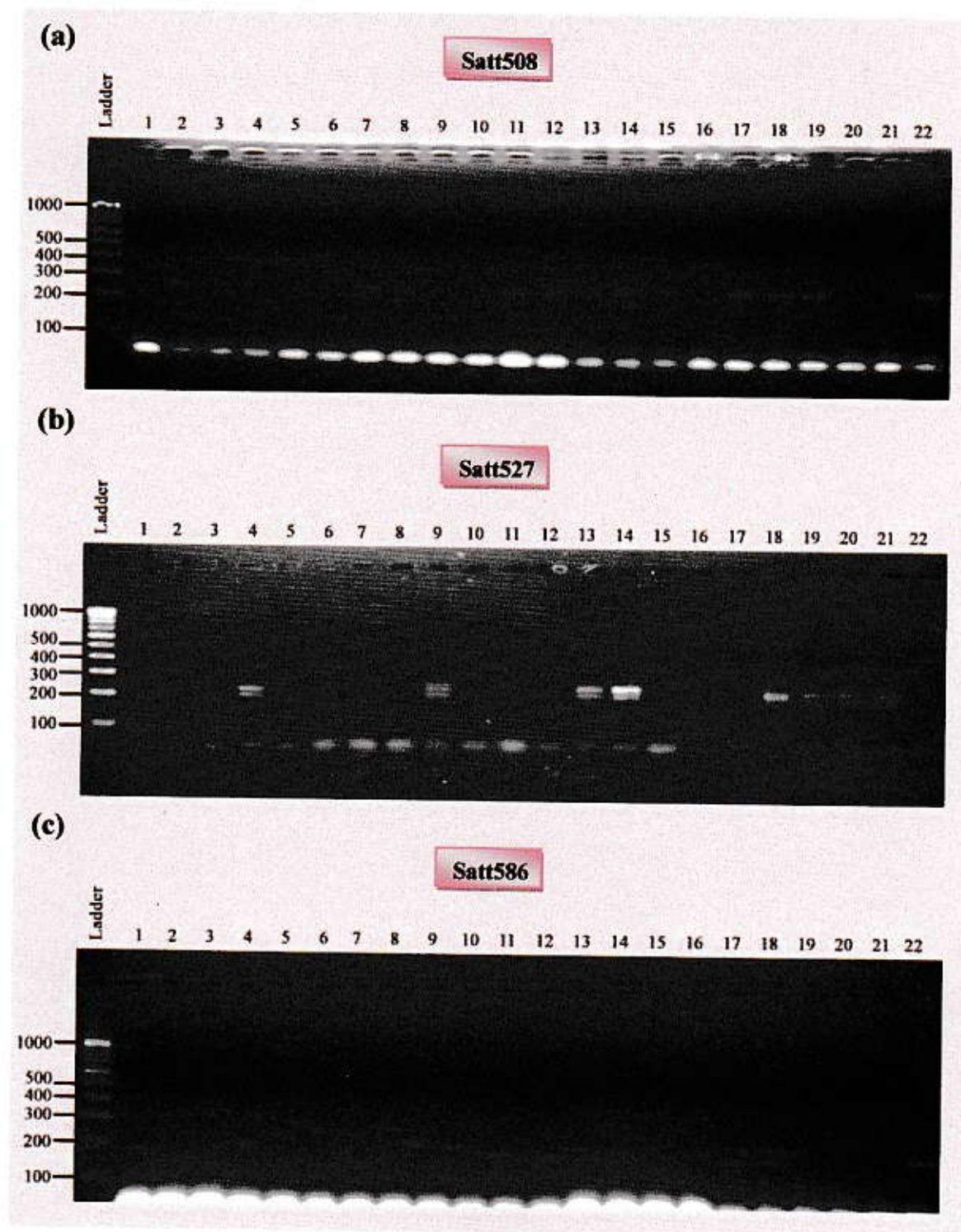
1=JS 20-59, 2=JS 20-64, 3=JS 20-69, 4=JS 97-52, 5=JS 20-54, 6=JS 20-63, 7=DS12-5, 8=PS 1584, 9=PS 1583, 10=PS 1092, 11=JS 20-41, 12=Bragg, 13=PS 1042, 14=JS 335, 15=PS 1225, 16=RVS 200-1, 17=PS 19, 18=Pb-1, 19=SL-688, 20=PS 1347, 21=JS 20-29, 22=JS 20-55.

Fig. 4.7.1.: Amplification profile of 22 soybean genotypes (1-22) by SSR markers (a) Satt184 (b) Satt187 and (c) Satt200



1=JS 20-59, 2=JS 20-64, 3=JS 20-69, 4=JS 97-52, 5=JS 20-54, 6=JS 20-63, 7=DS12-5, 8=PS 1584, 9=PS 1583, 10=PS 1092, 11=JS 20-41, 12=Bragg, 13=PS 1042, 14=JS 335, 15=PS 1225, 16=RVS 200-1, 17=PS 19, 18=Pb-1, 19=SL-688, 20=PS 1347, 21=JS 20-29, 22=JS 20-55.

Fig. 4.7.2: Amplification profile of 22 soybean genotypes (1-22) by SSR markers (a) Satt228 (b) Satt267 and (c) Satt268



1=JS 20-59, 2=JS 20-64, 3=JS 20-69, 4=JS 97-52, 5=JS 20-54, 6=JS 20-63, 7=DS12-5, 8=PS 1584, 9=PS 1583, 10=PS 1092, 11=JS 20-41, 12=Bragg, 13=PS 1042, 14=JS 335, 15=PS 1225, 16=RVS 200-1, 17=PS 19, 18=Pb-1, 19=SL-688, 20=PS 1347, 21=JS 20-29, 22=JS 20-55.

