

STUDIES ON GENETIC PARAMETERS FOR QUANTITATIVE AND QUALITATIVE TRAITS IN SOYBEAN [*Glycine max* (L.) Merrill]

Thesis

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By

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Pantnagar
July, 2016


(Kunduru Bharath)
Author

CERTIFICATE

This is to certify that the thesis entitled “**STUDIES ON GENETIC PARAMETERS FOR QUANTITATIVE AND QUALITATIVE TRAITS IN SOYBEAN [*Glycine max* (L.) Merrill]**” submitted in partial fulfilment of the requirements for the degree of **Master of Science in Agriculture** with major in **Genetics and Plant Breeding** of the college of Post Graduate Studies, G.B. Pant University of Agriculture and Technology, Pantnagar, is a record of *bona fide* research carried out by **Mr. Kunduru Bharath, Id. No. 48073**, under my supervision and no part of the thesis has been submitted for any other degree or diploma.

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

Pantnagar
July, 2016


(Kamendra Singh)
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CERTIFICATE

We, the undersigned, members of Advisory Committee of **Mr. Kunduru Bharath, Id. No. 48073**, a candidate for the degree of **Master of Science in Agriculture** with major in **Genetics and Plant Breeding** agree that the thesis entitled **“STUDIES ON GENETIC PARAMETERS FOR QUANTITATIVE AND QUALITATIVE TRAITS IN SOYBEAN [*Glycine max* (L.) Merrill]”** may be submitted in partial fulfilment of the requirements for the degree.



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(N. K. Singh)
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ABBREVIATIONS

million ha	–	million hectares
t/ha	–	tons per hectare
kg/ha	–	kilogram per hectare
(C)	–	Check
° C	–	Degrees centigrade
d.f.	–	Degrees of freedom
µl	–	Microliter
ml	–	Milliliter
nm	–	Nano meter
µg	–	Microgram
gm	–	Gram
mg	–	Milligram
% (m/m)	–	% (mass/mass)
mg/ml	–	Milligram/milliliter
gm/ml	–	Gram/milliliter
mM	–	Millimolar
kDa	–	Kilo Dalton
BPB	–	Bromophenyl Blue
BME	–	β-Mercaptoethanol (2- Mercaptoethanol)
EDTA	–	Ethylene diamine tetra acetic acid
EGTA acid	–	Ethylene glycol-Bis (β-amino ethyl ether)-N, N, N', N'-tetra acetic acid
HEPES	–	4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid
DTT	–	1, 4-Dithiothreitol
CBB R 250	–	Coomassie brilliant blue R 250
V	–	Volt

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INTRODUCTION

Soybean [*Glycine max* (L.) Merrill] is an important leguminous crop which is grown since age old times and is one of the oldest grown crops known to man. It is grown in tropical, sub-tropical and temperate regions of the world and is prominently recognized as an oil seed crop rather than a pulse since it contains about 40 per cent protein and 20 per cent oil (**Singh and Hymowitz, 1999**). Soybean ($2n=40$) is botanically placed under the family Papilionaceae. The North-eastern China region is believed to be the primary centre of origin of this crop, whereas the Manchuria region in China is considered to be the secondary centre of origin, from where it spread to different parts of Asia, USA, Brazil, Argentina etc. Soybean was first known to be domesticated in North-eastern China in 11th century B.C and from the time since, it has become one amongst the five major plant foods consumed in China along with rice, wheat, barley and millets (**Gibson and Benson, 2005**). Soybean is an important multi-purpose leguminous crop known for its highly valued protein and oil, and its use in food, feed and industrial applications. Hence it is popularly known as the “Golden Bean” or “Miracle crop” of the 20th century. Apart from that, soybean also enriches the soil productivity by fixing atmospheric nitrogen in soil at the rate of 65-100kg/hectare (**Patil et al., 2014**) through symbiosis with bacterium *Rhizobium japonicum* and thus rejuvenates and maintains the soil fertility.

Approximately 85% of the world's soybean produced annually is processed into soy-meal and oil and about 98% of the soy-meal is further processed into animal feed while the rest is used to produce soy flour and related proteins. From the total oil fraction extorted, about 95% is used for edible purpose, while the rest is used in the manufacture of industrial products like soaps, fatty acids, shortening, margarine, biodiesel and salad dressings (<http://www.soyatech.com>). Soy oil is also utilized in industrial paints, printing inks, varnishes, sealing compounds, linoleum, and other products. Lecithin is a natural extract from soybean oil which has an emulsifying property and is also used as a lubricant in many commercial and industrial applications. Soybeans in the recent past are being used for bio-fuel and ethanol production. Soybean hull is rich in carbohydrates and hence, could be used in ethanol production (**Mielenz et al., 2009**). For bio-fuel production, oil is first extracted from the seeds, degummed and converted into bio-fuel through a process called transesterification. About 1.5 gallons (1 gallon = 3.785 liters) of bio-diesel could be obtained from one bushel (one bushel = 60 pounds) of soybeans (**Hill et al., 2006**). But the production

cost of unit volume of bio-diesel is slightly higher than that of conventional petro-chemicals and hence cheaper methods of bio-diesel extraction should be worked out in order to popularize these eco-friendly energy resources.

Soybean is a highly valued crop in terms of its contribution towards human nutrition. It is rich in minerals like Calcium, Phosphorus and Iron along with providing Vitamins like A, B, D and E. It is a rich source of many essential amino acids (EAA) including lysine, which is generally defective in majority plant protein sources (**Mundewadikar and Deshmukh, 2014**). Soybean seed on an average is composed of 40% protein and 20% oil, 30% carbohydrates, besides high amounts of dietary fiber. Because of its high oil content, it is considered as a key crop for edible oil production. Soybean is the only cultivated crop that supplies a cheap and inexpensive source of high quality protein equivalent to meat, poultry and eggs. (<http://www.iita.org/soybean>). Soybean has been typically used in the preparation of traditional and as well as value added foods such as soy sprouts, tofu, okara, miso, natto, shoyu, soy milk, soya sauce, tempeh and soymilk yoghurt etc. (**Riaz, 2006**) which are being consumed on a regular basis in China, Japan, Korea and Southeast Asia. Consumption of soy protein alleviates the nutrient deficiencies caused by grain crops such as wheat and corn, which are defective in essential amino acids like lysine and tryptophan. Soy flour and grits, are used as chief ingredients to facilitate dough conditioning and bleaching in commercial baking industry. They have good moisture-holding capacity and could prevent staling in bakery products. In the western countries it is chiefly used in the preparation of meat and cheese alternatives, primarily due to its high protein content and is the reason why soybeans have been historically recognized as "meat of the field" or "meat without bones".

Lipid and protein are the two major constituents in soybean. Soybean oil is good for human health as it is rich in the essential fatty acids and low in saturated fat besides being an abundant source of vitamin E. Soybean oil contains 15% saturated and 85% unsaturated fatty acids. Among unsaturated fatty acids, poly- and mono-unsaturated fatty acids are 61% and 24%, respectively, including two essential fatty acids viz. linoleic and linolenic acid, which cannot be synthesized by the human body and hence, needed to be supplied through diet (**Balasubramaniyan and Palaniappan, 2003**). Therefore, soybeans besides providing omega-6 fatty acids, are among the few plant foods that provide omega-3 fatty acids. Apart from the high nutritional value attributed to its energy and protein content, an

important health benefit of soybean is the presence of high amounts of two isoflavones viz. genistein and daidzein in the seeds. These secondary metabolites have an important role in the symbiotic association of the plant with *Rhizobium* along with added health benefits to humans. Soybean isoflavones genistein and daidzein have good medicinal value that a daily intake of about 50 mg prevents the prostate cancer and breast cancer (**Liggins *et al.*, 2000**). A balanced intake of soy protein on a regular basis in the form of various soy based foods helps in prevention of cardio-vascular diseases, reduces the serum cholesterol as well as body fat and also helps in elevation of serum insulin. The isoflavones also help prevent osteoporosis, function as antioxidants and relieve menopausal symptoms (**Hasler, 1998**).

Soybean is a prominent oilseed crop across the world as well as in India. Soybeans contribute to 55% of the total oilseed production at the global level followed by rapeseed (14%), cottonseed (10%), groundnut (8%), sunflower (9%), oil palm kernel (3%) and coconut copra (1%) etc. It accounts to 25% of the global vegetable oil production and is a major commodity of domestic and International trade. Five countries viz. United State of America, Brazil, Argentina, China and India are the key players and they together contribute 90% of the global soybean output. At the global level, India is ranked fourth and fifth in terms of area and production, respectively. The estimates for world soybean area, production and productivity for 2015-16 were 120.78 million ha, 320.51 million tons and 2.65 t/ha, respectively, which is the highest ever recorded. But, however the global productivity level has not yet been achieved in tropical countries like India, where the estimates stand at 11.07 million ha, 8.64 million tons, and 781 kg/ha, for area, production and productivity, respectively (**ICAR-IISR, 2016**). The lower productivity in soybean could be attributed to several factors, and the important among them is the susceptibility of the crop to various pests and diseases. Several insect pests along with fungi, bacteria, viruses and nematodes cause quantitative as well as qualitative reduction of crop yields in soybean throughout the country. Rhizoctonia aerial blight (RAB), Bacterial pustule (BP) and Yellow mosaic virus (YMV) are the three important diseases of this crop prevalent in the plains of Uttarakhand causing significant deterioration of crop yields of this region.

Existence of genetic diversity in the germplasm of any crop is the basic pre-requisite for a sound crop improvement programme. Assessment of genetic diversity among the cultivars available in a particular crop helps in realizing the advancements made through any crop improvement programme (**Chen *et al.*, 1994**). Accurate estimates of level and

pattern of diversity are instrumental in any crop breeding programme for diverse applications, for example, in the choice of diverse parental lines for genetic crosses (**Barrett and Kidwell, 1998**) and in the introgression of desirable genes from diverse germplasm resources into available genetic base (**Thompson *et al.*, 1998**), which is the underlying principle of gene pyramiding and thereby helps in creation of better adaptable genotypes in terms of higher yield, improved quality and multiple resistance against biotic and abiotic stresses. Therefore, a reliable estimate of existent genetic diversity among the wild and cultivated soybeans is vital for conservation, management and efficient utilization of germplasm resources to meet the growing needs of varietal improvement for higher productivity. Conventionally the genetic diversity could be assessed through the analysis of morphological or biochemical traits, but with the technological advancements in the recent past, molecular approaches are employed now-a-days to obtain accurate results through detection of polymorphism among the genotypes at the gene level.

Genetic variability is a prerequisite in any crop as it is the source of variation and also the raw material for yield enhancement. A highly reliable and precise method for assessment of genetic variability devoid of environmental effects is essential to facilitate a valid estimate of parameters. The pedigree analysis of Indian soybean varieties showed that they hold a narrow genetic base which itself is evident through yield plateauing, increased susceptibility to pests and diseases and sensitivity to abiotic factors etc. The same is the scenario elsewhere in the world. **Hyten *et al.* (2006)** evaluated the genetic diversity among four soybean populations and inferred from their study that during crop domestication, about 50% of the existent diversity from germplasm and 81% of the rare alleles were lost, which led to about 60% changes in allele frequency in soybean. Hence, it is crucial to broaden the genetic base of elite gene pool by exploiting diverse exotic germplasm resources including wild forms, wild relatives and land races in the background of high yielding widely adopted soybean varieties. This could be accomplished through plant introductions (PIs), pedigree analysis, pre-breeding and population improvement schemes etc. applied in this direction.

A successful execution of a defined breeding strategy for yield enhancement in any given crop mandates a basic knowledge regarding the character association in such crop. Higher yields are the ultimate aim of any crop improvement programme. The grain yield in soybean as in other crop species is a complex trait, quantitative in nature and is dependent on a number of component traits. Hence, a direct selection for yield *per se* is inapt unless

different yield attributing traits are considered for selection. Correlation estimates provide a measure of association between different characters and thereby, helps in identification of important characters to be considered during selection. Knowledge of correlation between grain yield and other characters is helpful in selection of suitable plant type along with simultaneous improvement of several characters. Correlation coefficients, although very useful in quantifying the size and direction of trait associations, can be misleading if the high correlation between two traits is a consequence of the indirect effect of other traits. Hence, path coefficient analysis (**Sewall Wright, 1921**) should be employed to determine the direct and indirect effect for one variable upon another which further permits the separation of correlation coefficient into direct and indirect components (**Dewey and Lu, 1959**). Therefore, a combination of correlation co-efficient together with path co-efficient analysis serves a powerful tool to ascertain the character association in any crop and hence, its ultimate effect on overall yield.

Soybean is going to remain as the leading oilseed crop in India and improvement in its productivity would not only lead to self-sufficiency in edible oil production, but would also help millions of small and marginal farmers who depend for their lively hood on this crop. Therefore, in view of the above facts and considering the importance of soybean, the present investigation was undertaken with the following objectives.

1. To assess the existent genetic divergence in soybean genotypes.
2. To estimate the genetic variability.
3. To study the inter-character correlation among different characters and their direct and indirect effects on seed yield.
4. Identification of suitable donors for yield and yield attributing traits through diversity analysis.
5. Screening the genotypes for resistance against YMV (Yellow Mosaic Virus), BP (Bacterial Pustule) and RAB (Rhizoctonia Aerial Blight) to identify the donor sources.
6. Bio-chemical profiling of selected genotypes using SDS-PAGE to evaluate the diversity in protein content.

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REVIEW OF LITERATURE

Genetic diversity, whether naturally existing or artificially created, is the chief ingredient in any crop to start a planned crop improvement program. Selection is the cornerstone of all the plant breeding programs and selection is ineffective in any crop unless there exists certain amounts of variability for the trait(s) under selection. Correlation studies and Path-coefficient analysis also form an integral part of a planned crop breeding program as they facilitate a basic understanding of character association and contribution of different characters towards the enhancement of yield levels, which in turn is the ultimate objective of all the crop improvement programs. The relevant available literature pertaining to 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:

1. Genetic Divergence
2. Genetic variability parameters
3. Inter-character association (correlation) analysis
4. Path coefficient analysis
5. Screening for disease resistance
6. Bio-chemical profiling of genotypes

2.1 Genetic divergence

Genetic diversity is crucial in fulfilling the objectives of any crop breeding program, defined by the felt needs like, cultivar development, gene pool enhancement and end-product commercialization etc. Collection and documentation of genotypes for the assessment of existent genetic variability constitutes a key process in every crop improvement program. A basic knowledge regarding the existing variability in the germplasm of a crop enable breeders a better understanding of the evolutionary relationships among the genotypes, and thereby develop effective strategies to incorporate desirable traits in the crop improvement programs (**Bretting and Widrlechner, 1995**). Hence, it is mandatory to evaluate the level of genetic diversity contained in the available germplasm of a crop species. The genetic diversity analysis among the genotypes of a crop reveals the

genetic distance and similarity on whole genome basis i.e., dissimilarity in their genetic constitution throughout the genome. If lower levels of genetic diversity are realized in the germplasm of a crop, broadening of genetic base should be the prime objective in such a crop and also the germplasm should be evaluated from time to time to reveal the pattern of genetic diversity in the longer run. One approach to incorporate genetic diversity in a crop is through hybridization with introduced germplasm which increases genetic variability in the breeding populations, thereby ultimately enhancing the gains from selection (**Guedira et al., 2000**).

Pedigree analysis showed that the Indian soybean cultivars hold a narrow genetic base as evident from the inbreeding coefficient analysis and genetic variability studies using molecular markers (**Hiromoto and Vello, 1986; Priolli et al., 2002 and Bonato et al., 2006**). These studies concluded that majority of genes showcased in the present cultivars were derived from only a few accessions and that the genetic diversity in soybean elite germplasm is limited. This indicates a huge potential for soybean breeding. A narrow genetic base is a major setback in crop improvement programs where the lack of genetic variability results in attainment of yield plateaus, increased susceptibility of genotypes to pests and pathogens etc. (**Martin, 2000 and Fu, 2006**). Induction of novel germplasm sources in crop breeding programs, through Plant introductions (PIs) can incorporate adequate amounts of genetic variability necessary for continuous improvement and adaptation of genotypes to biotic and abiotic factors. Therefore, crop germplasm itself could be used as a natural source for broadening the genetic base of existing cultivars in soybean (**Chung & Singh, 2008**).

Strategies for broadening the genetic base of soybean for breeding and production in India have been suggested (**Tiwari, 2001**). They comprise of i) assessing the genetic base through pedigree and other analyses, ii) directed introductions, iii) consolidating the national germplasm collections, iv) evaluation and establishment of core collection of soybean genetic resources, v) pre-breeding and germplasm enhancement using cultigen as well as wild species, vi) population improvement, vii) enhancing genetic diversity at farm level by farmer participatory approaches and viii) facilitated access to soybean genetic resources for the users. Therefore, enhancement of genetic resources, pre-breeding and ultimate widening of the genetic base of the cultivars at the farm level will eventually lead to the realization of high productivity in soybean.

The success of a crossing program in any crop depends on the availability of genetically distant parents to generate adequate levels of genetic diversity between genotypes in terms of gene and gene frequencies, which could ultimately result in the formation of new heterotic groups and transgressive segregants. **Sandoval *et al.* (1997)** studied the genetic variability for seed yield and other agronomic traits in soybean and reported that the populations derived from genetic crosses of elite lines manifested limited diversity among the genotypes. This indicates a tremendous potential for utilization of natural variation that could be available among genotypes for important characters like protein content, oil content and seed yield per plant etc. to enhance the genetic potential of available cultivars. Therefore, an accurate estimate of genetic divergence and relatedness among soybean genotypes based on morphological traits as well as nutritional traits like oil and protein content is essential for identification of donors for improvement of concerned traits in soybean.

Earlier workers (**Vavilov, 1926; Joshi and Dhawan, 1966 and Ram and Panwar, 1970**) considered geographical diversity as a reliable measure of genetic diversity and hence, assumed heterosis among the crosses of such genotypes. But some workers reported that this statement could not be generalized and is not applicable to all the crops (**Moll *et al.*, 1962**). According to the literature available till date, in general, there exists no correspondence between geographical isolation and genetic diversity (**Das *et al.*, 2001; Barh *et al.*, 2014 and Poornima Jency and Kalaimagal, 2015**).