Fig. 4.7.4: Amplification profile of 22 soybean genotypes (1-22) by SSR markers
(a) Satt508 (b) Satt527 and (c) Satt586

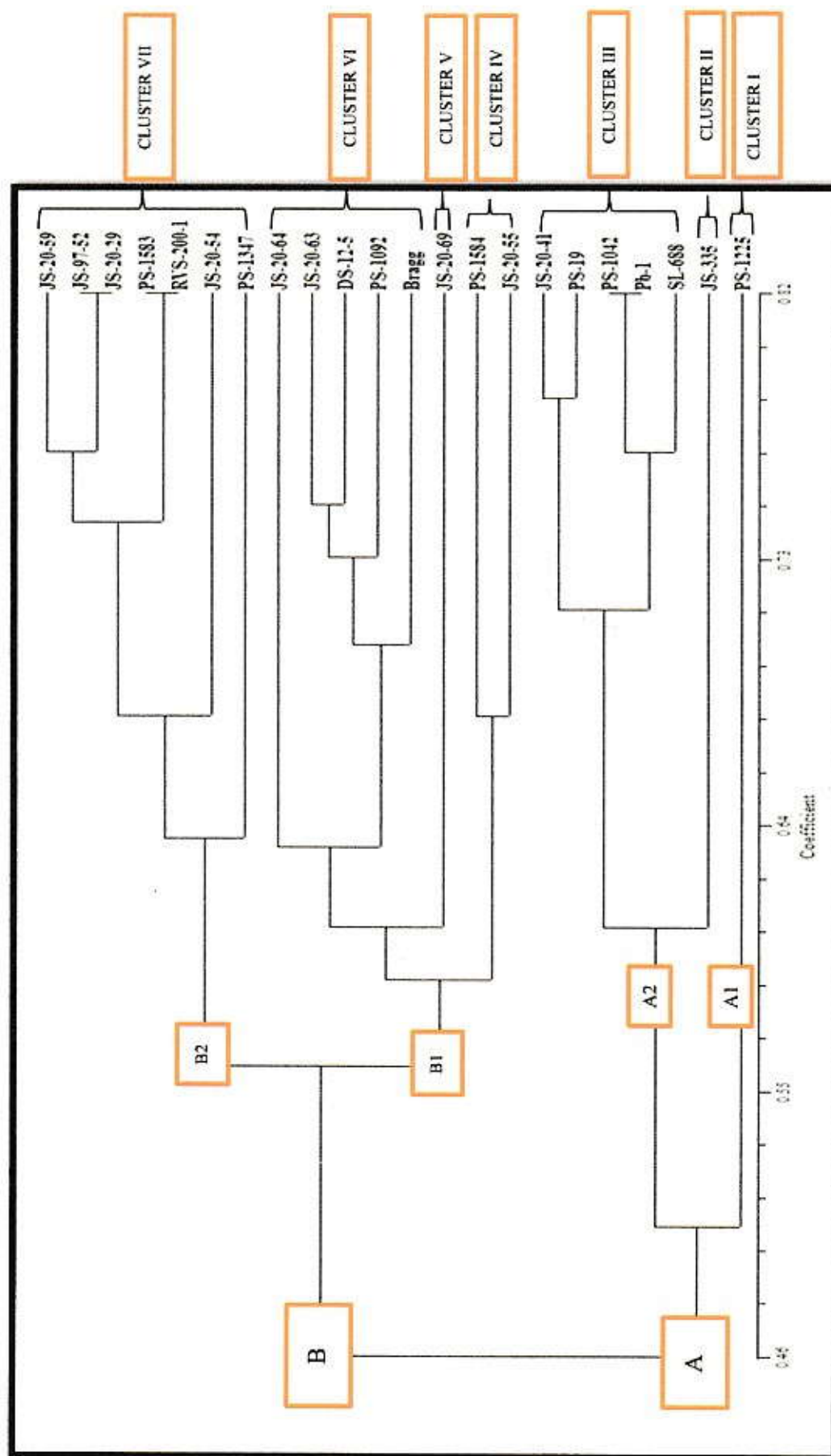


Fig. 4.7.5: Dendrogram of soybean genotypes based on the SSR marker data set using UPGMA analysis



Summary and Conclusions



The present investigation entitled “**Early generation selection based on genetic parameters and molecular diversity in parental lines of soybean [*Glycine max* (L.) Merrill**” was undertaken with the following objectives:

1. To estimate the effectiveness of early generation selection in F₂ and F₃ based on genetic parameters
2. To estimate the extent of genetic variability for various quantitative traits in early generation
3. To examine the frequency of transgressive segregants in F₂ generation.
4. To assess the inter-character associations and direct and indirect effects of different component characters on yield.
5. To study molecular genetic diversity among the parents using the molecular marker technique.

The present investigation was carried out during *kharif*, 2015 and 2016 at Norman E. Borlaug Crop Research Centre of G.B. Pant University of Agriculture & Technology, Pantnagar, Uttarakhand. In F₂ generation, the experimental material comprised of 36 genotypes (fourteen F₂ crosses along with twenty parents and two checks) were analyzed in randomized complete block design while in F₃ generation, fourteen F₃ crosses along with their twenty-one progenies were evaluated in compact family block design.

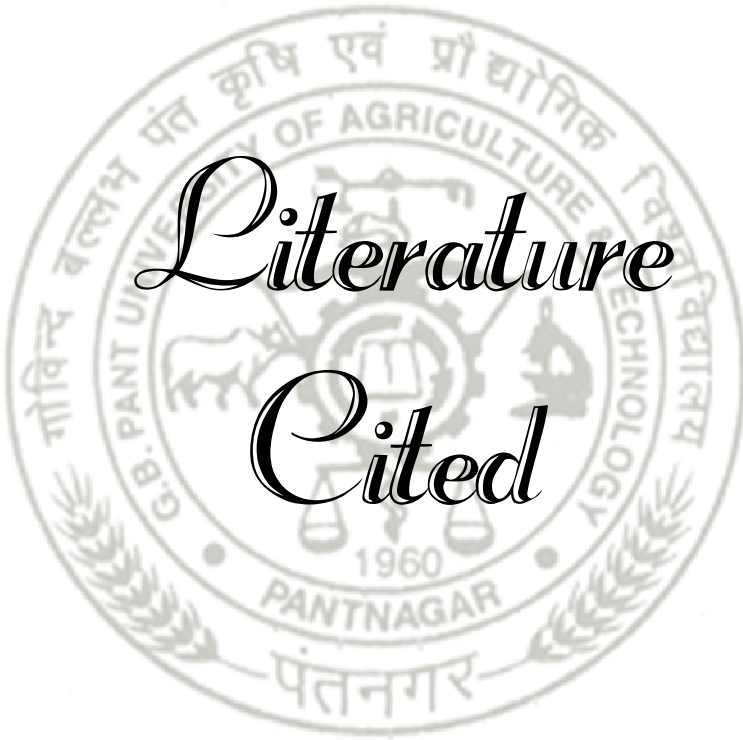
The data recorded on twelve different characters like days to 50% flowering, dry matter weight per plant, plant height, basal node height, basal pod height, number of nodes per plant, number of primary branches per plant, number of pods per plant, number of seeds per pod, seed yield per plant, 100-seed weight and harvest index were subjected to appropriate statistical and biometrical analysis and the results are summarized below:

- The analysis of variance for different characters revealed that highly significant differences among the treatments for all the characters studied in both the generations, indicating the presence of sufficient variability among the experimental material.
- The present study revealed adequate variation in all the characters under study in F_2 and F_3 generation. In both the generation, the estimated values of phenotypic coefficient of variation were higher than genotypic coefficient of variation for all the characters studied. Seed yield per plant exhibited highest phenotypic coefficient of variation and genotypic coefficient of variation in both the generations.
- Most of the traits included in this investigation were considered highly heritable as they have shown moderate to high estimate of broad sense heritability. In F_2 generation, highest heritability in broad sense was obtained for plant height and seed yield per plant, however, in F_3 highest heritability estimates were obtained for seed yield per plant, harvest index and dry matter weight per plant.
- The expected genetic advance in F_2 varied from 0.22 (number of seeds per pod) to 31.88 % (seed yield per plant). Similarly in F_3 , genetic advance varied from 0.19 (number of seeds per pod) to 34 % (seed yield per plant). Genetic advance as per cent of mean (5%), exhibited highest value for seed yield per plant (71.10%) and (62.25%) in F_2 and F_3 , respectively. High heritability coupled with high genetic advance was observed for plant height, number of nodes per plant, harvest index, dry matter weight per plant, basal pod height, number of pods per plant and seed yield per plant in both the generations.
- The estimates of inter-generation correlation revealed that four characters *i.e.*, days to 50% flowering, plant height, number of pods per plant and seed yield per plant showed positive and significant value for maximum number of crosses.
- The F_2 vs F_3 regression estimate was observed to be in correspondence with the correlation estimate. Three characters *i.e.*, days to 50% flowering, plant height and seed yield per plant exhibited significant and positive value of regression coefficient.

- The response to selection estimated for four characters *viz.*, dry matter weight per plant, number of pods per plant, harvest index and seed yield per plant revealed that number of pods per plant and seed yield per plant showed positive and significant response to selection for all the crosses in both the generations.
- For seed yield per plant, eight F₃ crosses of high value group showed higher mean performance than the mean performance of respective F₂ parents selected for high value, while six crosses showed the lowest value of seed yield in comparison to the lines selected for low value in F₂ generation.
- Out of fourteen, ten crosses showed higher value of mean performance of F₃ bulk progeny for seed yield per plant than the mean performance of high value group of F₃, while mean performance of bulk F₃ progeny exhibited higher value than the respective F₂ mean for all the crosses, implying that bulk method is more effective method than the pedigree method.
- The study of realized heritability revealed that maximum crosses displayed high value of realized heritability for days to 50% flowering, number of pods per plant and seed yield per plant. The range of realized heritability for high group in seed yield per plant was from 0.33 (JS 20-64 X JS 20-54) to 3.76 (RVS 200-1 X PS 1092).
- The *per se* performance of seed yield per plant in F₂ generation was highest for three crosses, *i.e.*, PS 1584 X JS 20-69 (20.7g), PS 1583 X JS 20-29 (20.08g) and PS 1225 X PS 1347 (19.58 g).
- The *per se* performance of F₃ high yielding group for seed yield per plant was observed highest in PS 1584 X JS 20-69 (42.63g), PS 1583 X JS 20-29 (33.40g) and PS 1584 X JS 20-41 (29.79g), similarly the *per se* performance of seed yield per plant in F₃ bulk was highest in PS 1584 X JS 20-69 (50.12g), JS 20-29 X JS 20-55 (39.76g) and JS 20-69 X JS 20-59 (35.63g). Out of fourteen crosses, only one cross, PS 1584 X JS 20-69 had showed higher mean performance in both the generation as well as in all the group, making it highly effective in early generation.
- Out of four characters, number of pods per plant and seed yield per plant had displayed maximum response to selection for all the crosses while estimates of response to selection for dry matter weight per plant and harvest index was not found to be significant for all the crosses.

- The study of effectiveness of early generation selection by all the genetic parameters revealed that seed yield per plant was found highly effective for selection in early generation by all the parameters studied.
- In F_2 , the range of residual heterosis for yield per plant varied from -63.58 (JS 20-64 X JS 20-54) to -3.91 (PS 1583 X Bragg) for mid parent heterosis, from -67.87 (JS 20-64 X JS 20-54) to -5.78 (PS 1042 X PS 1347) for heterobeltiosis, from -66.59 (JS 20-64 x JS 20-54) for residual heterosis over standard check PS 19 and from -66.59 (JS 20-64 x JS 20-54) for residual heterosis over standard check SL 688.
- In F_2 generation, none of the crosses showed significant and positive heterosis over mid parent, better parent and standard checks PS 19 and SL688 for seed yield per plant.
- In F_3 generation, PS 1584 X JS 20-41, PS 1583 X Bragg, PS 1584 X JS 20-69 and PS 1583 X JS 20-29 showed significant and positive residual heterosis over mid-parent. Over better parent, PS 1584 X JS 20-41 and PS 1583 X Bragg showed significant and positive residual heterosis over better parent, while PS 1584 X JS 20-69 showed positive and significant residual heterosis over both standard checks.
- Only one cross PS 1584 X JS 20-69 showed significant and positive residual heterosis over mid-parent and over both standard checks in F_3 generation for seed yield per plant.
- Most of the crosses exhibited presence of both positive and negative transgressive segregants for all the characters in F_2 . Both positive and negative transgressive segregants for days to 50 % flowering were observed in thirteen crosses. The maximum transgressive segregation for early flowering was exhibited in cross, RVS 200-1 X PS 1092.
- The maximum transgressive segregation for higher number of pods per plant was exhibited in crosses JS 20-63 X JS 97-52, PS 1583 X Bragg and JS 20-29 X JS 20-55. For higher number of seed per pod, maximum transgressive segregation was displayed by the cross, PS 1583 X Bragg. All the crosses showed positive transgressive segregants for seed yield per plant but frequency was moderate. Highest positive transgressive segregant for seed yield per plant was recorded in the cross, PS 1042 X PS 1347.

- In general, phenotypic correlations were smaller than genotypic correlations but in similar direction. In F_2 generation, seed yield per plant showed highly significant positive phenotypic and genotypic correlations for dry matter weight per plant, plant height, number of primary branches per plant, number of pods per plant, number of seeds per pod, 100-seed weight and harvest index. Whereas, in F_3 seed yield per plant showed significant and positive values of genotypic and phenotypic correlations with dry matter weight per plant, plant height, number of primary branches per plant, number of pods per plant, number of seeds per pod and harvest index.
- In F_2 , dry matter weight per plant and harvest index showed highly significant positive correlation as well as exhibited highly positive direct effect on seed yield per plant, while in F_3 number of pods per plant, displayed highly significant positive correlation and exhibited highly positive direct effect on seed yield. The positive and significant association of these traits with seed yield per plant and high direct effect of these traits towards the total yield indicated the true relationship between the characters. Hence, the direct selection for the component traits would result into the direct improvement of dependent variable, seed yield per plant.
- Out of seventeen SSR primers, thirteen were found to be polymorphic and were selected for analysis of molecular variability in twenty two soybean genotypes. The average number of alleles per primer was 1.88, while percentage of all bands that showed polymorphism was 100%. The PIC values of SSR primers ranged from 0.301 (Satt184) to 0.883 (Satt277) with mean value of 0.53.
- The Jaccard's similarity coefficient estimates between pair of different genotypes varied from 0.286 (JS 20-59 and Pb1, JS 20-54 and Pb1, PS 1584 and PS 1347, JS 20-41 and PS 1347) to 0.82 (JS 97-52 and JS 20-29, PS 1583 and RVS 200-1, PS 1583 and JS 20-29 and PS 1042 and Pb1) genetic similarity.
- The dendrogram constructed from SSR marker data divided the population of twenty-two genotypes into two main groups namely Group A and Group B. These groups further divided into subgroups which comprised the total seven clusters: Cluster I, II, III, IV, V, VI and VII. PS 1225 and JS 20-59 were found to be most distant.



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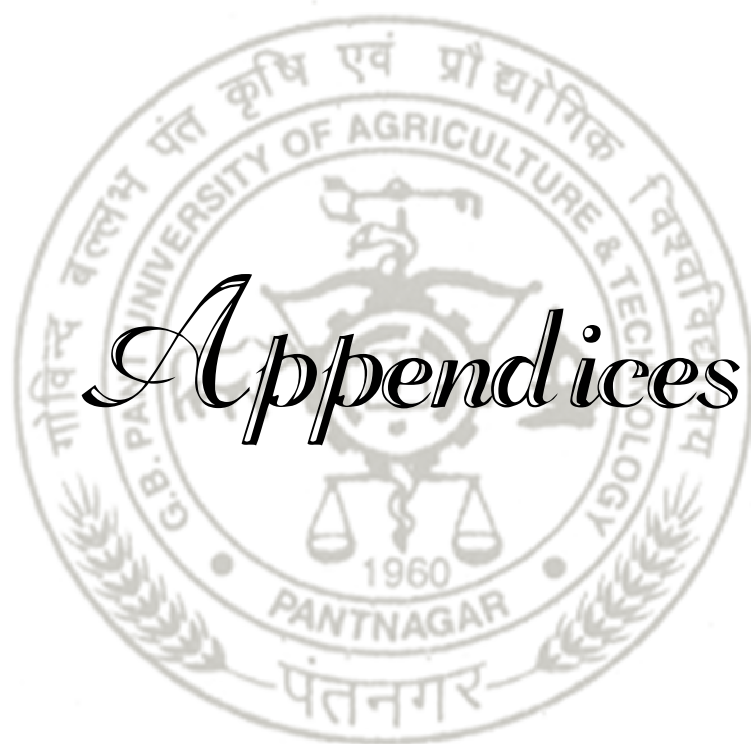
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Appendices

Appendix

Appendix 1a

Weekly weather data at Pantnagar for experimental period (June 2015 to Dec 2015)