Attempts were made by several researchers to study the extent and pattern of distribution of genetic diversity in various crops using different data sources including morphological, agronomical, biochemical and molecular traits.

Chauhan and Singh (1982) studied heterosis and variability in relation to genetic divergence involving 21 F_1 s and 17 F_2 populations which were derived from high, moderate and less diverse parents. The F_1 s and F_2 populations were evaluated to study the genetic diversity among their parents. Results obtained revealed that, high heterosis was observed in general for most of the characters among crosses involving diverse parents, but the maximum heterosis was reported among the crosses involving moderate divergent parents and such crosses also exhibited a larger variability in F_2 generations. Hybrid UPSM 533 x UPSL 18 involved the most divergent parents ($D^2 = 1311$), while Semmes x Bragg involved the least divergent parents ($D^2 = 23$). Intra-cluster crosses such as PK 71-39 x UPSM 229,

Lee x Bragg and Semmes x Bragg manifested little heterosis. The F₂ population derived from UPSM 726 x Type 49 cross ($D^2 = 23$) involving moderately diverse parents produced most variable progeny for pods per plant, primary branches and seed yield. The overall study concluded that heterosis in crosses increased with increase in genetic diversity of parents to a certain extent beyond which overall heterosis for seed yield gets partially cancelled due to negative heterosis for certain characters.

Jain and Ramgiry (2000) estimated genetic distance for 56 soybean genotypes of Indian and exotic origin. These genotypes were grouped into four clusters. The D^2 values were used for grouping genotypes into different clusters in such a way that genotypes within the same cluster exhibited smaller D^2 values as compared to those obtained between different clusters. Genotypes included in the clusters with maximum inter-cluster distance were found to be genetically more divergent irrespective of their place of origin.

Gawande et al. (2001) evaluated 50 indigenous and exotic soybeans (*Glycine max*) to study the genetic divergence and to identify potential parents for soybean improvement. All the 50 genotypes were grouped into 9 clusters using Anderson meteroglyph analysis method. The characters like growth habit, pubescence density, leaflet shape and pod colour contributed more towards genetic diversity as compared with the other characters such as flower colour, leaf colour, pod colour and seed coat colour. Two characters, growth habit and pubescence density contributed maximum towards variability among the genotypes. It was suggested that the parents should be selected for hybridization on the basis of these characters.

Sihag et al. (2004) determined the level of genetic diversity among 160 soybean genotypes using Mahalanobis D^2 analysis. Data on 8 yield components were recorded and later on subjected to multivariate analysis based on which the genotypes were grouped into 8 clusters. The maximum divergence was observed between the Clusters V and VIII followed by VI and VIII.

Yadav (2005) studied the genetic divergence using Mahalanobis D^2 statistic among 48 genotypes (31 elite breeding lines and 17 parental lines) of soybean for 12 quantitative and 11 morphological characters. Based on D^2 statistic, the 48 genotypes were grouped into 8 clusters. The maximum divergence was observed between Clusters III and VIII followed by Clusters III and VI. Based on D^2 analysis, the potential parental combinations were found to be Shilajeet x T-49, PK-327 X T-49, PK-1347 x T-49, Kalitur X Shilajeet, PK-327 X

Kalitur, PK-1347 X Kalitur, JS-335 X T-49, PK-1314 X Shilajeet, PK-1314 X PK-327, PK-1314 X PK-1347, PK-1308 X Shilajeet, PK-1307 X PK-327, PK-308 X PK-327 and Bragg X T-49. 100-seed weight contributed maximum towards genetic divergence followed by number of pods per plant and number of primary branches per plant. The diverse parents identified for different characters were PS-1382, Shilajeet, JS-335, PK-1347, PK-1314, Kalitur, Ankur, PS-1042, PS-1375, PK-515 and T-49 which could be useful to obtain better segregants for seed yield and its components.

Gaikwad *et al.* (2005) studied 50 genotypes of soybean to assess the genetic diversity and variability for days to 50% flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, pod length, number of seeds per pod, 100-seed weight, oil content and seed yield per plant. The genotypes were grouped into 19 clusters based on D^2 values. There were 10 solitary clusters, while the remaining clusters contained 2 to 8 genotypes. Based on D^2 values and *per se* performance, a hybridization programme involving ACPS-160 (Cluster XI), EC-18735 (Cluster X), JS-237 and MACS-250 (Cluster II), JS-335 (Cluster IV), PK-1 and MACS-291 (Cluster III), Kalitur (Cluster XV) and EC-34096 (Cluster XVI) was suggested to obtain superior genotypes for yield improvement in soybean.

Sharma *et al.* (2006) studied the genetic divergence using Mahalanobis D^2 analysis among 62 varieties of soybean based on 17 characters which led to their grouping into 15 clusters out of which 9 were monogenotypic. PK-472 and SL-295 were identified as the most potential parents for hybridization program. Among the 17 characters, protein percentage contributed maximum towards genetic divergence followed by number of pods per plant and seed yield per plant. This indicated that these characters were mainly responsible for genetic divergence in the parent material. The highest divergence was observed between Clusters IX and XV followed by Clusters XIV and XV, which may serve as potential parents for crossing.

Gohil *et al.* (2007) estimated the genetic distance for 55 genotypes of soybean collected from different soybean growing states of India using D^2 statistic. The results showed adequate diversity for all the traits among all possible 1485 pairs of genotypes with values ranging from 4.69 to 2324.12. This revealed that 55 genotypes were grouped into 11 clusters (Clusters I to XI) with substantial genetic divergence between them.

Zafar Iqbal *et al.* (2008) studied genetic diversity among 139 genotypes of soybean

for important morphological traits using Multivariate analysis. The results obtained from the cluster analysis revealed that the genotypes were divided into 5 clusters falling under two major groups A and B consisting one and 4 clusters, respectively. Cluster V was observed to be the largest which included 49 genotypes. Cluster mean values revealed that Cluster I showed highest mean values for number of filled pods per plant, grain yield per plant, 100-seed weight, biological yield and harvest index. Cluster II exhibited lowest means for harvest index, grain yield per plant and oil content. Cluster III showed maximum mean values plant height and number of branches per plant. Cluster IV included accessions with high means for oil content and low means for number of unfilled pods per plant, while Cluster V exhibited lowest mean value for days to maturity.

Kayande and Patil (2009) estimated the genetic diversity among 50 genotypes of soybean on the basis of 8 important yield attributes. The analysis based on D^2 statistic revealed high divergence among the genotypes for all the traits under consideration. The genotypes were grouped into 10 clusters, in which Cluster I comprised of 21 genotypes and was the largest, while the Clusters IV, VI, VIII, IX and X were the smallest which included one genotype each. Maximum inter-cluster diversity was reported between the Clusters II and V (49.60), whereas the minimum was observed between clusters V and VI (16.24). Hence, hybridization between genotypes selected from Clusters II and V may result in high manifestation of heterosis and also could yield superior segregants. On the basis of the results obtained from the above study, they concluded that genetic diversity was not necessarily associated with geographical diversity.

Bhartiya et al. (2011) studied genetic divergence by evaluating 282 black seeded soybean genotypes considering 11 metric and non-metric traits, each. Analysis of data based on non-hierarchical Euclidean cluster analysis grouped the genotypes into 9 clusters with Cluster II (67) comprising the maximum number of genotypes. The cluster mean values for different traits under study varied significantly among the clusters indicating the existence of substantial amounts of genetic variability among the genotypes. Intra-cluster distance varied from 2.316 (Cluster IV) to 2.968 (Cluster I), whereas the Inter-cluster distance ranged from 1.856 (between Clusters II and VII) to 6.385 (between Clusters IV and IX). Results obtained from the study showed that, the genotypes from the Cluster IX exhibited high mean values for pod length, seed yield per plant and 100-seed weight and hence, could be used as donors for development of superior genotypes in terms of grain yield and grain weight. The

genotypes from Cluster V exhibited high mean values for oil (17.79%) and protein (42.84%) contents and therefore, could serve as potential donors for the improvement of these concerned traits. Genotypes VBS 48 and VBS 25 (Cluster VII), VBS152 and VBS161 (Cluster VIII) were found to be outstanding among all the genotypes and hence, could be used as exceptional donors in different crossing programs to yield transgressive segregants for appropriate traits.

Shadakshari *et al.* (2011) evaluated the genetic diversity using D^2 analysis among 50 genotypes of soybean based on 12 morphological characters and reported that number of seeds per plant (40.24%) and seed yield per plant (20.12%) showed maximum contribution towards genetic diversity. The cluster analysis revealed that the genotypes under study were grouped into 10 clusters with Cluster II (16) and Cluster X (1) having maximum and minimum number of genotypes. Maximum and minimum differences among all the genotypes within the same cluster (intra-cluster average D^2 value) were exhibited by Clusters I (925.545) and X (0.00), respectively. Highest and lowest diversity was observed between the Clusters IX and X (3424.063) and III and VIII (266.431), respectively. This indicated an adequate opportunity for recombination of genes among the genotypes obtained from cluster combinations showing maximum diversity. Based on D^2 statistic, the genotypes JS 90-29, JS (SH) 93-37, IC93752 and IC93656 were identified as potential parents for hybridization to recover superior segregants with higher yield.

Bekele *et al.* (2012) evaluated genetic diversity based on 17 characters in 49 soybean germplasm introductions based on 17 characters including oil and protein contents. Divergence was estimated using Mahalanobis D^2 technique, based on which the genotypes were grouped into 16 clusters. Highest intra-cluster distance was observed within the Cluster XII (27.75) followed by Clusters XI (24.26) and XIII (23.65). Lowest intra-cluster distance was observed in Cluster VI (0.00) followed by Clusters V (5.53) and VI (6.05). Maximum inter-cluster distance was observed between the Clusters IX and X (66.56) followed by Clusters I and IX (60.53) and II and X (60.32). Thus genetic crosses among individuals from these clusters could result in maximum expression of heterosis and also a possible recovery of superior segregants for yield improvement in soybean.

Salimi *et al.* (2012) evaluated 19 genotypes of soybean to study the genetic diversity for 11 morphological traits under drought conditions using factor analysis and cluster analysis. Based on the results obtained from cluster analysis, the genotypes under study

were grouped into 7 clusters with in which Cluster VII with 2 genotypes (Streslland and Dw2) showed high mean values for traits like days to flowering, days to maturity, number of seed per plant, grain yield, oil and protein contents. The results from the study concluded that the genotypes TNH 56 and BP were the best donors for breeding soybean against drought resistance.

Pawar *et al.* (2013) studied the pattern of genetic diversity among 42 genotypes of soybean by evaluating their morphological characters using D^2 analysis, based on which the genotypes were grouped into 7 clusters. Cluster IV was found to be the largest which included 13 genotypes, while the Clusters III and VII were found to be the smallest comprising of one genotype each. Cluster VII (774.502) exhibited the maximum intra-cluster diversity, while the least intra-cluster diversity was observed in Clusters III and VII (0.00). Highest inter-cluster diversity was observed between Clusters III and VII (15964.430), while the lowest distance was observed between Clusters I and II (898.25). Oil content (%) contributed maximum towards the divergence (61.67%), followed by pods per plant (22.65%) and plant height (6.62%) which showed that emphasis should be given on these characters during hybridization and selection, while pod length and biological yield per plant contributed the least (0.00% each). Based on the results obtained, the genotypes MAUS 449, SL 778 and MACS 1201 were identified as suitable donors for improving grain yields in soybean.

Barh *et al.* (2014) evaluated the genetic diversity for 13 yield and yield contributing traits among 48 black soybean genotypes collected from Uttarakhand hills using Mahalanobis D^2 statistic. Cluster analysis revealed that the genotypes were grouped in 12 clusters. Cluster IV was the largest with 19 genotypes and Clusters V, VI, VIII, IX, X, XI and XII were the smallest which included one genotype each. Intra-cluster distance (average D^2 values) ranged from 0.00 (Clusters V, VI, VIII, IX, X, XII, XII) to 10.004 (Cluster IV). The highest inter-cluster distance (average D^2 value) was observed between the Clusters IX and XI (90.85), followed by Clusters IX and XII (84.10). Days to maturity (1.29%) contributed minimum, whereas number of pods per plant (14.703%) contributed maximum towards genetic diversity. Based on the results obtained, the genotypes BCK BHATT BOLD-2, MRN SOYBEAN -24, MOB-29, MOB-36, MOB-17, MOB-43 and BHATT CHOCHOLATE were considered as potential parents and MOB-41×MOB-6, MOB-29×RS SOYBEAN, MOB-36×MOB-6, MOB-17×MOB-6, BCK BHATT BOLD-2×BHATT CHOCOLATE and MOB-26×MOB-4 as potential parental combinations based on D^2

statistic. These combinations were expected to result in maximum heterosis and maximum number of useful segregants among the recombinants.

Chavan *et al.* (2014) evaluated genetic diversity among 40 genotypes of soybean with respect to 10 traits included in the study. Multivariate technique based on cluster analysis revealed that the genotypes under study were grouped into 12 clusters out of which Cluster I was the largest with 20 genotypes. Maximum genetic distance was observed between Clusters IV and VI ($D^2=361.76$), while the minimum was recorded between Clusters VIII and X ($D^2=36.72$). Maximum and minimum divergence between the genotypes within the same cluster was reported in Cluster IV ($D^2=36.24$) and Clusters III, IV, VII, VIII, IX, X, XI and XII ($D^2=0.00$ each). Among all the traits considered, number of pod per plant (35.90%) contributed maximum towards divergence followed by plant height (20.13%) and seed yield per plant (20.00%), whereas number of primary branches per plant (0.26%) contributed the least. The study concluded that simultaneous improvement in protein and oil contents along with seed yield per plant in soybean could be attained through hybridization between genotypes JS-335, M-108, JS-79214, EC-457159, EC-457159, EC-457159, DS-228, IC-15545, EC-457211 and EC-343307 which were selected based on the inter-cluster distance, divergent cluster combination, cluster means and *per se* performance of genotypes in the present study.

Kachhadia *et al.* (2014) carried out diversity analysis among 61 genotypes of soybean using Mahalanobis D^2 statistic. The results showed that the genotypes were grouped into 11 clusters. Maximum number of genotypes were included in Cluster I (29), while the lowest number of genotypes were included in the Clusters III, V, VI, VII, VIII, IX and X, which consisted of a single genotype each. Number of cluster per plant (33.61%) contributed maximum towards genetic divergence, followed by plant height (23.28%) and oil content (10.27%) together contributing to 67.16% of the total diversity among the material under study. Maximum inter-cluster distance (maximum divergence) was observed between Clusters II and IX ($D=150.36$) followed by Clusters II and XI ($D=129.64$) and II and VIII ($D=124.78$), indicating that the genotypes from these clusters showed extreme divergence from each other. Whereas the minimum inter-cluster distance was found between the Clusters V and VIII ($D=21.01$). The genotypes from the clusters showing maximum inter-cluster distance could be used as parents in genetic crosses to obtain a wide range of variation among the segregating generations. The results obtained from the study concluded that the genotypes from Clusters II (J-659), IX (PK-986), XI (PK-926) and VIII

(NRC-2-R) could be used as parents in crossing programs.

Malek et al. (2014) evaluated genetic diversity among 27 soybean mutants and 4 parent genotypes considering 9 morphological traits under study. All the 31 genotypes were divided into 5 major groups on the basis of cluster analysis. Cluster II was the largest including 13 genotypes, while Clusters IV and V were the smallest consisting of one genotype each. Cluster IV showed highest average means for majority of the traits under study except number of seeds per pod, while the Cluster III showed lowest cluster means for all the traits under consideration.

Promin et al. (2014) studied 46 lines to evaluate genetic diversity among 8 morphological traits. Analysis through D^2 statistic grouped the 46 genotypes under study into 9 different clusters. Cluster V was reported to be the largest with 13 genotypes. Inter-cluster estimates were found to be highest between the Clusters IV and V (36.07) followed by Clusters I and II (25.96) and VI and VII (20.15). Based on the cluster mean values and *per se* performance, 7 genotypes viz. RKS 15, RKS 36, RKS 416, DS 2309, CAUS 2, JS 79-81 and MPUS 308 were identified to be used as parents in hybridization programs with specific objectives for combining ability to obtain a wide spectrum of variability and transgressive segregants among recombinants.

Alpna et al. (2015) investigated 57 genotypes for their morphological characterization and assessment of genetic diversity within 16 morphological and yield attributing traits. Diversity analysis through D^2 statistic revealed that the genotypes under study were grouped into 10 clusters, whereas Cluster I constituted the highest number of genotypes (34). The lowest number of genotypes were recorded in Clusters VII, VIII, IX and X, comprising of one genotype each. Maximum genetic divergence (highest inter-cluster distance) was reported between the Clusters IX and X (8.00), whereas Clusters IV and VII (2.60) exhibited lowest genetic divergence (lowest inter-cluster distance) indicating higher similarity among genotypes. It was found that number of pods per plant contributed maximum (22.05%), while harvest index (3.63%) contributed minimum towards genetic divergence. From the results obtained, 9 genotypes viz. *Glycine soja*, UPSM 534, Bhatt, Alankar, Kalitur, PK 327, PK 308, MACS 450 and PS 1029 were identified as potential donors for important yield attributes under study. Whereas the parental combinations, especially the *Glycine soja* derived pre-breeding lines i.e., PS 1029 x *Glycine soja*, T-49 x *Glycine soja*, PK 564 x *Glycine soja*, Pusa 40 x *Glycine soja* and MACS 450 x *Glycine soja*

were found promising to obtain better recombinants for the economically important traits.

Kumar *et al.* (2015) evaluated 42 soybean genotypes considering agro-morphological traits and studied the existing genetic diversity. The results obtained showed that, based on agro-morphological traits, the 42 genotypes were divided into two clusters A and B. Cluster A was again sub-divided into two clusters A₁ and A₂. Cluster A included 36 genotypes, which constituted 85.71% of the total genotypes, while the cluster B included 5 genotypes constituting 11.90% of the total genotypes. Only one genotype i.e., JS 20-34 was present as an out group. Both the sub-clusters A₁ and A₂ had 18 genotypes, each, constituting 42.85 % of the total genotypes. The results obtained from the principal component analysis showed that 3 principal components with greater than one eigenvalues contributed 82.66% of the total genetic variation existing among 42 accessions of soybean.