Month	Date	Year	Metro Week No.	Temperature (°C)		Relative Humidity (%)		Rainfall (mm)	No. of Rainy Days	Sun Shine Hrs.	Wind Velocity (km/hr.)	Evap. (mm)
				Max.	Min.	712 am	1412 pm					
May-June	'28-03	2015	22	39.6	22.2	63.0	31.0	0	0	8.3	6.3	9.3
June	'04-10	2015	23	40.9	24.5	62.0	30.0	0	0	9.7	7.8	10.6
June	'11-17	2015	24	38.0	25.5	62.0	38.0	0.8	1	7.4	8.8	10.7
June	'18-24	2015	25	35.1	26.5	73.0	53.0	72.2	4	6.2	7.2	6.4
June-July	'25-01	2015	26	32.0	23.8	90.0	76.0	324.8	4	5	8.5	5.5
July	'02-08	2015	27	32.4	25.7	87.0	72.0	100	6	3.1	6.7	3.6
July	'09-15	2015	28	31.7	25.4	88.0	72.0	114.8	5	4.9	7	5.5
July	'16-22	2015	29	32.7	26.1	84.0	72.0	89.8	4	4.2	5.8	4
July	'23-29	2015	30	33.6	25.9	83.0	63.0	6.4	2	8.5	7.5	5.7
July-Aug	'30-05	2015	31	31.5	25.7	87.0	74.0	79.8	4	5	5.3	4.3
Aug	'06-12	2015	32	30.2	25.4	91.0	76.0	158.9	6	2.3	5.5	3.8
Aug	'13-19	2015	33	32.7	26.1	90.0	67.0	37.8	2	4.8	3.7	3.9
Aug	'20-26	2015	34	32.4	24.9	89.0	69.0	39	5	5.2	6.5	3.8
Aug-Sep	'27-02	2015	35	33.4	25.4	92.0	65.0	24.4	2	6.7	5.6	4.7
Sep	'03-09	2015	36	33.6	23.8	91.0	60.0	0	0	7.5	4.9	7
Sep	'10-16	2015	37	34.1	25.0	87.0	61.0	0	0	8.4	3.1	4.7
Sep	'17-23	2015	38	34.0	24.9	84.0	62.0	112	2	6.6	3.8	4.2
Sep	'24-30	2015	39	31.7	21.4	90.0	61.0	0	0	8.1	5	4
Oct	'01-07	2015	40	32.9	20.2	83.0	51.0	0	0	9.5	2.1	4.7
Oct	'08-14	2015	41	32.5	20.3	83.0	52.0	0	0	7.5	2.4	4.6
Oct	'15-21	2015	42	31.5	19.3	86.0	51.0	0	0	5.1	3.1	3.5
Oct	'22-28	2015	43	31.2	13.9	88.0	48.0	0	0	8.7	3	4
Oct-Nov	'29-04	2015	44	29.0	13.7	90.0	43.0	5	1	6.2	2.9	3
Nov	'05-11	2015	45	28.0	12.1	91.0	43.0	2	1	6.6	3	2.5
Nov	'12-18	2015	46	29.0	11.9	91.0	38.0	0	0	7.8	2.8	2.7
Nov	'19-25	2015	47	27.7	11.3	92.0	41.0	0	0	7.2	1.6	2.3
Nov-Dec	'26-02	2015	48	26.7	12.6	91.0	46.0	0	0	3.7	2.7	2.1
Dec	'03-09	2015	49	24.6	10.2	96.0	49.0	0	0	1.8	2.3	1.6
Dec	'10-16	2015	50	21.1	10.3	94.0	64.0	0	0	2.1	4.3	1.3
Dec	'17-23	2015	51	20.5	4.6	96.0	50.0	0	0	5.3	2.5	1.5
Dec	'24-31	2015	52	21.0	5.0	95.0	46.0	0	0	6.1	3	1.5

APPENDIX 1b

Weekly weather data at Pantnagar for experimental period (June 2016 to Dec 2016)

Month	Date	Year	Metro Week No.	Temperature (°C)		Relative Humidity (%)		Rainfall (mm)	No. of Rainy Days	Sun Shine Hrs.	Wind Velocity (km/hr.)	Evap. (mm)
				Max.	Min.	712 am	1412 pm					
May-June	'28-03	2016	22	33.8	24.3	72.6	51.4	35.2	1	7.7	7.5	7.4
June	'04-10	2016	23	35.3	26.6	68.7	55.1	17.4	2	6.0	8.4	6.6
June	'11-17	2016	24	35.5	25.8	77.4	52.9	40.8	3	6.5	7.1	6.5
June	'18-24	2016	25	32.9	26.0	84.6	65.0	66.2	4	6.3	5.9	4.7
June-July	'25-01	2016	26	33.3	26.3	86.7	66.3	80.4	5	4.0	7.3	4.4
July	'02-08	2016	27	30.7	25.9	90.1	77.0	72.2	5	2.0	6.4	3.4
July	'09-15	2016	28	33.0	26.2	89.4	71.0	52.6	5	4.2	5.6	4.3
July	'16-22	2016	29	32.0	25.5	91.4	74.3	119.2	4	2.8	5.9	4.6
July	'23-29	2016	30	30.8	24.9	89.1	76.7	125.9	6	3.9	6.5	3.8
July-Aug	'30-05	2016	31	31.7	25.7	86.1	75.3	151.8	4	5.5	7.1	5.0
Aug	'06-12	2016	32	33.0	26.3	89.4	69.3	40.2	4	5.7	6.8	4.5
Aug	'13-19	2016	33	32.9	25.9	92.6	69.9	100.6	5	4.7	3.9	3.9
Aug	'20-26	2016	34	33.1	26.3	87.0	67.7	2.4	2	7.8	4.7	4.4
Aug-Sep	'27-02	2016	35	34.0	25.5	88.9	63.6	26.6	3	5.5	3.8	3.6
Sep	'03-09	2016	36	32.7	25.3	91.0	68.9	2.4	1	6.2	6.2	4.6
Sep	'10-16	2016	37	32.1	24.5	88.9	72.4	59.4	1	4.5	4.3	3.6
Sep	'17-23	2016	38	32.7	24.2	89.9	65.9	76.6	1	5.9	3.6	3.2
Sep	'24-30	2016	39	32.6	23.2	87.0	61.9	3.4	1	8.9	2.9	3.2
Oct	'01-07	2016	40	32.7	24.9	88.0	65.4	0	0	3.9	2.4	3.0
Oct	'08-14	2016	41	32.2	19.9	88.7	61.6	0	0	5.9	2.9	2.9
Oct	'15-21	2016	42	31.6	17.2	80.0	48.7	0	0	7.7	2.3	2.8
Oct	'22-28	2016	43	31.2	13.8	90.1	38.4	0	0	7.7	2.1	2.8
Oct-Nov	'29-04	2016	44	30.4	13.5	84.9	38.6	0	0	7.9	1.9	2.6
Nov	'05-11	2016	45	29.0	11.4	90.3	36.9	0	0	7.9	2.6	2.4
Nov	'12-18	2016	46	28.3	10.6	90.9	36.9	0	0	8.1	2.1	2.8
Nov	'19-25	2016	47	26.6	9.8	93.4	38.1	0	0	7.3	2.2	1.9
Nov-Dec	'26-02	2016	48	26.1	11.3	92.6	46.6	0	0	4.2	2.6	1.8
Dec	'03-09	2016	49	23.4	11.5	83.2	54.9	0	0	4.1	3.1	1.3
Dec	'10-16	2016	50	20.0	9.9	94.4	66.4	0	0	2.2	2.7	1.1
Dec	'17-23	2016	51	23.1	6.5	94.6	48.7	0	0	6.1	2.3	1.8
Dec	'24-31	2016	52	22.5	8.7	93.4	55.3	11.2	1	5.9	3.6	1.7

APPENDIX-II

Reagents for Genomic DNA isolation and PCR amplification

I. Reagents for Genomic DNA isolation

Requirements:

Tris base, EDTA-Na₂, NaCl, Potassium Acetate, Glacial acetic acid, isopropanol, chloroform, isoamyl alcohol, and Absolute alcohol.

Preparation of solutions:

STOCKS SOLUTIONS:

1. 1M Tris-Cl buffer (pH 8.0), 100 ml

12.114 g Tris-base was dissolved in 80 ml ddw. The pH was adjusted to 8.0 by 6 N HCl. The volume was made upto 100 ml with ddw. Autoclaved and stored at 4°C.

2. 0.5 M EDTA (pH 8.0), 50 ml

9.3 g EDTA-Na₂ was dissolved in 30 ml of ddw (10N NaOH was added to make the pH 8.0). The final vol. was made upto to 50 ml, Autoclaved and stored at 4°C.

3. 10N NaOH, 50 ml

20 g of NaOH was dissolved in 30 ml of autoclaved ddw. The volume was made upto 50 ml. Stored in a plastic bottle at RT.

4. 5 M NaCl, 50 ml

14.6 g NaCl was dissolved in 30 ml of ddw. The final vol. was made upto 50 ml. Autoclaved and stored at RT

WORKING SOLUTIONS

1. DNA extraction buffer	25 ml
2% (w/v) CTAB	: 0.5 g
100 mM Tris-Cl	: 2.5 ml (1M stock)
1.4 M NaCl	: 2.0475 g
20 mM EDTA	: 1 ml (0.5 M stock)
0.2 % beta mercaptoethanol	: 50 µl

The final vol. was made upto to 25 ml with ddw.

2. 5 M potassium Acetate (pH 5.4) : 50 ml

3. Isopropanol	: Kept at 0°C.
4. Chloroform: isoamyl alcohol	: 24:1, 25 ml
5. 70% ethanol	: 10 ml
6. TE Buffer (pH 8.0)	25 ml
10 mM Tris-Cl	: 250 µl (1M stock)
1mM EDTA	: 50 µl (0.5 M stock)

Volume was made up by adding ddw to 25 ml. Autoclaved and stored at RT.

II. PCR Ingredients

(i) Design and Synthesis of the primers

The most essential requirement of PCR is the availability of short oligonucleotides called primers having sequence complementary to either ends of the target DNA segment called template DNA to be synthesized. The primers used in the study are synthesized from Eurofins, Bangalore

(ii) **Taq DNA polymerase**

Taq DNA polymerase is a thermostable enzyme that replicates DNA at 72-74⁰C and remains functional even after incubation at 95⁰C. The enzyme has 5'-3' polymerase and 3'-5' exonuclease activity. The concentration of the enzyme was 3units per µl (3U/ µl).

(iii) **dNTPs**

The dNTPs used in this reaction were obtained from Genei Pvt. Ltd. Bangalore as 10mM each (dATP, dGTP, dCTP, dTTP).

(iv) **Assay Buffer (10X)**

Assay buffer (10X) contained 10 mM Tris-Cl (pH 9.0), 15 mM MgCl₂, 50 mM KCl and 0.01% gelatin.

III. Running buffer, Dye and Reagents Running Buffer

1 X TBE buffer

Dye

98% formamide, 10mM EDTA, 0.023mg Bromophenol Blue, 0.023mg Xylene Cynol

Reagents used and preparation

1. Electrophoresis buffer (5X)	100ml
Tris base (0.045M)	54 g
Glacial acetic acid	27.5g
EDTA (0.001M)	10ml (1M stock)

Components were dissolved in 80ml of de-ionized water. pH was adjusted to 8.0 with 6N. Final volume was made up to 10 ml, autoclaved and stored at 4⁰C. 0.5X was the working solution of TBE buffer.

2. DNA loading dye (Double Dye)	10ml
Bromophenol Blue (0.25% w/v)	0.025g
Xylenecynol FF (0.25% w/v)	0.025g
Sucrose (40% w/v)	

The components were dissolved in 8.0ml of sterile de-ionized water. pH was adjusted to 8.0 and finally volume was made 10ml. Aliquots were made and stored at -20⁰C.

3. DNA staining solution and Ethidium Bromide (10000X)

Ethidium Bromide	10ml
Sterile de-ionized water	1ml

Note:

- x Working solution for staining gel was made by dissolving 60μl ethidium bromide Stock (10mg/ml) in 3000ml of de-ionized water.
- x Stock was stored at 40C

Ethidium bromide being highly carcinogenic was handled wearing gloves.

Meenakshi Bisht, the authoress of this manuscript was born on February 11th, 1990 in Lucknow (Uttar Pradesh). She passed secondary and higher secondary examination with 1st division from Central Board for Secondary Education. Then she joined Isabella Thoburn College (University of Lucknow), Lucknow, Uttar Pradesh in 2008 and completed the degree of B.Sc (ZBC) with 1st division in the year 2011. She completed her MSc(Ag) in Agriculture with major in Genetics and Plant Breeding. Thereafter, she joined PhD. with major in Genetics and Plant Breeding and minor in Molecular Biology and Biotechnology from G.B.P.U.A.T Pantnagar and qualified ICAR NET examination

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ABSTRACT

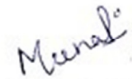
The present investigation was carried out with the objectives to study the efficiency of early generation selection, residual heterosis, transgressive segregation, inter-character association and their direct and indirect effects on yield and molecular marker analysis using seventeen different SSR primers for effective selection of genotypes and improvement of soybean. For field experiment, 36 genotypes of soybean comprising 14 crosses, 20 parents and two checks (PS 19 and SL 688) were evaluated in F_2 generation using randomized block design with two replications in *kharif* 2015 and 14 crosses along with their 21 progenies (10 high value group, 10 low value group and 10 bulk) were evaluated in compact family block design with two replications in *kharif* 2016 at the Norman E Borlaug Crop Research Centre, G.B. Pant University of Agriculture and Technology, Pantnagar.