De Sousa *et al.* (2015) evaluated the genetic divergence and variability using multivariate analysis among 110 progenies (F₅) obtained from 22 biparental crosses (5 progenies from each cross) of soybean along with 5 cultivars viz. UFUS Riqueza, UFUS Impacta, UFUS Xavante, UFUS Millionária and MSoy 8211 used as control. Observations were recorded on 11 traits and the analysis revealed that plant height at maturity contributed maximum to divergence (31%), followed by number of pods with one grain and grain yield contributing 19.6% and 13.2%, respectively. The estimates of genetic divergence determined through Mahalanobis generalized distance (D^2), based on 11 characters, varied from 3.2 (between the crosses of CR6 and CR16) to 155.5 (between cultivar UFUS Impact and CR21). This indicated that UFUS Impact and CR21 were the most divergent, while crosses CR6 and CR16 were the most identical. Further, a dendrogram obtained through UPGMA method grouped the material under study into 8 clusters with Cluster I encompassing 14 genotypes and was found to be the largest. It was concluded from the study that, genetic hybridization between lines derived from crosses CR13, CR14 with cultivar UFUS Impact or hybridization of lines derived from crosses CR5 and CR10 with crosses CR21 and CR12 showed a great promise to obtain segregating populations in soybean.

Poornima Jency and Kalaimagal (2015) evaluated 50 genotypes of soybean for assessment of genetic diversity among 10 morphological characters. The diversity analysis was carried out using the D^2 statistic and the results revealed that the 50 genotypes under

study were grouped into 6 clusters. Cluster III was found to be the largest with 21 genotypes. Cluster VI showed the maximum intra-cluster distance (26.85), while minimum intra-cluster distance was observed for Cluster I (3.90). Maximum inter-cluster distance was recorded between Clusters IV and V (41.59) and the minimum between Clusters II and I (7.28). Cluster V showed highest mean values for 6 characters under study, while Clusters I and II exhibited lowest mean values for majority of the characters under study. Clusters V and VI were reported to be the superior among all the clusters and hence crossing between the genotypes from these clusters offers a promising scope in generating variability for yield.

Mahbub et al. (2016) evaluated morpho-physiological divergence among 28 genotypes of soybean using D^2 statistic. The diversity analysis classified the genotypes into 5 clusters. Cluster III contained the maximum number of genotypes (9) followed by Clusters I and II (6 each), V (5) and IV (2) which had the least number of genotypes. Maximum and minimum intra-cluster distance was observed for Clusters V (0.113) and IV (0.012), respectively. The maximum inter-cluster distance was found between the Clusters II and IV (11.19) followed by II and V (9.36) and III and IV (8.74). The lowest inter-cluster distance was observed between the Clusters II and III (4.04). Among the 11 physiological traits under study, plant height contributed maximum towards genetic divergence, followed by seed yield per plant and days to first flowering. The results obtained from the present study concluded that the genotypes CHINA-1, F-85-11347, PI-4174-75, YESOY-4, MTD-451, AUSTRALIA and BARI SOYBEAN-6 can be selected as potential parents in future breeding programs for yield improvement in soybean.

2.2 Genetic variability parameters

Genetic variability is indispensable for successful implementation of any crop breeding programme. A basic understanding of genetic variability is essential, since it renders crop breeding easier by facilitating the selection of superior genotypes in different generations (**Skaloud and Kovacik, 1994**). Genetic variability forms a key element in any agricultural production system (**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**). Several studies have been conducted in soybean reporting the nature and magnitude of variability.

Johansson (1909) attributed the genetic and environmental components of variation

to both heritable and non-heritable factors and he concluded that the variation in a pureline was exclusively due to environmental factors and hence non-heritable.

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

Heritability refers to the index of transmissibility, which measures the genetic relationship between the parents and their offspring's. Heritability infers as to how much emphasis should be laid on a particular trait for its selection. Heritability is defined as the ratio of additive genetic variance to the total phenotypic variance (**Wright, 1921**).

Lush (1949) partitioned heritability into broad sense and narrow sense. Broad sense heritability is the ratio of total genotypic variance to total phenotypic variance expressed in percentage. Narrow sense heritability is the ratio of additive genetic variance to total phenotypic variance 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 through selection is the product of its heritability, phenotypic standard deviation and selection differential (**Burton and De Vane, 1953**).

Puspendra and Ram (1987) obtained large heritability values for plant height, seed weight and days to flowering when they analyzed the heritability estimates from F₂ to F₅ generations of the two crosses viz. UPSM 534 x PK 86 and UPIR 1 x Bragg, using the North Carolina Design I, correlation and regression techniques and suggested that the selection would be effective for these traits.

Singh et al. (1995) also derived information on genetic variability, heritability and correlation coefficients from data on 8 yield related traits in 51 soybean genotypes grown during *kharif*, 1987. Highest heritability was estimated for hundred 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) studied the genetic variability among 25 genotypes of soybean for 16 yield and its attributing traits including oil and protein contents. They reported highly significant differences among genotypes for all the traits under study. They reported 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 which indicates additive type of gene action, while the remaining characters showed 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) studied genotypic and phenotypic variability, heritability and genetic advance among 33 genetically diverse genotypes of soybean for 12 quantitative traits including seed yield and vigour. The results obtained from the study showed that the highest magnitude of genetic variability was exhibited by number of pods per plant, followed by seed vigour, seed yield per plot and number of seeds per pod. They reported highest values of heritability (98.91%) and expected genetic advance (40.22%) for number of pods per plant.

Balla and Elrayah (2010) evaluated the genetic variability among 21 genotypes of soybean for which 6 traits were considered into study. Analysis of variance revealed significant dissimilarities among genotypes for all the traits under study. A general comparison among the PCV and GCV values revealed small to very large variations among the magnitudes of PCV over GCV for all the corresponding traits. Minimum values of PCV and GCV were reported for days to maturity (17% and 16%, respectively), while the maximum values varied among the characters. The estimates of heritability (h^2) varied from 43% (number of pods per plant) to 85% (grain yield). Genetic advance as % mean (GAM) was recorded highest for grain yield (17.9%), while the lowest was observed for days to maturity (3.0%). High estimates of heritability coupled with genetic advance indicated the existence of sufficient amount of variability for selection to bring about the improvement in such traits.

Ramteke et al. (2010) studied the genetic variability among 92 released varieties of soybean in India. They studied important economic characters like plant height, days to 50% flowering, days to maturity, nodes per plant, branches per plant, 100-seed weight, grain yield, oil and protein contents. They reported highly significant differences among the genotypes for all the characters under study. The characters like days to maturity, days to 50% flowering, plant height, nodes, oil and protein contents manifested high heritability indicating an additive gene action for the concerned characters and hence an improvement

of these characters through selection.

Aditya et al. (2011) studied the genetic parameters considering 8 quantitative traits among 31 soybean genotypes. The results obtained showed significant differences among the genotypes for all the concerned traits under study. The magnitude of GCV and PCV were obtained 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 reported 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 reported for number of pods per plant (45.46%) and the lowest value was reported for number of primary branches per plant (1.24%). High heritability coupled with high genetic advance holds an adequate scope for improvement of concerned characters through selection.

Bekele et al. (2012) studied genetic variability among 49 soybean germplasm introductions on the basis of 17 characters including oil and protein contents. The results showed that the estimates of PCV were significantly higher than that of GCV for all the characters under study. The highest value of PCV (%) and GCV (%) were observed for plant height (28.54% and 18.4%), followed by seed yield per plant (25.53% and 7.40%) and lodging (25.47% and 17.39%). Moderate to low levels of heritability were observed 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 reported for plant height (24.69%) followed by lodging (24.51%) and shattering (23.60%), while the lowest values are reported 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 to study the genotypic variation and heritability in broad sense (h^2_b) for seed yield and other quality traits. The results obtained showed significant differences for seed yield and quality characters under study suggesting 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 reported for the number of nodes per plant, days to flowering and plant height, respectively. However, lowest values for heritability and genetic advance were observed 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 Koteshwara rao (2013) studied genetic variability among 45 genotypes of soybean to estimate the variability, heritability and expected genetic advance with reference to 13 traits including yield and its attributes. Analysis of variance showed significant deviations among the genotypes for all the traits under study. 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%), suggesting a broader adaptability for these traits with minimal environmental interference in the expression of such traits. High heritability (%) combined with high expected genetic advance (GA%) was reported 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, suggesting a role of additive gene action in the expression of these traits and hence, an abundant scope for improvement through direct selection.

Adsul and Monpara (2014) evaluated 100 germplasm lines of soybean to study the selection indices and variability for 6 quantitative traits. They reported moderate to high GCV values along with high heritability and high genetic advance for all the characters under study, thereby indicating a scope of improvement in these traits through selection. Highest PCV (%) and GCV (%) values were observed 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 estimates of heritability (broad sense) ranged from 86.91% (biological yield per plant) to 70.55% (harvest index), whereas those for genetic advance as % mean (GAM) ranged from 65.80% (pods per plant) to 24.49% (harvest index).

Amrita et al. (2014) studied different genetic parameters including genetic variability, heritability, correlation and path coefficient analysis among 26 advanced generation lines of soybean. The analysis of 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 indicated selection to be effective in these traits.

Baruah *et al.* (2014) evaluated the genetic variability in 44 genotypes of soybean indigenous to North-eastern India by including seed yield and its component traits under study. The results showed that all the traits under study exhibited a wide variation among the genotypes. Highest PCV and GCV values were reported 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 the lowest values were reported for days to maturity (2.74% and 2.25%) and days to 50% flowering (8.96% and 7.35%). The estimates of heritability showed highest value for seed number per plant (99.19%), while the lowest being reported for days to maturity (44.67%). Estimates of genetic advance (GA %) showed highest value for 100-seed weight (139.24%) and lowest value for days to maturity (3.80%), respectively.

Hakima *et al.* (2014) studied genetic variability and expected genetic advance in the

F₂ progenies of soybean obtained from crosses of 3 parental combinations. They included 8 characters into study, for which the reported values of mean variability ranged from 11.7% (branches per plant) to 52.6% (seed weight per plant). The estimates of variability for different traits under study among F₂ progenies were found to be low to moderate, whereas their mean values ranged from 18.7% (seed weight per plant) to 56.1% (for both pods per plant and seed size). The estimates of expected genetic advance (%) were also found to be low to moderate with a range from 12.3% (branches per plant) to 47.2% (pods per plant). The results obtained concluded that, agronomic characters like plant height, seed size, pods per plant and days to maturity exhibited high coefficients of variability coupled with high heritability and genetic advance and hence, development of early maturing and high yielding soybean varieties based on the selection for plant height, pods per plant and seed size should be feasible.

Kumar *et al.* (2014) evaluated 9 soybean genotypes along with 3 checks viz. PS 1347, SL 688 and Bragg to study the genetic variability and character association for 11 characters including yield and its contributing traits. Analysis of variance revealed significant differences among genotypes for all the characters under study. The values of PCV and GCV were in correspondence with each other with the values of PCV slightly higher than that of GCV. The range of PCV varied 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). High estimates of heritability were observed for most of the characters with the maximum values observed for biological yield per plant (99.80%), while the lowest was observed for pod length (50.00%). Estimates of genetic advance revealed highest value for plant height (17.85%), while the lowest value was recorded for pod length (0.14%). Hence, a direct selection of the characters manifesting high heritability and high genetic advance should bring about adequate improvement in the characters concerned.

Malek *et al.* (2014) studied genetic variability among 27 soybean mutants and 4 parent genotypes considering 9 morphological traits. The reports revealed significant differences among the mutants and parent genotypes for all the traits under study. Eighteen mutants showed superior performance over parents with respect to grain yield and other morphological traits including yield attributes. They reported narrow differences between phenotypic and genotypic coefficients of variation (PCV and GCV) for majority of the characters under consideration, indicating minimum environmental influence. The highest

and lowest values of PCV and GCV were reported for branches per plant (38.11% and 35.03%) and days to maturity (7.22% and 6.35%). Highest values of heritability were reported for 100-seed weight (93.73%) followed by plant height (87.74%) and branches per plant (84.70%), while the lowest heritability was recorded for days to maturity (77.40%). Highest GA (%) was reported for branches per plant (66.33%), while the lowest for days to maturity (11.50%). High heritability coupled with high GA (%) could be considered as promising attributes for improvement through phenotypic selection.

Sureshrao *et al.* (2014) evaluated 12 genotypes of soybean to study the genetic variability parameters considering 13 yield component traits into study. Results from analysis of variance showed significant differences for all the characters under study except number of grains per plant indicating substantial amount of genetic variability. The estimates of PCV and GCV showed similar correspondence of values, with the highest values being recorded for number of pod per plant (PCV = 40.83% and GCV = 40.42%), while number of grains per pod recorded lowest values (PCV = 3.85% and GCV = 2.33 %). The estimates of heritability recorded moderate to high values for all the traits under study. High heritability was reported for days to maturity (98.50%), while the lowest value was reported for number of grains per pod (36.70%). The estimates of genetic advance (GA %) showed highest value for number of pod per plant (82.43%), while the lowest value was reported for number of grain per pod (2.91%).

Badaya *et al.* (2015) studied the genetic variability and path analysis based on reproductive phase in 60 genotypes of soybean and also evaluated the quality traits for their association with seed yield. Results revealed that 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). Highest heritability was observed for days to full flowering (97.93 %), while the least was reported for protein content (67.30%) and oil content (77.78%). The highest values of genetic advance as percentage of mean (GAM) were reported for seed yield per plant (49.28%), while the lowest were reported for protein content (5.75%) and oil content (8.67%). Low estimates of heritability and genetic advance for oil and protein contents suggested that expression of these traits could be due to non-additive gene action.

Kumar *et al.* (2015) evaluated 42 soybean genotypes to evaluate agro-morphological traits and studied the extent of genetic variability. Analysis of variance for yield and its component traits showed significant differences among all the genotypes for

all the characters under study. Results obtained revealed that the phenotypic and genotypic coefficients of variation (PCV and GCV) showed similar trends of distribution with highest PCV (21.30%) and GCV (19.24%) observed for number of pod clusters per plant. High heritability was reported 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%). Estimates of genetic advance as percentage of mean (GAM) showed higher values for number of clusters (35.81%) followed by number of pods (33.89%) and grain yield (25.07%). Higher values of heritability coupled with adequate levels of genetic advance suggested a scope for improvement of concerned characters through selection.

Dubey *et al.* (2015) studied genetic variability among 50 genotypes of soybean and the results obtained showed that the phenotypic coefficients of variation (PCV) were higher than that of genotypic coefficients of variation (GCV) for all the traits under consideration. A same range of magnitude between the values of PCV and GCV for most of the characters was due to a lesser environmental interference on the expression of traits under study. Study on heritability reported high values for majority of the characters included. High heritability (h^2_b) combined with higher values of genetic advance as per cent of mean (GAM) were observed for biological yield per plant, harvest index, number of seeds per plant, seed yield per plant and number of pods per plant indicating scope of improvement for these traits through direct selection.

Jain *et al.* (2015) evaluated the genetic variability and also studied correlation and path analysis among 41 genotypes of soybean for 9 important yield and its related characters. The estimates of PCV were found to be higher than those of GCV with only a slight deviation between both the estimates for all the traits under study. Highest value of GCV was reported for plant height, followed by number of primary branches and seed yield per plant. High estimates of heritability (%) were reported for days to 50% flowering, 100-seed weight and seed yield per plant which inferred that improvement of yield through selection based on these characters should be conceivable.

Mahbub *et al.* (2015) studied genetic variability among 28 genotypes of soybean for 11 morphological characters and reported significant differences among the genotypes for all the traits under consideration. They reported additive gene action 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 and hence a good scope for improvement of

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

2.3 Inter-character association (correlation) analysis

Correlation analysis is a handy technique, which provides information about the degree of relationship between important plant traits and is also a good index to predict the yield response in relation to the change of a particular character. The knowledge of correlation between yield and its attributes is highly essential as it helps in bringing about simultaneous response through selection in all such characters which are associated with one other.

Many of the earlier workers reported positive associations between pods per plant, days to maturity and seed yield in soybean (**Jadhav *et al.*, 1995**).

Rajput *et al.* (2000) studied the interrelationships between yield and growth parameters of soybean in Madhya Pradesh, India during *Kharif* seasons of 1995 and 1996. Out of 78 character pair associations, 66 and 71 pairs were positively and significantly correlated during 1995 and 1996, respectively. Seed yield was positively and significantly correlated with all growth parameters especially dry matter per plant, leaf area index, leaf area ratio, canopy growth rate, average growth rate and plant height, during both the years. Among yield components, pods per plant were most highly correlated with seed yield. The majority of growth and yield parameters exhibited positive and significant correlations among themselves.

Thorat *et al.* (2001) estimated the phenotypic and genotypic correlations of yield and its components using 30 soybean cultivars. Seed yield was positively correlated with the number of pods per plant and days to 50% flowering, but negatively correlated with 100-seed weight. Negative correlations were also observed for number of seeds per pod, oil and protein contents.

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.

Malik et al. (2006) studied the correlation between 16 yield and its attributing traits including oil and protein contents among 25 genotypes of soybean. They reported significant and positive correlation of grain yield with number of pods per plant but negative correlation with days to 50% flowering and days to flowering completion. Therefore, selection in the direction of more number of pods per plant would result in higher yields in soybean.

Malik et al. (2007) studied the genotypic, phenotypic and environmental correlations between 16 yield and its attributing traits including oil and protein contents among 27 genotypes of soybean. The results showed that the estimates of genotypic correlation were higher than that of phenotypic and environmental correlations which indicated a high degree of genetic association among the traits under study. Positive correlations were observed 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 indicating that high mean values for these traits can increase the grain yield.