The Analysis of variance was found highly significant for all the characters undertaken in both the generations. The study on early generation selection with various genetic parameters revealed that characters days to 50% flowering, plant height, number of pods per plant and seed yield per plant exhibited positive and significant value for intergeneration correlation coefficient. The estimate of intergeneration regression coefficient revealed that days to 50% flowering, plant height and seed yield per plant were positive and significant. The number of pods per plant and seed yield per plant displayed significant and positive value for response to selection. High heritability coupled with high genetic advance was observed for seed yield per plant in both the generations. The value of realized heritability was found higher for days to 50% flowering, number of pods per plant and seed yield per plant. High performance of F_3 bulk than F_2 generation and F_3 high group proved bulk method to be more effective than the pedigree method. The *per se* performance of F_2 generation for seed yield per plant was highest for three crosses, PS 1584 X JS 20-69 (20.7g), PS 1583 X JS 20-29 (20.08g) and PS 1225 X PS 1347 (19.58 g), for F_3 high yielding group it was highest in PS 1584 X JS 20-69 (42.63g), PS 1583 X JS 20-29 (33.40g) and PS 1584 X JS 20-41 (29.79g), similarly the *per se* performance in F_3 bulk was highest in PS 1584 X JS 20-69 (50.12g), JS 20-29 X JS 20-55 (39.76g) and JS 20-69 X JS 20-59 (35.63g). On overall basis, seed yield per plant was found to be effective for early generation selection.

The study of nature and magnitude of residual heterosis revealed that PS 1584 X JS 20-41, PS 1583 X Bragg, PS 1584 X JS 20-69 and PS 1583 X JS 20-29 showed significant and positive residual heterosis over mid-parents. Over better parent, PS 1584 X JS 20-41 and PS 1583 X Bragg showed significant and positive residual heterosis over better parent, while PS 1584 X JS 20-69 showed positive and significant residual heterosis over both the checks, in F_3 generation while none of the crosses showed significant residual heterosis in F_2 generation. All the F_2 crosses showed positive transgressive segregants for seed yield per plant but moderate frequency was observed. Highest positive transgressive segregant for seed yield per plant was recorded in the cross, PS 1042 X PS 1347. Occurrence of transgressive segregants in segregating generation is helpful for development of homozygous lines by continued selfing in crops like soybean. The present study revealed that in F_2 and F_3 , dry matter weight per plant, plant height, number of primary branches per plant, number of pods per plant, number of seeds per pod and harvest index exhibited significant and positive correlation with seed yield per plant. The component characters which showed highest direct effect on seed yield per plant were harvest index and dry matter weight per plant in F_2 generation and number of pods per plant in F_3 generation indicating selection of these characters will bring direct improvement in seed yield.

The molecular diversity analysis of twenty two soybean genotypes revealed that the Jaccard's similarity coefficient estimates varied from 0.29 (JS 20-59 and Pb1, JS 20-54 and Pb1, PS 1584 and PS 1347, JS 20-41 and PS 1347) to 0.82 (JS 97-52 and JS 20-29, PS 1583 and RVS 200-1, PS 1583 and JS 20-29 and PS 1042 and Pb1) genetic similarity. The average number of alleles per marker was 1.88, while percentage of all bands showed the polymorphism was 100%. The dendrogram constructed from SSR marker data divided twenty two genotypes into two main groups A and group B which consisted of seven clusters: Cluster I, II, III, IV, V, VI and VII. On the basis of dendrogram, genotypes PS 1225 and JS 20-59 was found to be most distant.


 (Kamendra Singh)
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 Authoress

नाम	: मीनाक्षी बिष्ट	परिचयांक	: ४२५१५
सत्र एवं प्रवेश वर्ष	: प्रथम, २०१४-१५	उपाधि	: पी.एच.डी
मुख्य	: आनुवंशिकी एवं पादप प्रजनन	विभाग	: आनुवंशिकी एवं पादप प्रजनन
अल्प	: आणविक जीव विज्ञान एवं जैव प्रौद्योगिकी		
शोध शीर्षक	: “आनुवंशिक मापदंडों के आधार पर आरंभिक पीढ़ी का चयन एवं सोयाबीन की पैतृक लाइनों में आणविक विविधता [ग्लाइसिन मेक्स (एल.) मेरिल]”		
सलाहकार	: डॉ. कामेन्द्र सिंह		

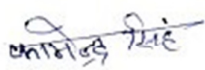
सारांश

प्रस्तुत शोध शीर्षक का उद्देश्य आरंभिक पीढ़ी चयन की दक्षता, अवशिष्ट संकर ओज, उत्क्रामी पृथक्करण, अन्तर-लक्षण संबंध का अध्ययन था एवं उनका उपज पर प्रत्यक्ष व अप्रत्यक्ष प्रभाव एवं १७ एस एस आर आणविक चिह्नको का प्रयोग कर प्रभावी जीन प्रारूप का चयन व सोयाबीन में सुधार करना था। क्षेत्र प्रयोग में ३६ जीन प्रारूप थे उनमें १४ क्रॉस, २० पैरेंट्स एवं २ चेक यादृच्छिक खण्ड अभिकल्पना में दो प्रतिकृतियों में खरीफ २०१५ में लिए गए एवम १४ क्रॉस उनके २१ वंशजों (१० उच्च मूल्य समूह, १० निम्न मूल्य समूह एवम १० बल्क) को कॉम्पैक्ट फैमिली अभिकल्पना में दो प्रतिकृतियों में खरीफ २०१६ में नॉर्मन ई बोर्लॉग फसल अनुसंधान केंद्र, जी.बी. पंत कृषि और प्रौद्योगिकी विश्वविद्यालय, पंतनगर में लगाया गया।