Ramteke et al. (2010) carried out correlation studies among 92 released varieties of soybean in India. They included important economic characters under this study and reported that yield showed significant negative correlation with days to flowering and days to maturity. 100-seed weight was found to be negatively correlated with days to flowering, days to maturity, plant height and nodes per plant but showed positive correlation with oil content. Protein content was found to be positively correlated with number of branches and days to 50% flowering but negatively correlated with oil content.

Aditya et al. (2011) studied the correlation between 8 quantitative traits among 31 soybean genotypes. The results obtained showed higher values for genotypic correlation coefficients than phenotypic correlation coefficients. At the genotypic level, grain yield per plant showed 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 ($r_g = 0.403$), while the remaining characters showed non-significant correlation. At phenotypic level, seed yield per plant showed highly significant and positive correlation with number of pods per plant ($r_p = 0.511$) and significant positive correlation with dry matter weight per plant ($r_p = 0.410$) and harvest index ($r_p = 0.385$), while the remaining characters showed non-significant correlation.

Koladiya et al. (2012) studied the correlation and path co-efficient analysis among

40 genotypes of soybean by including 12 characters in the study. They reported higher values of genotypic correlations over phenotypic correlations for majority of the characters under consideration suggesting a strong association between character pairs at genotypic level. Positive correlation was observed for seed yield per plant with days to 50% flowering, days to maturity, plant height and pods per plant.

Sarutayophat (2012) evaluated 22 genotypes of vegetable soybean to determine the association among yield and its component traits. The results reported positive and significant correlation for number of marketable pods per plant (0.821**) and marketable pod yield (0.520*) with plant height, and between number of marketable pods per plant and marketable pod yield (0.822**), whereas significant and negative correlation was observed for green pod weight with plant height (-0.620**) and number of marketable pods per plant (-0.588**).

El-Mohsen *et al.* (2013) studied the correlation and regression analysis among 6 soybean cultivars for seed yield and its attributes under varying irrigated conditions. The correlation analysis revealed that seed yield per hectare showed 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). But, it exhibited significant and negative correlation with oil content (-0.426) and protein content (-0.399). Oil and protein contents exhibited highly significant and negative correlation (-0.661) with each other indicating that selection for higher oil content would reduce protein levels in soybean.

Ghodrati (2013) evaluated 12 soybean genotypes during three crop growing seasons to study the genotypic and phenotypic correlation for seed yield and other quality traits. The results showed higher magnitudes of genotypic correlation over phenotypic correlation suggesting strong association between each pair of traits. About 21.7% of genotypic and 25.5% of phenotypic correlations showed significance at 5% probability level. Significant and positive genotypic and phenotypic correlations were reported between plant height, oil yield, protein yield and seed yield. Plant height showed highly significant and positive genotypic and phenotypic correlations with number of nodes per plant, pods per plant, seeds per pod and number of seeds per plant.

Moe and Girdthai (2013) studied the genetic correlation among 94 soybean cultivars based on physiological and agro-morphological traits. They reported positive and

significant correlations between yield and other agro-morphological traits under consideration, except number of seeds per pod.

Salimi *et al.* (2013) evaluated 19 soybean genotypes to study the effect of drought stress on yield and its components by considering 15 characters into study. 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 showed a negative and non-significant correlation (-0.139). However, they reported that grain yield showed non-significant negative and positive correlations with protein (-0.068) and oil contents (0.129), respectively.

Attia (2014) evaluated 10 soybean genotypes for seed yield and its attributes, pubescence density and trypsin inhibitor content as resistant factor against defoliation %. Among 14 characters studied, seed yield per plant showed a significant and positive correlation with plant height (0.308), while it showed highly significant and positive correlation with branches per plant (0.795), pods per plant (0.978), seeds per plant (0.828) and 100-seed weight (0.869). However, it showed positive and non-significant correlation with oil content % (0.058) and significant and negative correlation with protein content % (-0.346).

Barh *et al.* (2014) studied the inter-character correlation co-efficients at the genotype level, between 13 yield and yield attributing traits among 48 black soybean genotypes obtained from Uttarakhand hills. Results obtained revealed that number of pods per plant, number of primary branches per plant, number of seeds per pod and 100-seed weight showed highly significant and positive correlations with seed yield per plant, whereas days to 50% flowering, days to maturity, plant height and protein content showed negative correlations with seed yield per plant. However oil and protein contents showed negative correlation with each other.

Malek *et al.* (2014) studied the genotypic and phenotypic correlation between 9 morphological traits among 27 soybean mutants and 4 parent genotypes. The magnitudes of genotypic correlation co-efficients were found to be higher than that of phenotypic correlation co-efficients. All the characters under study except 100-seed weight showed significant and positive correlations with seed yield per plant and seed yield per hectare,

both at phenotypic and genotypic levels. They also reported that 100-seed weight showed significant and negative correlation with all the characters under study except seed yield per plant.

Ali *et al.* (2015) evaluated character associations among yield and yield attributes in 10 accessions of soybean considering 8 traits into study. Results obtained from the correlation studies showed that positive and significant correlation was reported between seed yield, days to 50% flowering, days to maturity, pods per plant and 100-seed weight, while positive correlation was observed between seed yield and pod length. However, seed yield showed negative correlation with plant height.

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). The results obtained from the study revealed highly significant and positive correlation between seed yield and biological yield (0.996) in the maturity group IV, whereas in maturity group III, weight of seeds per plant (0.997), biological yield (0.996) and plant dry weight (0.996) showed highly significant and positive correlation with seed yield. With regard to seed yield, oil and protein contents, they reported a negative and non-significant correlation of seed yield with oil and protein contents in maturity group IV but a significant and negative correlation of oil and protein contents with seed yield in maturity group III indicating that selection for high oil and protein contents could reduce the seed yields in soybean.

Kumar *et al.* (2015) conducted correlation studies among agro-morphological traits in soybean considering 42 genotypes under this study. Correlation studies revealed significant associations of seed yield with its component traits. Results obtained showed that days to flowering showed positive correlation with yield and negative correlation with seed weight, whereas the number of branches per plant and yield were positively correlated.

Chandrawat *et al.* (2015) evaluated 41 germplasm lines of soybean along with 3 national checks (Bragg, JS-93-05 and JS-335) and 2 local checks (MAUS-158 and MAUS-71) to study the correlation and path analysis for 11 quantitative traits. Results obtained from the study showed that the magnitude of genotypic correlations were higher than the phenotypic correlations suggesting a higher influence of genetic factors in the development of dependent variable i.e., seed yield. Phenotypic and genotypic correlations of seed yield were found positive and highly significant with harvest index (0.582 and 0.662) and 100

seed weight (0.363 and 0.451). But seed yield per plant showed highly significant and non-significant negative correlations with protein content (-0.268 and -0.205) at the genotypic and phenotypic levels, respectively, whereas oil content showed non-significant positive (0.025) and negative (-0.016) correlations with protein content at genotypic and phenotypic levels, respectively. The other traits like days to 50% flowering, days to maturity and branches per plant exhibited positive but non-significant association with seed yield per plant.

Mahbub *et al.* (2015) conducted correlation studies among 28 genotypes of soybean for 11 morphological characters and reported that plant height, number of pods per plant, pod length, number of seeds per pod, 100-seed weight and branches per plant exhibited significant positive genotypic and phenotypic correlation with seed yield. They concluded that emphasis should be given on characters like plant height, pod length, seeds per pod and 100-seed weight to improve seed yields in soybean.

Rodrigues *et al.* (2015) studied the correlation among 15 soybean genotypes infected with Asian soybean rust (*Phakopsora pachyrhizi*), which were evaluated for 14 phenotypic traits contributing to yield. The study revealed that the genotypic and phenotypic correlation coefficients were positive. Highly significant and positive phenotypic correlations were observed for seed yield with total number of pods per plant (0.89) and number of pods with 2 (0.87) or 3 seeds (0.74), suggesting them to be the important traits for selection in soybean for enhanced grain yields. Also they reported a strong environmental correlation between plant height at blooming and maturity with grain yield and its components. A negative and non-significant phenotypic (-0.05) and genotypic (-0.07) correlation was observed between seed yield and severity of rust infection.

Thakur *et al.* (2015) estimated the correlation and path analysis among 40 genotypes of soybean by including 12 yield and its components traits under the study. Correlation analysis revealed that pod bearing nodes (0.578), number of seeds per pod (0.368) and 100-seed weight (0.471) showed highly significant and positive correlation with seed yield per plant, whereas number of pods per plant (0.397) showed significant and positive correlation with seed yield per plant. The traits like days to 50% flowering (-0.328) and days to maturity (-0.391) exhibited significant negative correlation, meanwhile plant height (-0.420) exhibited highly significant and negative correlation with seed yield per plant. The oil (0.271) and protein (-0.297) contents showed non-significant positive and

negative correlation, respectively, with seed yield per plant and non-significant negative correlation (-0.194) with each other.

2.4 Path coefficient analysis

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

Path coefficient analysis measures the direct and indirect effect for one variable upon another and permits the separation of the correlation coefficient into components of direct and indirect effects (**Dewey and Lu, 1959**).

Iqbal et al. (2003) evaluated 10 soybean varieties to determine the interrelationship among 5 characters including yield and its attributes through genotypic correlation and path co-efficient analysis. Results obtained from the study revealed that pods per plant (0.816) exhibited highest positive and direct effect on seed yield, followed by 100-seed weight (0.420) and number of seeds per pod (0.076), whereas plant height (-0.097) showed negative and direct effect on seed yield. The study concluded number of seeds per pod, number of pods per plant and 100-seed weight as the important yield components.

Malik et al. (2006) studied the path co-efficient analysis between 16 yield and its attributing traits including oil and protein contents among 25 genotypes of soybean. The reports suggested that chlorophyll content, number of branches per plant, days to pod initiation, number of pods per plant and 100-seed weight exerted direct and positive effects on yield. Days to pod initiation (6.297) showed the maximum direct effect. The other characters like plant height, days to 50% flowering, days to flowering completion, first pod height, days to maturity, leaf area, oil content and protein contents showed direct and negative effects on yield.

Arshad et al. (2007) evaluated 33 genotypes of soybean to study the path co-efficient analysis in which they reported that, among the 10 characters included under study, 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, suggesting that the emphasis should be laid on these characters during selection to enhance yield levels in soybean. The remaining characters showed negative and direct effects on seed yield, which indicated that positive selection for these traits could result in reduced yield levels.

Malik et al. (2007) conducted path co-efficient analysis for 16 yield and its attributes including oil and protein contents among 27 genotypes of soybean. Results obtained showed that first pod height, days to 50% flowering, days to maturity, leaf area, branches per plant, 100-seed weight, protein and oil contents had negative direct effects on yield, suggesting that selection based on these traits could lead to reduced grain yield. On the other hand, days to flowering completion, days to pod initiation, chlorophyll content, plant height and pods per plant showed direct and positive effects on grain yield. Maximum direct effect on seed yield was shown by days to flowering completion (32.75) followed by days to pod initiation (19.46).

Oz et al. (2009) studied the correlation and path analysis among 8 cultivars of soybean to evaluate yield and its components over different locations and years. Path co-efficient analysis revealed that, number of seeds per pod had the maximum direct and positive effect (0.473) on seed yield, followed by number of pods per plant (0.399) which correspond to 57.0% and 50.4% of direct effects on seed yield, respectively. Direct and positive effect of number of pods per plant was found stable in expression over the years and locations and hence, could be included as the chief trait for enhancing yield along with seeds per pod in soybean.

Machikowa and Laosuwan (2011) evaluated 14 genotypes of soybean to study correlation and verify direct and indirect effects through path co-efficient analysis for 8 characters. Results from the study revealed that, number of pods per plant (1.203) showed highest positive and direct effect on seed yield, followed by number of branches per plant (0.344). Also, most of the characters showed 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.

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) studied the correlation and path analysis among 30 genotypes of vegetable soybean for fresh pod yield and other yield attributes. Path coefficient analysis revealed that number of 3-seed pods per plant (0.58) showed highest direct and positive effect on fresh pod yield followed by number of 2-seed pod per plant (0.56), 2-seed pod width (0.31), and 100-fresh seed weight (0.23), whereas highest negative and direct effect on fresh pod yield was shown by plant height (-0.36) and 2-seed pod length (-0.35). The results showed that more emphasis should be given on 3-seed and 2-seed pods per plant, 2-seed pod width, 100-fresh seed weight and number of seed pod per plant to increase fresh pod yield in the vegetable soybean.

Amrita et al. (2014) evaluated 26 advanced generation lines of soybean to study phenotypic and genotypic path analyses for 11 traits. They reported 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) exhibited positive direct effect at genotypic and phenotypic levels, and also that these traits exhibited positive indirect effect through each other indicating a scope for simultaneous improvement of these traits and yield ultimately. Whereas 100-seed weight (-1.083 and -0.064) and seeds per pod (-1.528 and -0.373) exhibited negative and direct effects at both genotypic and phenotypic levels on grain yield.

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.

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. lpa 5-1, lpa 5-2, lpa 5-3, lpa 13-1 and lpa 18 all as parents and crossed them in a line x tester design to generate 25 F₁s 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 levels in soybean.

Shruti et al. (2015) evaluated 13 genotypes of soybean to study the correlation and 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.

2.5 Screening for disease resistance

Singh et al. (1974) evaluated 1014 and 3047 germplasm accessions of soybean during 1970 and 1971, respectively, in an effort to find a stable source of resistance against two important diseases viz. rust and yellow mosaic (YMV) in soybean. They also tested 5 wild species of soybean viz. *Glycine tabacina*, *G. tomentella*, *G. formosana*, *G. wightii* and *G. ussuriensis* for resistance during the study. The selected lines were further evaluated in 1972 and 1973 and they reported 6 lines to be resistant and 13 lines to be moderately resistant to rust and most of these accessions were obtained from Shikoku, Japan. In case of YMV, they reported one line, PI 171443 (UPSM 534), an accession from China, to be highly immune against the disease which was confirmed after testing in multiple locations for years. Among the wild species only *G. ussuriensis* succumbed to the disease, while the remaining 4 species showed resistance to YMV but *G. formosana* was found susceptible to rust and bacterial pustule.

Sharma et al. (1993) screened 20 genotypes of soybean for resistance against bacterial pustule by following excised leaf inoculation method. The results obtained

revealed a differential susceptibility among the test genotypes against the disease. Two genotypes (P- 169-3 and P-4-2) showed complete resistance, while 4 genotypes (Bragg, Kalitur, EC 34160 and PK 472) exhibited moderate resistance and all other remaining genotypes showed susceptible reaction to the disease.

Shehzad azad *et al.* (2006) screened 91 entries of soybean against three common diseases occurring in the crop viz. bacterial pustule, anthracnose and yellow mosaic. Out of total entries screened, results showed that 68 entries were infected by bacterial pustule to variable extent, 67 entries were infected by Anthracnose to varying intensity and 64 entries manifested the Yellow mosaic virus infection with some entries showing severe infection as compared to the other entries which were infected by the disease.

Suryadi *et al.* (2012) screened 100 genotypes of soybean for three important foliar diseases i.e., soybean stunt virus (SSV), bacterial blight (BB), and bacterial pustule (BP). The results obtained from the study showed that among the 100 genotypes for bacterial blight, 48 were found to be resistant (R), 31 were moderately resistant (MR), 13 were moderately susceptible (MS) and 8 were found to be susceptible (S). In case of Bacterial pustule, 43 genotypes showed R, 41 were MR, 14 were MS and 2 were S. The overall results obtained from the screening of genotypes against SSV, BB and BP diseases showed that a total of 19 out of 100 genotypes were categorized as MR to R for all the three diseases. The genotype GM 4779 Si showed the lowest severity for all the three diseases and was ranked first with a stable resistance.

Talukdar *et al.* (2013) evaluated 100 germplasm lines of soybean for 3 years under field conditions to screen the genotypes against Yellow mosaic (YMV) in soybean. They reported that 24 lines showed stable resistance which included UPSM 534, DS 9814, DS 9712, Jupiter, PK 1223 and SL 528 etc. These resistant lines were of both exotic and indigenous collections, especially from North-India, indicating that these lines could be used as promising donors in breeding for resistant genotypes against YMV.

Baruah *et al.* (2014) evaluated 44 genotypes of soybean to study the genetic variability for Yellow mosaic virus (YMV) resistance. The results obtained from the study showed that among 44 genotypes evaluated, only a few genotypes showed moderate to high level of susceptibility. One genotype (JS 335) was found to be highly susceptible for YMV, while two genotypes (DS 9712 and DS 9814) were found to be highly resistant for the disease.

Kumar et al. (2014) evaluated 500 germplasm lines of soybean collected from across the globe to screen them against Yellow mosaic virus. The study was conducted for three consecutive years and the results obtained revealed that a total of 96 genotypes out of 500 evaluated showed stable reaction with 48 genotypes each, showing resistance and susceptibility towards the disease. They reported that 21 genotypes including PS 1042, UPSM 534 and PK 1347 etc. showed complete resistance for three years, while the others showed resistant reaction. Similarly, 31 genotypes showed high susceptibility for three consecutive years like EC 472211, SKAF 106 and JS 335 etc., while the rest showed susceptible reaction. These resistant genotypes could be used as promising donors for incorporating the resistance into cultivated background.

Ingle et al. (2016) evaluated 13 advanced lines of soybean obtained from DSR (ICAR-IISR), Indore and screened them for resistance against 4 important diseases viz, Alternaria leaf spot, root rot/charcoal rot, bacterial pustule and yellow mosaic by comparing with 5 standard checks both in protected as well as un-protected conditions. The results obtained revealed that 4 entries i.e., JS-20-69, NRC-94, KDS-699 and JS 20-71 exhibited Resistant High Yield (R-HY) reaction to the disease complex, whereas JS 20-41, NRC-92, KDS-378 and KDS 705 showed Susceptible High Yield Tolerance {S-HY (T)} reaction to the disease complex. Only one entry, SL-958 exhibited Resistant Low Yield (R-LY) reaction, while the rest of the advance lines evaluated showed Susceptible Low Yield (S-LY) reaction to the disease complex.

Kumar et al. (2016) screened 42 accessions against the aerial blight caused by *Rhizoctonia solani* and the results obtained showed that two accessions (SL 752 and RKS 48) were found to be absolutely resistant, while 6 accessions were found to be highly resistant to the pathogen. They reported that maximum losses occurred in the crop sown under flooded field condition, where the incidence of pathogen was high. These resistant lines could be used as donors for developing soybean varieties resistant against the aerial blight (RAB).

2.6 Bio-chemical profiling of genotypes

The molecular approaches have become the choicest methods for the evaluation of crop diversity during the recent past. It is primarily due to their high precision in detecting polymorphism among genotypes. They also facilitate a precise estimation of genetic and

environmental components of variation. Among the biochemical methods, seed protein electrophoresis (SDS-PAGE) has been widely used as a promising tool for distinguishing the genotypes of a particular crop species. The SDS-PAGE is a reliable and handy technique for the differentiation of genotypes because the total seed storage proteins were not influenced by environmental variations (**Gepts, 1989**). Seed protein profiles obtained through electrophoresis were successfully utilized in resolving taxonomic problems and understanding evolutionary patterns in various crop species (**Khan, 1992 and Rao *et al.*, 1992**). This technique can also be utilized to evaluate the genetic diversity among genotypes based on seed storage proteins (**Das and Mukarjee, 1995**). The contrary was also reported by some workers indicating limitations of SDS-PAGE in the identification of genotypes (**De Vries, 1996**). SDS-PAGE has been found to be a powerful and easy tool in not only separation but also in identifying the types of seed protein and any variation within them in soybean (**Liu *et al.*, 2007**).

Soybean seed has 40% protein on average (**Patil *et al.*, 2014**) and the seed storage protein in soybean could be divided into two major fractions i.e., β -conglycinin (7S) and glycinin (11S). They together contribute nearly 70% of the total seed storage protein in soybean, of which the glycinin fraction is the major accounting for 60% of the seed storage protein, while the remaining 40% is constituted by β -conglycinin (**Ajdukovic *et al.* 2010**).

Han *et al.* (1999) and **Hirata *et al.* (1999)** evaluated the genetic diversity and variability pattern among the Asian soybean germplasm based on their seed storage proteins.

Bushehri *et al.* (2000) evaluated genetic diversity among 21 soybean genotypes using the SDS-PAGE. Based on the analysis of banding pattern of seed storage proteins, they categorized the genotypes into four distinct groups. They also inferred that seed protein electrophoresis could be more effective in differentiating soybean genotypes as compared to the isoenzyme profiling.

Ghafoor *et al.* (2005) studied the seed storage proteins in 9 genotypes of black gram (*Vigna mungo* (L.) Hepper) using SDS-PAGE to study the pattern of genetic variability. Results obtained from SDS-PAGE revealed low polymorphism among genotypes indicating low genetic diversity and also failed to differentiate genotypes based on their origin.

Iqbal *et al.* (2005) studied the seed protein profile among 20 genotypes of chickpea and reported that 6 out of 12 bands observed were polymorphic and also they reported low

level of genetic diversity in terms of polypeptide polymorphism among the genotypes having diverse origins. They further recommended 2-D electrophoresis and DNA analysis using molecular markers for assessing the genetic diversity among genotypes showing similar banding patterns.

Zarkadas *et al.* (2007) evaluated the protein quality among 14 genotypes of soybean through amino acid analysis and 2-DE (2-Dimensional electrophoresis). They obtained a similar banding pattern for the 14 genotypes evaluated using 1-DE on a large gradient (8-18%) gel. They reported 14 distinct bands which showed a M_r (migratory distance of protein) ranging from 7.0 to 166.0 kDa. These bands correspond to different protein subunits of β -conglycinin (α' , α and β subunits), the acidic (A_1 – A_4) and basic (B_1 – B_4) glycinin subunits and other major bands like lipoxygenase, lectins, Kunitz trypsin inhibitor and Gly m Bd (which is an allergen).

Malik *et al.* (2009) studied the genetic diversity using seed protein electrophoresis among 92 soybean genotypes belonging to five different origins (USA, AVRDC, Pakistan, North Korea and Japan). SDS-PAGE revealed 26 reproducible bands and genetic diversity among the genotypes was estimated based on the difference in number of polypeptide bands. Out of 26 bands, 50% were found to be polymorphic among which 10 major bands were detected. Dendrogram based on Ward's method divided the genotypes into 2 main groups comprising of 4 clusters. They inferred from the cluster analysis that genetic diversity between Pakistani and US or AVRDC genotypes is much higher as compared to that between Pakistani and North Korean or Japanese genotypes.

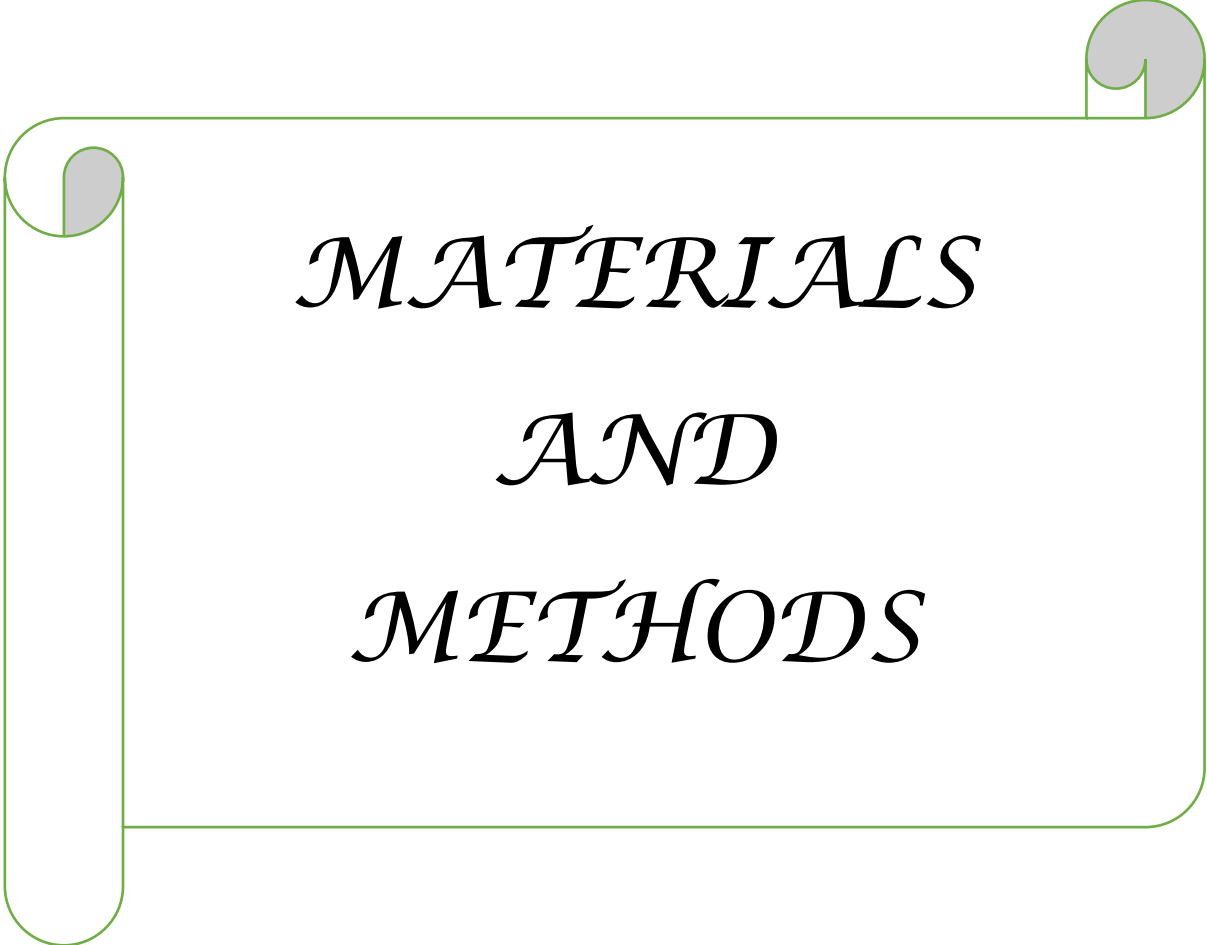
Emre *et al.* (2010) studied the pattern of seed storage proteins in 9 *Lathyrus* species using SDS-PAGE and reported that their protein content ranged from *L. cilicicus* (65.860 $\mu\text{g/ml}$) to *L. lycicus* (79.906 $\mu\text{g/ml}$) when the protein contents were quantified. They observed significant differences in banding pattern for all the 9 species and they found that *L. annuus* and *L. hierosolymitanus* were more genetically close to each other than the other species included.

Chaudhary and Dantu (2011) studied the genetic diversity among 14 germplasm accessions of soybean using SDS-PAGE and observed a total of 29 bands in their electrophoregrams. The genotypes are scored for the presence or absence of bands and the data obtained was analyzed using Jackard's similarity matrix based on which the 14

genotypes were differentiated and grouped into four clusters. Also, they observed a protein content range from 42 µg/µl (PS1029) to 14 µg/µl (JS335).

Arefrad *et al.* (2014) assessed the seed storage protein composition among 6 Iranian soybean genotypes. The seed protein was extracted and quantified using **Bradford (1976)** method in which they reported a range of protein concentration from 63.38 mg/gm (genotype 032) to 76.86 mg/gm (genotype DPX). The protein fractions extracted were subjected to SDS-PAGE to identify the different variants of seed storage protein sub-units. They observed a low level of polymorphism among the test genotypes and also reported that the protein profile consisted of 16 distinct scorable bands corresponding to different sub-units of 11S (glycinin), 7S (β-conglycinin) and other bulk storage proteins.

Masoomeh *et al.* (2015) surveyed the genetic relationship among 11 genotypes of ground nut genotypes using SDS-PAGE in which they reported 17 major bands in their protein profiles. Based on the cluster analysis based on UPGMA from banding pattern obtained, the 11 genotypes under study were grouped into 4 clusters. They reported significant differences in the banding pattern of the 11 cultivars, based on which specific bands were assigned to certain genotypes through the analysis of their protein profiles.



MATERIALS AND METHODS

The details of the material and methodology followed during the present investigation have been described in this chapter.

3.1 Experimental site:

The present study was conducted during *Kharif*, 2014 at N. E. Borlaug Crop Research Centre, Govind Ballabh Pant University of Agriculture and Technology, Pantnagar, Udham Singh Nagar, Uttarakhand. The University is located at an altitude of 243.84 meters above the mean sea level and its geographical coordinates are 29° 3' 0'' N and 79° 31' 0'' E. The University comes under the *Tarai* region of Uttarakhand state which falls in the humid sub-tropical climatic zone, in the *Shivalik* range at the foothills of 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 employed in the present study include a constellation of 160 genotypes obtained from ICAR-Indian Institute of Soybean Research, Indore, along with 5 checks viz. SL 688, PS 1347, PS 1092, Bragg and PS 1042, all maintained at G. B. P. U. A. T, Pantnagar. The details of the experimental material used were given in **Table 3.2.1**.

Table 3.2.1: List of 165 soybean genotypes included in the present investigation

Sl. No.	Genotype	Sl. No.	Genotype	Sl. No.	Genotype
1	AGS 129	14	EC 65772	27	Himso 175
2	EC 389148	15	RVS 2006-27	28	GP 448
3	Jupiter	16	EC 95291	29	WT 150
4	T-49	17	EC 100027	30	MAUS 76
5	P RAB 1	18	IC 13051	31	MAUS 102
6	AMS 155 (A)	19	EC 14626	32	MAUS 489
7	TGX 855-39E	20	JS 82	33	MAUS 38
8	AMS 77-3-6	21	PI 283327	34	MAUS 85
9	AMS 2005-19	22	PK 765	35	MAUS 149
10	EC 16738	23	MACS 1394	36	AMS 2005-24
11	EC 37937	24	GP 305	37	MAUS 164
12	EC 39362	25	RPSP 935-E	38	EC 963805
13	EC 39491	26	GP 465	39	EC 281462

Contd....

Table 3.2.1 Concluded

Sl. No.	Genotype	Sl. No.	Genotype	Sl. No.	Genotype
40	EC 116343	82	Cat. 3284	124	PS 1551
41	EC 172607	83	Cat. 2430	125	PS 1480
42	EC 33940	84	Cat.103	126	Shilajeet
43	EC 2581	85	Cat. 537	127	Ankur
44	EC 118443	86	Cat. 366	128	PS 1029
45	RKS 30	87	Cat. 3327	129	Alankar
46	RKS 27	88	Cat. 783	130	PK 416
47	AMS 243-7-3	89	Cat. 181	131	PK 262
48	AMS 42	90	Cat. 307	132	PS 19
49	AMS 50B	91	Cat. 195	133	Kalitur
50	AMS 100-16-4-1-3	92	Cat. 2388	134	EC 250608
51	AMS 25-5-1	93	EC 2581	135	JS 20-41
52	AMS 100-25-5	94	RVS 2002-6	136	EC 251358
53	AMS 100	95	RVS 2002-7	137	JS 20-27
54	AMS 115	96	MACS 993	138	JS 20-61
55	AMS 2005-13	97	RVS 2006-1	139	JS 20-34
56	AMS MB 5-19	98	EC 457161	140	JS 20-38
57	AMS MB 5-18	99	Chocolate Bold	141	JS 20-30
58	AMS 56	100	Cat. 2755	142	AMS 62
59	AMS 59	101	IC 49685	143	EC 250619
60	AMS 38-24	102	Cat 2511	144	JS 20-75
61	EC 685243	103	Cat. 779	145	JS 20-60
62	RVS 2006-19	104	Cat. 710	146	JS 20-21
63	EC 457174	105	Cat. 891	147	JS 20-31
64	IC 437079	106	Cat. 340	148	JS 20-23
65	SL 983	107	Cat. 805	149	EC 396053
66	K 88-262A	108	F4P21	150	EC 250607
67	GP 393	109	MACS 303	151	EC 325099
68	GP 67	110	G 620	152	JS 20-29
69	SL(E) 1	111	G5P22 (PI)	153	JS 20-25
70	AGS 751	112	EC 457198	154	JS 20-51
71	DT 21	113	Cat. 135A	155	JS 20-54
72	Cat. 118	114	Cat. 902	156	JS 20-79
73	Cat. 50 (A)	115	G 11	157	JS 20-53
74	Cat. 209	116	Cat. 746	158	JS 20-52
75	Cat. 142	117	Cat. 938	159	AMS 77-3
76	Cat. 133	118	PP 6 (PI)	160	AMS 210-6
77	Cat. 886	119	PS 1024	161	SL 688 (C)
78	Cat. 305	120	Typical Bhatt (B)	162	PS 1347 (C)
79	Cat. 2503	121	PK 327	163	PS 1092 (C)
80	Cat. 780	122	PS 564	164	Bragg (C)
81	Cat. 148	123	PS 1225	165	PS 1042 (C)

3.3 Layout plan

The experiment was laid out in an augmented design (**Federer 1956, 1961 and Federer and Raghavarao, 1975**) and the material was sown on 7th August, 2014 in four

blocks containing 45 genotypes each including 5 checks which were repeated in each block. Each genotype was planted in a single row of 4 m length with a spacing of 45 cm between rows and 5-7 cm between plants. All the recommended package of agronomic practices were followed for raising a healthy crop.

3.4 Characters studied and observation procedure:

A total of 23 qualitative and quantitative characters that include morphological, derived and nutritional traits were taken up for the present investigation which included discrete as well as continuous measurements for data recording. Five representative plants from the single row of each genotype were randomly selected and all the necessary observations were recorded at appropriate stages of crop growth which include plant height, number of primary branches per plant, number of nodes per plant, number of pod bearing nodes per plant, number of pods per plant, number of seeds per pod, dry matter weight per plant and seed yield per plant. Observations on characters like germination, leaf colour, leaf shape, flower colour, pubescence colour, pod colour, days to 50% flowering and days to maturity were recorded on whole plot basis. The observations on seed coat colour, hilum colour, 100-seed weight, oil and protein contents were recorded on composite sample basis. Finally, derived characters like harvest index and seed yield efficiency were also recorded. The data on disease reaction for three important diseases i.e., Yellow mosaic virus, Rhizoctonia aerial blight and Bacterial pustules was also recorded on whole plot basis.

3.4.1 Qualitative characters: In the present investigation, eight qualitative characters were included in the present study as described below.

3.4.1.1 Germination

On the basis of germination the material was classified under three categories:

- a. Poor : Below 50% germination
- b. Fair : 50 to 75% germination
- c. Good : More than 75% germination

3.4.1.2 Leaf colour

On the basis of leaf colour, three categories were recorded among the genotypes:

- a. Dark green
- b. Green

3.4.1.3 Leaf shape

On the basis of leaf shape, three categories were recorded among the genotypes:

- a. Lanceolate
- b. Pointed ovate
- c. Round ovate

3.4.1.4 Flower colour

On the basis of flower colour, two classes were recorded among the genotypes:

- a. White
- b. Purple

3.4.1.5 Pod colour

On the basis of pod colour, the genotypes were categorized into three classes:

- a. Yellow
- b. Brown
- c. Black

3.4.1.6 Pubescence colour

Two classes were recorded among the genotypes on the basis of pubescence colour:

- a. Grey (White pubescence)
- b. Tawny (Brown pubescence)

3.4.1.7 Seed coat colour

Seed coat colour showed a wide range of variation in colour and the given genotypes in the present study were classified into three phenotypic classes viz. yellow, black and brown.

3.4.1.8 Hilum colour

Hilum colour also showed a range of variation in colour, and in the present study, the genotypes were classified into the following phenotypic classes on the basis of hilum colour viz. yellow, brown and black.

3.4.2 Quantitative characters: Eleven characters were included under this group for the present study which are described below:

3.4.2.1 Days to 50% flowering

Observation was noted on the date during which about 50% of the plants in the single row bloomed with each bearing a minimum of one opened flower, and the days to 50% flowering were further calculated from the date of sowing.

3.4.2.2 Days to maturity

The date on which almost all the leaves were shed from the plant and about 95% of the pods showed maturity was recorded and then starting from the date of sowing, days to maturity were calculated.

3.4.2.3 Plant height (cm)

Plant height was recorded at maturity. It was measured in centimeters (cm) from the ground level to the tip of the main stem. The mean height of 5 selected plants was recorded as the average plant height for the concerned genotype.