विभिन्नता विश्लेषण द्वारा सभी लक्षणों के लिए दोनों ही पीढ़ियों में सार्थक विभिन्नता देखी गई। आरंभिक पीढ़ी चयन के अध्ययन में विभिन्न आनुवंशिकी मापदंडों ने दर्शाया कि ५० प्रतिशत पुष्पन, पौध ऊंचाई, फलियों की संख्या प्रति पौध, बीज उपज प्रति पौध का अंतरवंशीय सहसंबंध गुणांक के लिए सकारात्मक एवम सार्थक दर्शाया। अंतरवंशीय प्रतिगमन गुणांक आँका गया जिसमें ५० पुष्पन दिवस, पौध ऊंचाई एवं बीज उपज प्रति पौध सार्थक व सकारात्मक थे। फलियों की संख्या प्रति पौध एवं बीज उपज प्रति पौध में चयन प्रतिक्रिया के लिए सकारात्मक मूल्य दर्शाया। उच्च आनुवंशिकता के साथ जिनैटिक एडवांस, बीज उपज प्रति पौध के लिए दोनों पीढ़ियों में प्रेक्षित हुआ। रियलाइज्ड आनुवंशिकता का मान ५० प्रतिशत पुष्पन, फलीयो की संख्या प्रति पौध एवम बीज उपज प्रति पौध के लिए अधिक पाया गया। एफ ३ बल्क का उच्च प्रदर्शन एफ २ पीढ़ी की तुलना में एवम एफ ३ उच्च समूह ने दर्शाया कि समूहिक पद्धति, वंशावली पद्धति कि तुलना में अधिक प्रभावी थी। पर से प्रदर्शन बीज उपज प्रति पौध के लिए तीन क्रॉस में अत्यधिक था पी.एस. १५८४ X जे.एस. २०-६९ (२०.७ ग्रा.), पी.एस. १५८३ X जे.एस. २०-२९ (२०.०८ ग्रा.) व पी.एस. १२२५ X पी.एस. १३४७ (१९.५८ ग्रा.), एफ ३ के उच्च उपज समूह में पी.एस. १५८४ X जे.एस. २०-६९ (४२.६३ ग्रा.), पी.एस. १५८३ X जे.एस. २०-२९ (३३.४० ग्रा.) एवम पी.एस. १५८४ X जे.एस. २०-४१ (२९.७९ ग्रा.) अधिक था इसी तरह एफ ३ बल्क अधिक था पी.एस. १५८४ X जे.एस. २०-६९ (५०.१२ ग्रा.), जे.एस. २०-२९ X जे.एस. २०-५५ (३९.७६ ग्रा.) व जे.एस. २०-६९ X जे.एस. २०-५९ (३५.६३ ग्रा.)। अतः सभी प्रकार से बीज उपज प्रति पौध आरंभिक पीढ़ी चयन के लिए प्रभावी लक्षण था।

अवशिष्ट संकर ओज की प्रकृति एवं मात्रा के अध्ययन से पता चला कि पीएस १५८४ x जेएस २०-४१, पीएस १५८३ x ब्रैग, पीएस १५८४ x जेएस २०-६९ और पीएस १९८३ x जेएस २०-२९ ने मध्य-जनक के ऊपर महत्वपूर्ण और सकारात्मक अवशिष्ट संकर ओज दिखाया। एफ ३ पीढ़ी में पीएस १५८४ x जेएस २०-४१ और पीएस x ब्रैग ने बेहतर-जनक के ऊपर महत्वपूर्ण और सकारात्मक अवशिष्ट संकर ओज दिखाया जबकि पीएस १५८४ x जेएस २०-६९ ने पीएस १९ और एसएल ६८८ के ऊपर महत्वपूर्ण और सकारात्मक अवशिष्ट संकर ओज प्रदर्शित किया जबकि किसी भी क्रॉस ने एफ २ पीढ़ी में महत्वपूर्ण अवशिष्ट संकर ओज नहीं दिखाया। सभी एफ २ संकरो ने बीज उपज प्रति पौध के लिए सकारात्मक उत्क्रामी पृथक्करण दिखाया लेकिन उनकी आवृत्ति मध्यम देखी गई। बीज उपज प्रति पौध के लिए उच्चतम सकारात्मक उत्क्रामी पृथक्करण पीएस १०४२ x पीएस १३४७ में लेख्यंकित किया गया। सोयाबीन जैसे फसलों में उत्क्रामी पृथक्करण द्वारा निरंतर आत्म प्रजनन द्वारा समयुग्मजी लाइनों के विकास करने में सहायक है। वर्तमान अध्ययन से पता चला है कि एफ २ और एफ ३ में, सूखा भार प्रति पौध, पौध ऊंचाई, प्राथमिक शाखाओं की संख्या प्रति पौध, फलियों की संख्या प्रति पौध, बीजों की संख्या प्रति फली एवम हार्वेस्ट सूचकांक एवं बीज की संख्या प्रति पौध में महत्वपूर्ण और सकारात्मक सह-संबंध है। एफ २ पीढ़ी में घटक वर्ण जैसे की हार्वेस्ट सूचकांक व सूखा भार प्रति पौध तथा एफ ३ पीढ़ी में फलियों की संख्या प्रति पौध ने बीज उपज प्रति पौध पर उच्च सीधा प्रभाव दिखाया जिसका उपयोग इन पात्रों के चयन से बीज उत्पादन में प्रत्यक्ष सुधार किया जा सकता है।

२२ सोयाबीन जीन प्रारूपों के आणविक विविधता विश्लेषण से पता चला कि जैकार्ड समानता गुणांक अनुमानों में भिन्नता ०.२९ (जेएस २०-५९ और पीबी१, जेएस २०-५४ और पीबी१, पीएस १५८४ और पीएस १३४७, जेएस २०-४१ और पीएस १३४७) से ०.८२ (जेएस १७-५२ और जेएस २०-२९, पीएस १५८३ और आरवीएस २००-१, पीएस १५८३ और जेएस २०-२९, पीएस १०४२ और पीबी१) तक पायी गयी। अलील प्रति मार्कर की औसत संख्या १.८८ पायी गयी तथा सभी बैंडों का प्रतिशत दिखाता है कि बहुरूपता १०० प्रतिशत थी। एस एस आर मार्कर डेटा से बना डेन्ड्रोग्राम दो मुख्य समूहों ग्रुप ए और ग्रुप बी में विभाजित हुए जो की पुनः सात क्लस्टर में विभाजित हुए: क्लस्टर I, II, III, IV, V, VI और VIII डेन्ड्रोग्राम के आधार पर, जीन प्रारूप पीएस १२२५ और जेएस २०-५९ को सबसे भिन्न पाया गया।


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सलाहकार


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लेखिका