3.4.2.4 Number of primary branches per plant

At maturity, the total number of branches radiating from the main stem were counted from all the five representative plants, and the value for this parameter was recorded as the average of five plants.

3.4.2.5 Number of nodes per plant

From all 5 selected plants, the total number of nodes present on the main shoot were counted from base to the tip, and the average value of all the five plants was recorded as the final observation for this parameter.

3.4.2.6 Number of pod bearing nodes per plant

The total number of nodes bearing pod(s)/pod cluster(s) on the entire plant were counted. The average value thus obtained for 5 plants was further noted down as the estimate of this parameter.

3.4.2.7 Number of pods per plant

It was recorded at maturity, during which the total number of seed bearing pods were counted from all the five representative plants and the average of five plants was recorded to obtain a value for this parameter.

3.4.2.8 Number of seeds per pod

At maturity, about 20 pods were randomly selected from the composite sample and total number of seeds in 20 pods were calculated and the average value was worked out to get number of seeds per single pod.

3.4.2.9 Dry matter weight per plant (g)

When the plants were completely dried at maturity, all five representative plants from each single row were cutoff from the ground level, weighed and the average value was worked out to get the dry matter weight per plant in grams (g). To estimate this parameter the weight of leaves and roots were not considered.

3.4.2.10 100-seed weight (g)

From the composite sample, one hundred sun dried, sound and healthy, complete seeds were taken and weighed to record the 100-seed weight in grams (g).

3.4.2.11 Seed yield per plant (g)

At maturity, the five representative plants were harvested, threshed and their seed yield was recorded. Their average is worked out to obtain the seed yield per plant in grams (g).

3.4.3 Derived characters: Two derived characters viz. seed yield efficiency and harvest index were considered for the present study.

3.4.3.1 Seed yield efficiency

Seed yield efficiency was calculated as follows:

$$\text{Seed yield efficiency(\%)} = \frac{\text{Economical yield (seed weight)}}{\text{Total dry matter weight (excluding seed)}} \times 100$$

3.4.3.2 Harvest index (%)

The harvested plants were threshed separately and seed yield of representative plants was recorded separately and individually. Harvest index of the selected representative plants was estimated using the formula:

$$\text{Harvest index (\%)} = \frac{\text{Economical yield (seed weight)}}{\text{Total dry matter weight (including seed)}} \times 100$$

3.4.4 Nutritional quality traits: Two important nutritional quality traits included in the present study were protein and oil contents in the seed. The protocols for the estimation of these two traits are given below.

3.4.4.1 Estimation of crude fat or ether extractive (oil content %)

a. Principle

The solvent extraction was conducted using petroleum ether (boiling point of 40-60° C) as the extraction solvent. The oil was extracted from 2 g of finely powdered seed samples in Soxhlet apparatus. The samples were prepared by drying soybean seeds at $103 \pm 2^\circ \text{C}$. The water content in all the seed samples was reduced to $<10\%$ (m/m). For each test sample, the extraction should be carried out for 16 hours to ensure complete oil recovery from the powdered sample. The oil percentage in the seeds was then determined gravimetrically and expressed as a weight percent relative to initial weight of the raw soybean seeds.

b. Procedure

The seeds after drying were finely powdered and this powdered sample after moisture determination were transferred in to a thimble which is then plugged at the top with a wad of fat free cotton. The thimble was then dropped into the fat extraction tube of a Soxhlet apparatus. The bottom of the extraction tube was then attached to a Soxhlet flask. About 75 ml or more of petroleum ether was poured through the sample in the tube into the flask. The top of fat extraction tube was then attached to the condenser. Now, oil was extracted from the sample for 16 hours on a water bath. The water bath was regulated in such a way that the ether which volatilizes would condense, and again drop on the sample without any appreciable loss.

At the end of extraction period, the thimble was removed from apparatus and most of the ether was distilled off and allowed to collect in the Soxhlet tube. Ether was removed when the tube is nearly full. When the ether has reached a small volume, it is poured into a small, dry, (previously weighed) beaker through a small funnel containing a plug of cotton. The flask and filter are rinsed thoroughly, using several small portions of ether. The ether is then evaporated on a steam bath at low heat, under a current of air. The sample was further dried at 100°C for 1 hour, cooled and weighed. The difference in the weights gives the fat-soluble material present in the sample (**Ranganna, 1977**).

c. Calculation

$$\text{Percent crude fat} = \frac{\text{Weight of fat soluble material}}{\text{Weight of sample}} \times 100$$

3.4.4.2 Protein content (%)

The total protein content present in a given plant sample could be estimated indirectly through the quantification of total nitrogen content present in that particular sample. The same was followed to estimate the total protein content in the selected genotypes for the present investigation.

a. Principle

The protein content of the selected genotypes under study was estimated using the CHNS (**Jimenez and Ladho, 1993**) analyzer which quantifies a total of four elements present in the analyzed sample viz. Nitrogen (N), Carbon (C), Hydrogen (H) and Sulphur (S). The method is highly sensitive to low concentrations of N, yielding results accurate up to 0.3% (**Barbarino and Lourenço, 2009**) and is based on the modification of the classical Pregl-Dumas method. Samples of 8-10 mg weighed in tin capsules were fed into a vertical quartz combustion chamber maintained at 950° C, through which a constant flow of helium gas is circulated. When the sample is introduced into the chamber, the helium flow is temporarily enriched with a bout of pure oxygen. Flash combustion occurs, mediated by the oxidation of the tin container. Quantitative combustion is further achieved by passing the mixture of gases over tungstic oxide. The mixture of gases is then passed over copper to remove excess of oxygen and reduce oxides of nitrogen to nitrogen. It then passes through a gas chromatography (GC) column followed by a thermal conductivity (TC) detector. The gases eluted are N₂, CO₂, H₂O and SO₂. A series of separate infra-red and thermal conductivity cells were provided for the detection of individual compounds. The CHNS analyzer used in the present study was Thermo Electron Corporation-Flash EA 1112/MAS200 model. The standard used for calibration was BBOT [2, 5 Bis (5-tert-butyl-benzoxalol-2-yl) thiophene] (C₂₆H₂₆N₂O₂S), manufactured by Thermo Electron Corporation (Milan, Italy) which has 72.53% C, 6.51% N, 6.09% H, 7.44% S and 7.43% O.

b. Procedure

The estimates of total Nitrogen content available in the seed samples under study as obtained from above were later used to quantify the protein content by using a correction factor of 6.25. The seed samples of all selected genotypes were crushed into fine powder using pestle and mortar. Now the instrument was turned on and the temperature of the furnace was set at 950° C. Once the temperature was attained, the CNHS analyzer was then calibrated using the BBOT standard. After calibration, the powdered seed samples were weighed on a standard microbalance into the tin capsules (Thermo Scientific-Delft,

Netherlands, 8x5 mm size) which are then sealed air tight and fed into the combustion tube. The instrument was then given command to RUN the samples using a programmed software on the computer, which moves the samples into furnace. The amount of Nitrogen, Carbon, Hydrogen and Sulphur present in the given samples were displayed by the monitor after 12 minutes into combustion of sample in the furnace. The same procedure was followed and all the samples were fed one after another into the furnace to estimate the total nitrogen content which were recorded simultaneously. The readings were recorded and the protein content was estimated as given below.

c. Calculation

Protein content in the sample = Total nitrogen content in the sample x 6.25

3.4.5 Disease reaction

The 160 genotypes along with 5 checks employed in the present study were screened against three important diseases prevailing in the region viz. Yellow mosaic virus (YMV), Rhizoctonia aerial blight (RAB) and Bacterial pustules (BP) as per the standard protocol recommended for screening against these concerned diseases and relevant data for the disease reaction was recorded. The procedure followed for disease screening was described below.

For screening of genotypes, especially against Yellow mosaic virus (YMV) and Rhizoctonia aerial blight (RAB), one row of highly susceptible genotype (JS 335) was planted on both side of the block whereas one row of standard variety (PS 1347) was planted in middle of the block. Uniform method of disease rating (**46th AICRP on soybean report, 2016-17**) was followed to screen the genotypes against the three diseases. In this method, the point scale (0 to 9) was divided into 6 categories to classify the screened genotypes as per their resistance level. General interpretation of the scale is as follows:

0	–	Absolutely resistant
1	–	Highly resistant
3	–	Moderately resistant
5	–	Moderately susceptible
7	–	Susceptible
9	–	Highly susceptible

3.4.5.1 Rating scale for Yellow mosaic virus (viral disease):

Rating	Description
0	– No symptoms on any plants
1	– Yellow mottle or necrotic mottle in up to 1% plants
3	– Yellow mottle or necrotic mottle in up to 1.1 to 10% plants
5	– Necrotic mottle/mild mottle/mild symptoms on 10.1 to 25% plants and no reduction in plant growth; no yield loss.
7	– Yellow mottling symptoms not covering the whole leaf lamina on 25.1 to 50% plants; reduction in leaf and plant growth.
9	– Yellow mottle symptoms on more than 50% plants; severe reduction in leaf and plant growth as well as pod formation and death of plants.

3.4.5.2 Rating scale for Rhizoctonia aerial blight (RAB) and Bacterial pustule (BP):

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

3.5 Bio chemical profiling of genotypes

Among 165 genotypes of soybean evaluated in the present study, based on the estimates

of protein content, 11 genotypes were selected which exhibited considerable diversity in terms of their protein content. These 11 genotypes fall under three arbitrary categories with respect to their total seed protein content:

- a) EC 389148, Typical Bhatt (B), PS 1092, Cat 2503 and EC 39491 (>42% protein).
- b) RVS 2002-7, RVS 2002-6 and PS 1042 (38-40% protein)
- c) SL (E) 1, PS 1024 and PK 416 (<38% protein).

These genotypes were further analysed through SDS-PAGE (Sodium Dodecyl Sulfate Poly Acrylamide Gel Electrophoresis) to study their protein profiles.

3.5.1 Extraction of protein from seeds

Two grams of dried seeds of each genotype were finely crushed and about 10 ml of extraction buffer was added to the sample and thoroughly grinded to form a slurry. This was then transferred to eppendorf tubes. These tubes were then shaken for 5 minutes and kept in the refrigerator for 4-5 hours. These samples were further centrifuged at 4° C for 20 minutes at 10,000 rpm. The supernatant was later on transferred into fresh eppendorf tubes and stored at 4°C. These protein samples were used for further analysis and quantification of crude protein.

3.5.2 Seed protein quantification

Seed protein content was quantified using **Bradford (1976)** method. The procedure for quantification of seeds protein was explained in detail below:

3.5.2.1 Principle

The assay relies on the binding of the dye Coomassie Brilliant Blue G-250 to the protein molecule. The cationic form of the dye, which predominates in the acidic assay reagent solution, has a $\lambda_{\max}$ of 470 nm. The dye binds to protein as anionic form, which has a $\lambda_{\max}$ of 595 nm and this change in absorption maxima could be monitored through spectrophotometer. The dye basically reacts with arginine residues (but not to the free amino acid) and to a lesser extent with histidine, lysine, tyrosine, tryptophan and phenylalanine residues. Hence the absorbance of light by the dye-protein complex at 595 nm is proportional to the amount of protein bound (over a limited range), i.e., there is a linear relationship between absorbance and total protein concentration of the sample over a narrow range. This assay has a good colour stability for one hour and dye binding process virtually

completes within two minutes, and hence, it is reproducible and rapid. Carbohydrates like sucrose and cations like sodium and potassium ions offer little or no interference with results.

3.5.2.2 Requirements

Coomassie Brilliant Blue (CBB) G-250 dye, Ethanol, Ortho-phosphoric acid, Bovine serum albumin standard (BSA), double distilled water, funnel, filter paper, coloured bottles, test Tubes and test tube stand.

3.5.2.3 Reagents

a. Extraction Buffer

- | | | |
|---------------|---|--------|
| 1. D-Mannitol | – | 250 mM |
| 2. EGTA | – | 3 mM |
| 3. HEPES | – | 50 mM |
| 4. DTT | – | 1 mM |

b. BSA standard solution (1 mg/ml concentration)

Working solution - 0.1 mg/ml.

c. Bradford dye

- | | | |
|-----------------------------------|---|-------|
| 1. Coomassie brilliant blue G-250 | – | 10 mg |
| 2. Absolute ethanol | – | 5 ml |
| 3. Ortho-phosphoric acid (85%) | – | 10 ml |

The dye was dissolved in absolute ethanol, Ortho-phosphoric acid was added and the solution was stirred constantly for half an hour. The final volume was made up to 100 ml by adding distilled water. The dye solution was filtered in dark and stored in amber colored bottle.

3.5.2.4 Procedure

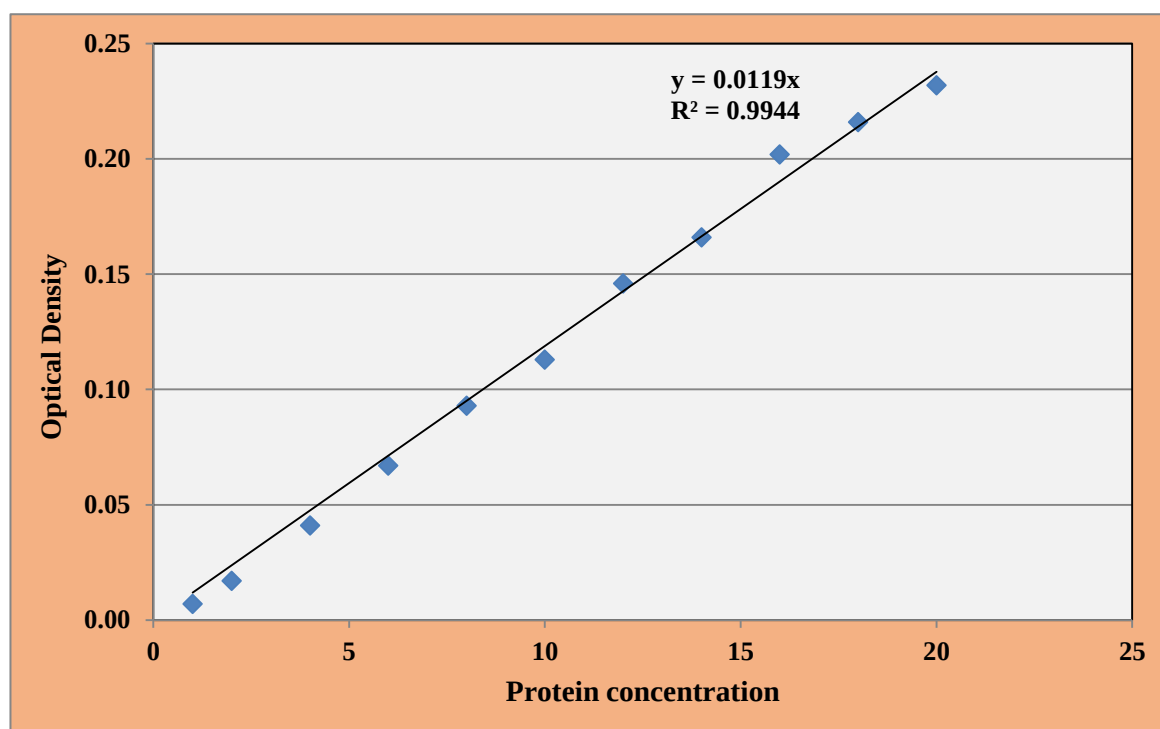
- 1) A dilution series of BSA working solution was prepared by adding 5, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100 μ l to 12 test tubes.
- 2) Blank was prepared by adding 300 μ l of double distilled water to test tube.
- 3) Samples and blank were prepared according to **Table 3.5.2.4a**.
- 4) All the tubes were incubated at room temperature in dark for 30 minutes.

- 5) Standard graph was plotted between BSA concentration (X-axis) and absorbance (Y-axis) as shown in the **Figure 3.5.2.5a**.

Table 3.5.2.4a: Blank and sample preparation to obtain the BSA standard curve using spectrophotometer

BSA working Solution (µl)	Double distilled water (µl)	Total volume (µl)	Dye (ml)	Optical Density (595 nm)	Concentration (µg)
5	295	300	3	0.007	1
10	290	300	3	0.017	2
20	280	300	3	0.041	4
30	270	300	3	0.067	6
40	260	300	3	0.093	8
50	250	300	3	0.113	10
60	240	300	3	0.146	12
70	230	300	3	0.166	14
80	220	300	3	0.202	16
90	210	300	3	0.216	18
100	200	300	3	0.232	20
Blank	300	300	3	-	-

Figure 3.5.2.5a: BSA standard graph obtained by plotting protein concentration against optical density



3.5.2.5 Preparation of standard curve

A standard curve was plotted and protein concentration was estimated by extrapolation from standard curve. The standard curve was obtained as per the procedure given below:

- 1) Different concentrations of BSA working solution in duplicate were taken to plot standard curve.
- 2) The following mixture was incubated at 37 °C for 30 minutes and optical density was measured at a wavelength of 595 nm.
- 3) The concentration versus absorbance curve was plotted by taking 5, 10, 20, 30, 40, 50, 60, 70, 80, 90 and 100 µl of BSA working solution.

3.5.2.6 Analysis of sample

The amount of protein present in an unknown sample can be calculated with the help of the standard graph by using the following formula:

$$y = mx + c$$

Where, 'x' and 'y' are the coordinates of the points and lie on the straight line graph. 'm' is the slope of the straight line graph,

$$m = (y_2 - y_1)/(x_2 - x_1)$$

and 'c' is the y intercept of the straight line graph.

3.5.3 Protein characterization using Sodium dodecyl sulfate (SDS) polyacrylamide gel electrophoresis (PAGE)

3.5.3.1 Principle

SDS-PAGE is a method by which protein molecules are separated on the basis of molecular weight. SDS is an anionic detergent and the amount of SDS that binds the polypeptide chains is directly proportional to the size of molecules. Most of the complex structures are destroyed by SDS and are attracted towards anode in an electric field. Larger molecules migrate slower as compared to smaller and hence get separated. In a gel of uniform density the relative migratory distance of a protein (Rf) is negatively proportional to the log of its molecular weight. If proteins of known molecular weight run simultaneously with the unknown, the relationship between Rf and molecular weight can be plotted and the molecular weight of unknown protein can be determined.

Polyacrylamide gel is prepared by the free radical induced polymerization of acrylamide and N-N methylene Bis acrylamide, which is a cross linking agent.

3.5.3.2 Requirements

Gel electrophoresis assembly (Genei.), power supply for electrophoresis (Genei.), eppendorf tubes, 30% Bis acrylamide and acrylamide solution, 10% SDS, stacking and separating gel buffer, 10% Ammonium persulfate (APS), TEMED, double distilled water, PAGE rigs like glass plates, spacers, comb and clamps, sample buffer, molecular marker, staining solution, de-staining solution, magnetic shaker, micropipette, staining container and glass tray etc.

3.5.3.3 Reagent preparation

a. 30% Acrylamide and Bis-acrylamide solution

1. Acryl amide
2. N,N-methylene Bis acrylamide
3. Double distilled water

29.2 gm of acrylamide and 0.8 gm of N, N- methylene Bis acrylamide were dissolved in 100 ml of double distilled water and solution was stirred on a magnetic stirrer to completely dissolve the solutes. The solution was then filtered through Whatman No. 4 filter paper in a dark bottle and stored at 4⁰ C.

b. 10% Sodium dodecyl sulfate (SDS)

1. SDS
2. Double distilled water

One gram of SDS was dissolved in 10 ml of double distilled water and warmed slightly to dissolve the solute completely.

c. Seperating gel buffer 1.5 M (pH 8.8)

- | | | |
|--------------------|---|---------|
| 1. Tris base | – | 18.15 g |
| 2. Distilled water | – | 50 ml |

Concentrated HCl was added drop wise until pH reached 8.8. Final volume was made up to 100 ml and filtered through Whatman No. 1 and stored at 4⁰ C.

d. Stacking gel buffer 0.5 M (pH 6.8)

1. Tris base – 6.05 g
2. Distilled water – 50 ml

Concentrated HCl was added until pH reached 7.2 and then 1 N HCl was added drop wise to attain a final pH of 6.8. Final volume was made up to 100 ml and stored at 4⁰ C.

e. Ammonium per sulphate (APS) (0.1 gm/ml concentration)

Ammonium per sulfate 100 mg was mixed in 1 ml of double distilled water and was dissolved completely.

f. Sample buffer preparation

1. Tris HCL (pH of 6.8) – 62 mM
2. SDS – 2%
3. Glycerol – 10%
4. BME – 5%
5. EDTA – 0.1%
6. BPB – 0.1%

g. Electrophoresis buffer (1X)

1. Tris-base – 6.06 gm
2. Glycine – 28.84 gm
3. SDS – 2 gm

The above compounds were dissolved in double distilled water and the final volume was made up to 200 ml by adding double distilled water.

h. Staining solution (100 ml)

1. Glacial acetic acid – 10 ml
2. Methanol – 50 ml
3. CBB R 250 – 0.1 mg

These compounds were dissolved and final volume was made up to 100 ml by adding double distilled water. Solution was filtered through Whatman No. 1 and stored in dark bottle at room temperature.

i. Destaining solution (500 ml)

- | | | |
|------------------------|---|-------|
| 1. Glacial acetic acid | – | 50 ml |
| 2. Methanol | – | 35 ml |

Dissolved and final volume was made up to 500 ml by double distilled water.

3.5.3.4 Procedure:

a. Gel cassette assembly

- 1) Glass plates, combs and other related materials were cleaned, washed and dried.
- 2) The short plate was placed over spacer plate. Based on the need, two gels could be electrophoresed simultaneously, whereas in case of single gel electrophoresis, a dummy plate could be used for balancing. The casting frame was clamped and checked for any non-uniform surface and level at bottom.
- 3) Casting frame was then put into the casting stand.

b. Preparation of separating gel (50 ml)

10% separating gel was used. For making 50 ml of separating gel, the following ingredients were mixed together.

- | | | |
|--------------------------------------|---|---------|
| 1. 30% Acrylamide stock | – | 16.2 ml |
| 2. Separating gel buffer (pH of 8.8) | – | 12.4 ml |
| 3. Ultra-pure water | – | 20.6 ml |
| 4. 10% SDS | – | 0.25 ml |
| 5. 10% APS | – | 0.5 ml |
| 6. TEMED | – | 25 µl |

- 1) When the gel was ready to be poured, 10% APS and TEMED were quickly added to the above solution. The solution was then thoroughly mixed and the gel was loaded into the casting frame about $\frac{3}{4}$ inch below short plate. Little amount of water was added onto the top of separating gel to avoid zig-zag surface and was removed after 15 minutes.
- 2) A time lapse of 10 minutes was further provided to allow the polymerization of separating gel.

c. Preparation of stacking gel (8 ml)

5% stacking gel was used.

- | | | |
|---------------------------------|---|---------|
| 1. 30% Acrylamide | – | 1.3 ml |
| 2. Stacking gel buffer (pH 6.8) | – | 2.0 ml |
| 3. Ultra-pure water | – | 4.53 ml |
| 4. 10% SDS | – | 80 µl |
| 5. 10% APS | – | 80 µl |
| 6. TEMED | – | 10 µl |

- 1) When the gel is ready, quickly 10% APS and TEMED were added to the above solution and the contents were thoroughly mixed, and the gel was loaded into the casting frame about $\frac{3}{4}$ inch below the short plate.
- 2) As soon as the separating gel (10%) was polymerized, the stacking gel (5%) was poured into glass plates and combs were inserted and left undisturbed.
- 3) Further, an interval of 10 minutes was provided to allow the stacking gel get polymerized.

d. Sample preparation for electrophoresis

- 1) 40 µg of each sample from stock was mixed with equal volume of dye
- 2) The samples were then denatured in boiling water for 5 minutes.
- 3) Further, the samples are centrifuged at 10000 rpm for 2 minutes.

e. Electrophoresis

- 1) The gel is removed from the casting stand and placed in an electrode assembly in such a way that the short plate is facing towards inside.
- 2) The electrode assembly was slid into the clamping frame and the clamps were locked.
- 3) Then, 1X electrophoresis buffer was filled into the space of the casting frame between the gel cassettes. Enough buffer was added so that the wells in the gel were submerged completely within the buffer.
- 4) 20 µg sample was loaded in each well and 4 µg marker with 16 µl dye in one well.

- 5) The electrophoresis tank was connected to power supply and run at a voltage of 60 V till the samples left the wells after which, the voltage was increased to 100 V and then maintained constant till the dye front reached the bottom of gel.
- 6) The power supply was turned off after completion of electrophoresis i.e., when loading dye starts to come out of gel and diffuse into electrophoresis buffer.

f. Removing the gel

- 1) The gel cassette was removed from the buffer chamber.
- 2) All the clamps were loosened.
- 3) Spatula was put in between the 2 plates and slightly pressed with lower plate serving as fulcrum.
- 4) Starting from one corner, gel was removed and placed in staining solution.

g. Staining and destaining of gel

Gel was kept in the staining solution for overnight. On the next day, it was taken out from staining solution and kept in destaining solution. Destaining step was repeated 2-3 times to obtain a clear background of gel which took nearly 12-14 hours. The gel was further documented after proper destaining and saved for further analysis.

h. Analysis of gel

The gel was then documented using the Gel documentation unit. Protein bands of different intensities were observed through visual observation the gel obtained after destaining. The differences in polypeptide expression among the genotypes as visualized through the varying intensities of polypeptide bands were recorded to differentiate between genotypes.

3.6 Statistical Analysis

The following statistical procedures were followed for the analysis of data obtained during the present investigation:

1. Analysis of Variance
2. Mean and range of variation
3. Estimation of Genetic Divergence
4. Estimation of Variability parameters

5. Estimation of Correlation coefficient
6. Path-coefficient analysis

3.6.1 Analysis of Variance

Augmented block design-II (**Federer, 1956**), is the choice of design opted for the evaluation of genotypes during this present study. It is the choicest method when the resources available are limited and a large number of genotypes are to be evaluated simultaneously. Augmented design facilitates the accommodation of each genotype as a single treatment without replication into a single block and the overall concept is that all the genotypes to be evaluated are distributed into a set of blocks (b) such that each block has equal number of treatments (genotypes), along with a set of checks (c) which are repeated in each block to facilitate the statistical analysis. So in this design, only checks are replicated in each block but not the treatments. The entire experimental material under evaluation is randomized in such a manner that all the checks (c) and a part of test genotypes appear only once in each block. ANOVA for augmented design-II is presented in **Table 3.6.1.1** below.

Table 3.6.1.1: Structure of ANOVA (Analysis of variance) for Augmented Design-II

Source of variation	d.f.	SS	MSS	F
Blocks	b - 1	bSS	bMS	bMS/EMS
Entries	e - 1	eSS	eMS	eMS/EMS
Checks	c - 1	cSS	cMS	cMS/EMS
Varieties	v - 1	vSS	vMS	vMS/EMS
Checks vs genotypes	1	cvSS	cvMS	cvMS/EMS
Error	(c-1)(b-1)	ESS	EMS	
Total	N-1	TSS		

Where,

b = Number of blocks c = Number of checks v = Number of test genotypes

e = c + v N = bc + v

N = Total number of plots into which the experimental material is sown.

The analysis of variance for the augmented design-II as shown above was carried out as per the method suggested by **Federer (1956, 1961)** and as described by **Federer and Ragavarao (1975) and Petersen (1985)**.

Partitioning of ANOVA into different components could be done from the equations given below. Since only the checks (c) but not the test genotypes (v) are replicated within each block, adjustment of means of 'v' should be done in this design before partitioning the ANOVA into its components, with the help of the following effects.

$$\text{Block effects (b}_j\text{)} = 1/c (T b_j - \bar{c} - T v b_j) \quad (j = 1 \text{ to } b)$$

$$\text{Counter check: } \sum_{j=1}^b b_j \approx 0$$

$$\text{Mean effect (m)} = 1/e (GT - (b-1) \bar{c} - \sum_{j=1}^b n_j b_j)$$

Where, n_j is the number of 'v' occurring in j^{th} block

$$\text{Check effects (c}_i\text{)} = c_i - m \quad (i = 1 \text{ to } c)$$

$$\text{GCF (General correction factor)} = (GT)^2 / N \quad (GT = \text{grand total})$$

$$bSS = \sum_{j=1}^b T b_j^2 / (c + n_j) - \text{GCF}$$

$$bMS = bSS / (b-1)$$

$$TSS = \sum_{i=1}^c \sum_{j=1}^b c_{ij}^2 + \sum_{i=1}^v v_i - \text{GCF}$$

$$cCF (\text{Check correction factor}) = T c^2 / bc$$

$$cSS = \sum_{i=1}^c T c_i / b - cCF$$

$$cMS = cSS / (c-1)$$

$$eSS = (m \times GT) + \sum_{j=1}^b b_j (T b_j) + \sum_{i=1}^c T c_i (C_i) + \sum_{i=1}^v v_i (v_i) - \left[\sum_{j=1}^b T b_j^2 / (c + n_j) \right]$$

$$eMS = eSS / (e-1)$$

$$vCF = \sum_{i=1}^v v_i^2 - vCF$$

$$vMS = vSS / (v - 1)$$

$$cvSS = cvMS = eSS - cSS - vSS$$

$$ESS = TSS - eSS - bSS$$

$$EMS = ESS / (c - 1) (b - 1)$$

If the block effect is found significant, then the following four standard errors are helpful in drawing conclusion.

$$SEd_1 \text{ (between any two check means)} = \frac{\sqrt{2EMS}}{b}$$

$$SEd_2 \text{ (between any two means of test genotypes)} = \sqrt{2EMS}$$

$$SEd_3 \text{ (between any two entries of the same block)} = \sqrt{2EMS (1 + 1/c)}$$

$$SEd_4 \text{ (between means of a check and a test genotype)} = \sqrt{EMS (1 + 1/b + 1/c + 1/bc)}$$

C.D is then calculated using these SEd's x 't' at 5% or 1% levels.

Adjusted means of test genotypes (v_i') and genotypic effects (v_i'') were computed by using the following formula

$$\text{Adjusted mean } (v_i') = v_i - b_j$$

Where, b_j is the effect of the block under which v_i falls into.

$$\text{Genotypic effects } (v_i'') = v_i' - m$$

3.6.2 Mean and range of variation

The mean and range of variation were estimated for all the genotypes and for each of the character included in the present study.

3.6.2.1 Mean

Mean of the individual genotypes were calculated as arithmetic average of values for each character.

$$\bar{X} = \sum_i^n \frac{X_i}{n}$$

Where,

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

X_i = sum of all the observations recorded for i^{th} character, and

n = number of observations

3.6.2.2 Range

Range denotes the difference between the maximum and minimum values for a parameter. Here, it was considered as the largest and smallest value of the character among the experimental material.

3.6.3 Estimation of Genetic Divergence

The genetic divergence was estimated using the Hierarchical cluster analysis which was performed on the basis of Euclidean distance between the genotypes. Euclidean distance was determined by the following method:

3.6.3.1 Euclidean distance

The Euclidean distance between the i^{th} and k^{th} genotypes could be calculated from the equation:

$$D_{ik} = \left[\sum_{j=1}^n (A_{ij} - A_{kj})^2 \right]^{1/2}$$

Where,

D_{ik} = Euclidean distance between i^{th} and k^{th} genotype

A_{ij} = performance of i^{th} genotype for j^{th} character

A_{kj} = performance of k^{th} genotype for j^{th} character

m = number of genotypes (I or $k = 1, 2, \dots, m$)

n = number of characters ($j = 1, 2, \dots, n$)

When the similarity matrix is computed from distance function, the hierarchical clustering method begins by finding the link between the two closest genotypes and the procedure accordingly is given in the following steps (**Adenberg, 1973**).

1. The lower triangular similarity matrix (S) was computed where, S_{ij} be the similarity between genotype i and j , as defined by Euclidean distance. The compute schedule of similarities for all $n(n-1)/2$ possible pair-wise combinations of entities was arrayed in lower triangular similarity matrix (n = No. of entries/ genotypes)

2. Then the collections of S_{ij} were arranged into ascending sequence and recorded as (s_{ij}, i, j) . Then start up with “n” clusters, each consisting of exactly one genotype.
3. For the first merger, the pair of genotype corresponding to the first similarity value in the sorted list, that is, the smallest distance in the entire similarity matrix. Then the chosen clusters were labelled as p and q and their associated similarity (Euclidean distance) by s_{pq} , $p > q$.
4. The no. of clusters was reduced down by 1 through merger of cluster p and q. The product of merger was labelled and the similarity matrix entities were updated, in order to reflect the revised similarities between cluster t and all other existing clusters. The row and column of S pertaining the cluster p were then deleted.
5. At each succeeding stage for the next link on merger was chosen in such a way that pair of genotypes corresponding to the next largest similarity value (Euclidean distance) provided the two genotypes are not already in the same cluster (connected to each other through a chain of links). If the genotypes were already in the same cluster, bypass the link and move on to the next triple.
6. Step 3 and 4 were performed a total of n-1 times. At each stage the identity of the clusters which were merged and the Euclidean distance between them was recorded in order to have a complete record of the results.
7. Maximum link (i.e. Euclidean distance) was fixed between groups arbitrarily among the minimum links between pair-wise combinations, to discriminate the given genotypes into different clusters.

3.6.4 Estimation of Variability parameters

The different parameters estimated include the following:

3.6.4.1 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)**.

$$\text{Genotypic Variance } (\sigma_g^2) = \text{vMSS} - \text{EMSS}$$

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

3.6.4.2 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

3.6.4.3 Heritability (Board 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.

3.6.4.4 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)

$$\text{GAM} = \frac{\text{GA}}{\overline{X}} \times 100$$

Where,

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

3.6.5 Estimation of correlation coefficient

The estimation of correlation coefficient is based on the variance and covariance of x and y variables (characters). Correlation is ranged between +1 to -1 and the intensity of relationship is measured by correlation coefficients (r). Correlations between all the characters under study were estimated as per the method suggested by **Searle (1961)** using the following formula:

Simple correlation between characters X and Y,

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

Where,

r_{xy} = Correlation coefficient between characters X and Y

Cov. (XY) denotes covariance between characters X and Y, respectively.

Var. X and Var. Y denote variances for characters X and Y, respectively.

Variance and covariance were calculated by the following formula

$$\text{Var. (X)} = \left[\sum x^2 - \frac{(\sum x)^2}{n} \right]$$

$$\text{Var. (Y)} = \frac{1}{n} \left[\sum y^2 - \frac{(\sum y)^2}{n} \right]$$

$$\text{Cov.}(XY) = \frac{1}{n} \left[\sum xy - \frac{(\sum x)(\sum y)}{n} \right]$$

To test the significance of correlation coefficient the calculated t-value was compared with tabulated value on n-2 degrees of freedom (**Snedecor and Cochran, 1967**).

$$t_c = \frac{r\sqrt{n-2}}{\sqrt{1-r^2}} ; \text{ (n-2) d.f.}$$

Where, r = correlation coefficient and

n = number of observations.

3.6.6 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.

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

Where,

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

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

p_{iy} = 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,

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

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



RESULTS AND DISCUSSION

The present study was taken up in an attempt to assess the genetic diversity and variability, inter-character correlation and their direct and indirect effects among 165 genotypes (including 5 checks) of soybean that are collected and maintained at G.B.P.U.A.T, Pantnagar and the experimental results thus obtained in this context were reported under the following heads:

1. Characterization of genotypes based on qualitative characters
2. Analysis of variance
3. Mean performance and range of variation for quantitative characters
4. Genetic divergence
5. Genetic variability parameters
6. Inter-character association (correlation) analysis
7. Path coefficient analysis
8. Screening for disease reaction
9. Bio-chemical profiling of selected genotypes

4.1 Characterization of genotypes based on qualitative characters

Characterization of a genotype/variety is essential for its identification and avoiding duplication. Qualitative characters show stable inheritance over generations and hence are reliable for characterization of genotypes (**Raut 2003**) as they are less influenced by environmental fluctuations. The 165 genotypes under study were classified into discrete groups under 8 major categories representing 8 qualitative characters viz. germination, leaf colour, leaf shape, pubescence colour, flower colour, pod colour, seed coat colour and hilum colour. On the basis of results obtained, it could be outlined that morphological characters play an important role and they do contribute towards genotype divergence in soybean. Similar studies were taken up by **Ramteke and Muralidharan (2012)**, who characterized soybean accessions on the basis of qualitative characters. **Yadav and Sharma (2001)** reported large variation for hilum colour in soybean.

Characterization of genotypes on the basis of 8 qualitative characters was given in **Table 4.1.1**. Further, they were classified into distinct groups under each character as shown

Table 4.1.1: Characterization of 165 genotypes under study in soybean based on eight qualitative characters

S.No.	Genotypes	Leaf colour	Leaf shape	Pod colour	Seed coat colour	Hilum colour	Flower colour	Pubescence colour	Germination
1	AGS 129	Green	Lanceolate	Yellow	Yellow	Yellow	Purple	Grey	Good
2	EC 389148	Green	Pointed ovate	Brown	Yellow	Brown	Purple	Tawny	Good
3	Jupiter	Green	Pointed ovate	Brown	Yellow	Black	Purple	Tawny	Good
4	T-49	Green	Pointed ovate	Brown	Yellow	Black	Purple	Tawny	Good
5	P RAB 1	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good
6	AMS 155 (A)	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good
7	TGX 855-39E	Green	Pointed ovate	Brown	Yellow	Brown	Purple	Tawny	Good
8	AMS 77-3-6	Green	Pointed ovate	Brown	Yellow	Brown	Purple	Tawny	Good
9	AMS 2005-19	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good
10	EC 16738	Green	Pointed ovate	Yellow	Yellow	Brown	Purple	Grey	Good
11	EC 37937	Green	Pointed ovate	Brown	Yellow	Yellow	Purple	Tawny	Good
12	EC 39362	Green	Pointed ovate	Brown	Yellow	Yellow	Purple	Tawny	Good
13	EC 39491	Green	Pointed ovate	Brown	Yellow	Brown	Purple	Tawny	Good
14	EC 65772	Dark Green	Round ovate	Brown	Yellow	Yellow	Purple	Tawny	Good
15	RVS 2006-27	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good
16	EC 95291	Green	Pointed ovate	Brown	Yellow	Black	Purple	Tawny	Fair
17	EC 100027	Green	Pointed ovate	Brown	Yellow	Yellow	Purple	Tawny	Good
18	IC 13051	Green	Pointed ovate	Brown	Yellow	Brown	Purple	Tawny	Good
19	EC 14626	Dark Green	Pointed ovate	Brown	Yellow	Yellow	Purple	Tawny	Good
20	JS 82	Green	Pointed ovate	Brown	Yellow	Black	Purple	Tawny	Good
21	PI 283327	Green	Pointed ovate	Brown	Yellow	Black	Purple	Tawny	Good
22	PK 765	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good
23	MACS 1394	Green	Pointed ovate	Brown	Yellow	Brown	Purple	Tawny	Good
24	GP 305	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good
25	RPSP 935-E	Green	Pointed ovate	Yellow	Yellow	Brown	White	Grey	Good
26	GP 465	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good
27	Himso 175	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good
28	GP 448	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good
29	WT 150	Green	Pointed ovate	Brown	Yellow	Black	White	Tawny	Good
30	MAUS 76	Green	Pointed ovate	Brown	Yellow	Black	White	Tawny	Good
31	MAUS 102	Green	Pointed ovate	Brown	Yellow	Black	Purple	Tawny	Good
32	MAUS 489	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good
33	MAUS 38	Green	Pointed ovate	Brown	Yellow	Black	Purple	Tawny	Good

Contd....

Table 4.1.1 Contd....

S.No.	Genotypes	Leaf colour	Leaf shape	Pod colour	Seed coat colour	Hilum colour	Flower colour	Pubescence colour	Germination
34	MAUS 85	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good
35	MAUS 149	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good
36	AMS 2005-24	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good
37	MAUS 164	Green	Pointed ovate	Brown	Yellow	Brown	Purple	Tawny	Good
38	EC 963805	Green	Pointed ovate	Brown	Yellow	Yellow	Purple	Tawny	Good
39	EC 281462	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good
40	EC 116343	Green	Pointed ovate	Brown	Yellow	Black	Purple	Tawny	Good
41	EC 172607	Green	Pointed ovate	Brown	Yellow	Black	Purple	Tawny	Good
42	EC 33940	Green	Pointed ovate	Brown	Yellow	Brown	Purple	Tawny	Good
43	EC 2581	Green	Pointed ovate	Brown	Yellow	Black	Purple	Tawny	Good
44	EC 118443	Dark Green	Pointed ovate	Brown	Yellow	Black	Purple	Tawny	Good
45	RKS 30	Green	Pointed ovate	Yellow	Yellow	Brown	Purple	Grey	Good
46	RKS 27	Green	Pointed ovate	Brown	Yellow	Brown	Purple	Tawny	Good
47	AMS 243-7-3	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good
48	AMS 42	Green	Pointed ovate	Brown	Yellow	Brown	Purple	Tawny	Good
49	AMS 50B	Green	Pointed ovate	Brown	Yellow	Black	Purple	Tawny	Good
50	AMS 100-16-4-1-3	Green	Pointed ovate	Brown	Yellow	Brown	Purple	Tawny	Good
51	AMS -25-5-1	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Poor
52	AMS 100-25-5	Green	Lanceolate	Yellow	Yellow	Brown	Purple	Grey	Good
53	AMS 100	Green	Lanceolate	Yellow	Yellow	Brown	Purple	Grey	Good
54	AMS 115	Green	Pointed ovate	Brown	Yellow	Black	Purple	Tawny	Good
55	AMS 2005-13	Dark Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Fair
56	AMS MB 5-19	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good
57	AMS MB 5-18	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good
58	AMS 56	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good
59	AMS 59	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good
60	AMS 38-24	Green	Pointed ovate	Yellow	Brown	Brown	White	Grey	Good
61	EC 685243	Dark Green	Pointed ovate	Yellow	Yellow	Brown	Purple	Grey	Good
62	RVS 2006-19	Green	Pointed ovate	Brown	Yellow	Black	White	Tawny	Good
63	EC 457174	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good
64	IC 437079	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good
65	SL 983	Green	Pointed ovate	Brown	Yellow	Black	White	Tawny	Good
66	K 88-262A	Green	Pointed ovate	Brown	Yellow	Brown	Purple	Tawny	Good

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Table 4.1.1 Contd....

S.No.	Genotypes	Leaf colour	Leaf shape	Pod colour	Seed coat colour	Hilum colour	Flower colour	Pubescence colour	Germination
67	GP 393	Green	Pointed ovate	Yellow	Yellow	Black	White	Grey	Good
68	GP 67	Green	Pointed ovate	Yellow	Yellow	Black	White	Grey	Good
69	SL(E) 1	Green	Pointed ovate	Brown	Yellow	Black	White	Tawny	Good
70	AGS 751	Green	Pointed ovate	Brown	Yellow	Brown	Purple	Tawny	Good
71	DT 21	Green	Pointed ovate	Yellow	Yellow	Brown	White	Grey	Good
72	Cat. 118	Green	Pointed ovate	Brown	Yellow	Black	Purple	Tawny	Good
73	Cat. 50 (A)	Green	Pointed ovate	Brown	Yellow	Yellow	Purple	Tawny	Good
74	Cat. 209	Green	Pointed ovate	Yellow	Yellow	Yellow	White	Grey	Good
75	Cat. 142	Green	Pointed ovate	Brown	Yellow	Black	Purple	Tawny	Good
76	Cat. 133	Green	Pointed ovate	Brown	Yellow	Yellow	Purple	Tawny	Good
77	Cat. 886	Green	Pointed ovate	Brown	Yellow	Brown	Purple	Tawny	Good
78	Cat. 305	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good
79	Cat. 2503	Green	Pointed ovate	Brown	Yellow	Brown	Purple	Tawny	Fair
80	Cat. 780	Green	Pointed ovate	Yellow	Yellow	Black	White	Grey	Good
81	Cat. 148	Green	Pointed ovate	Yellow	Yellow	Yellow	Purple	Grey	Good
82	Cat. 3284	Green	Pointed ovate	Brown	Yellow	Black	Purple	Tawny	Good
83	Cat. 2430	Green	Pointed ovate	Brown	Yellow	Black	Purple	Tawny	Poor
84	Cat.103	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good
85	Cat. 537	Green	Pointed ovate	Brown	Yellow	Yellow	Purple	Tawny	Good
86	Cat. 366	Green	Pointed ovate	Brown	Yellow	Yellow	Purple	Tawny	Good
87	Cat. 3327	Green	Pointed ovate	Brown	Yellow	Yellow	Purple	Tawny	Good
88	Cat. 783	Green	Pointed ovate	Brown	Yellow	Brown	Purple	Tawny	Poor
89	Cat. 181	Green	Pointed ovate	Yellow	Yellow	Brown	Purple	Grey	Good
90	Cat. 307	Green	Pointed ovate	Brown	Yellow	Brown	Purple	Tawny	Good
91	Cat. 195	Green	Pointed ovate	Brown	Brown	Brown	White	Tawny	Good
92	Cat. 2388	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good
93	EC 2581	Green	Pointed ovate	Brown	Yellow	Black	Purple	Tawny	Good
94	RVS 2002-6	Green	Lanceolate	Brown	Yellow	Black	White	Tawny	Good
95	RVS 2002-7	Green	Pointed ovate	Brown	Yellow	Black	White	Tawny	Good
96	MACS 993	Dark Green	Pointed ovate	Brown	Yellow	Brown	Purple	Tawny	Good
97	RVS 2006-1	Green	Pointed ovate	Brown	Yellow	Black	White	Tawny	Good
98	EC 457161	Green	Pointed ovate	Brown	Yellow	Black	White	Tawny	Good
99	Chocolate Bold	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good

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Table 4.1.1 Contd....

S.No.	Genotypes	Leaf colour	Leaf shape	Pod colour	Seed coat colour	Hilum colour	Flower colour	Pubescence colour	Germination
100	Cat. 2755	Green	Pointed ovate	Brown	Brown	Brown	White	Tawny	Good
101	IC 49685	Green	Pointed ovate	Brown	Yellow	Yellow	Purple	Tawny	Good
102	Cat 2511	Green	Pointed ovate	Brown	Yellow	Yellow	Purple	Tawny	Good
103	Cat. 779	Green	Pointed ovate	Brown	Yellow	Yellow	Purple	Tawny	Good
104	Cat. 710	Green	Pointed ovate	Brown	Yellow	Black	Purple	Tawny	Good
105	Cat. 891	Green	Pointed ovate	Brown	Yellow	Yellow	White	Tawny	Poor
106	Cat. 340	Green	Pointed ovate	Brown	Yellow	Brown	Purple	Tawny	Good
107	Cat. 805	Green	Pointed ovate	Brown	Yellow	Black	Purple	Tawny	Good
108	F4P21	Green	Pointed ovate	Brown	Yellow	Black	White	Tawny	Good
109	MACS 303	Dark Green	Pointed ovate	Brown	Yellow	Black	White	Tawny	Good
110	G 620	Green	Pointed ovate	Brown	Yellow	Brown	Purple	Tawny	Good
111	G5P22 (PI)	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good
112	EC 457198	Dark Green	Pointed ovate	Brown	Yellow	Yellow	White	Tawny	Fair
113	Cat. 135A	Green	Pointed ovate	Brown	Yellow	Yellow	Purple	Tawny	Good
114	Cat. 902	Green	Pointed ovate	Brown	Yellow	Black	Purple	Tawny	Good
115	G 11	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good
116	Cat. 746	Green	Pointed ovate	Brown	Yellow	Brown	Purple	Tawny	Good
117	Cat. 938	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good
118	PP 6 (PI)	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good
119	PS 1024	Dark Green	Lanceolate	Brown	Yellow	Brown	White	Tawny	Good
120	Typical Bhatt (B)	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good
121	PK 327	Green	Pointed ovate	Yellow	Yellow	Brown	Purple	Grey	Good
122	PS 564	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good
123	PS 1225	Green	Pointed ovate	Yellow	Yellow	Yellow	White	Grey	Good
124	PS 1551	Green	Pointed ovate	Brown	Yellow	Black	Purple	Tawny	Good
125	PS 1480	Green	Pointed ovate	Yellow	Yellow	Black	White	Grey	Good
126	Shilajeet	Dark Green	Pointed ovate	Brown	Yellow	Yellow	Purple	Tawny	Good
127	Ankur	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good
128	PS 1029	Green	Pointed ovate	Brown	Yellow	Black	White	Tawny	Good
129	Alankar	Green	Pointed ovate	Brown	Yellow	Yellow	White	Tawny	Good
130	PK 416	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good
131	PK 262	Green	Pointed ovate	Yellow	Yellow	Brown	White	Grey	Good
132	PS 19	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good

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Table 4.1.1 Concluded

S.No.	Genotypes	Leaf colour	Leaf shape	Pod colour	Seed coat colour	Hilum colour	Flower colour	Pubescence colour	Germination
133	Kalitur	Green	Pointed ovate	Black	Black	Black	Purple	Tawny	Good
134	EC 250608	Green	Pointed ovate	Brown	Yellow	Brown	Purple	Tawny	Good
135	JS 20-41	Green	Pointed ovate	Brown	Yellow	Black	White	Tawny	Good
136	EC 251358	Green	Pointed ovate	Brown	Yellow	Black	Purple	Tawny	Good
137	JS 20-27	Green	Pointed ovate	Brown	Yellow	Black	White	Tawny	Good
138	JS 20-61	Green	Pointed ovate	Brown	Yellow	Yellow	White	Tawny	Good
139	JS 20-34	Green	Pointed ovate	Brown	Yellow	Black	White	Tawny	Good
140	JS 20-38	Green	Pointed ovate	Brown	Yellow	Black	Purple	Tawny	Good
141	JS 20-30	Green	Pointed ovate	Brown	Yellow	Black	White	Tawny	Good
142	AMS 62	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Fair
143	EC 250619	Green	Pointed ovate	Brown	Yellow	Brown	Purple	Tawny	Good
144	JS 20-75	Green	Pointed ovate	Brown	Yellow	Black	White	Tawny	Good
145	JS 20-60	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good
146	JS 20-21	Green	Pointed ovate	Brown	Yellow	Black	White	Tawny	Good
147	JS 20-31	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good
148	JS 20-23	Green	Pointed ovate	Brown	Yellow	Brown	Purple	Tawny	Good
149	EC 396053	Dark Green	Pointed ovate	Brown	Yellow	Yellow	Purple	Tawny	Good
150	EC 250607	Green	Pointed ovate	Brown	Yellow	Brown	Purple	Tawny	Good
151	EC 325099	Dark Green	Pointed ovate	Brown	Yellow	Brown	Purple	Tawny	Good
152	JS 20-29	Green	Pointed ovate	Brown	Yellow	Black	White	Tawny	Good
153	JS 20-25	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good
154	JS 20-51	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good
155	JS 20-54	Green	Pointed ovate	Brown	Yellow	Brown	Purple	Tawny	Good
156	JS 20-79	Green	Pointed ovate	Brown	Yellow	Brown	Purple	Tawny	Good
157	JS 20-53	Green	Pointed ovate	Brown	Yellow	Black	Purple	Tawny	Good
158	JS 20-52	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good
159	AMS 77-3	Green	Pointed ovate	Brown	Yellow	Black	Purple	Tawny	Good
160	AMS 210-6	Green	Pointed ovate	Brown	Yellow	Brown	White	Tawny	Good
161	SL 688 (C)	Green	Round ovate	Brown	Yellow	Brown	Purple	Tawny	Good
162	PS 1347 (C)	Green	Lanceolate	Brown	Yellow	Yellow	White	Tawny	Good
163	PS 1092 (C)	Green	Pointed ovate	Brown	Yellow	Black	Purple	Tawny	Good
164	Bragg (C)	Dark Green	Pointed ovate	Brown	Yellow	Black	Purple	Tawny	Good
165	PS 1042 (C)	Green	Pointed ovate	Black	Yellow	Brown	White	Tawny	Good

Table 4.1.2: Classification of 165 genotypes under study into distinct groups based on eight qualitative characters in soybean

S.No.	Character		Serial number of genotypes included in the group	Number of genotypes included
1.	Germination	Good	1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,52,53,54,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,80,81,82,84,85,86,87,89,90,91,92,93,94,95,96,97,98,99,100,101,102,103,104,106,107,108,109,110,111,113,114,115,116,117,118,119,120,121,122,123,124,125,126,127,128,129,130,131,132,133,134,135,136,137,138,139,140,141,143,144,145,146,147,148,149,150,151,152,153,154,155,156,157,158,159,160,161,162,163,164,165	156
		Fair	16,55,79,112,142	5
		Poor	51,83,88,105	4
2.	Leaf colour	Green	1,2,3,4,5,6,7,8,9,10,11,12,13,15,16,17,18,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,45,46,47,48,49,50,51,52,53,54,56,57,58,59,60,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95,97,98,99,100,101,102,103,104,105,106,107,108,110,111,113,114,115,116,117,118,120,121,122,123,124,125,127,128,129,130,131,132,133,134,135,136,137,138,139,140,141,142,143,144,145,146,147,148,150,152,153,154,155,156,157,158,159,160,161,162,163,165	152
		Dark green	14,19,44,55,61,96,109,112,119,126,149,151,164	13
3.	Leaf shape	Lanceolate	1,52,53,94,119,162	6
		Pointed ovate	2,3,4,5,6,7,8,9,10,11,12,13,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93,95,96,97,98,99,100,101,102,103,104,105,106,107,108,109,110,111,112,113,114,115,116,117,118,120,121,122,123,124,125,126,127,128,129,130,131,132,133,134,135,136,137,138,139,140,141,142,143,144,145,146,147,148,149,150,151,152,153,154,155,156,157,158,159,160,163,164,165	157
		Round ovate	14,161	2
4.	Pubescence colour	Tawny	2,3,4,5,6,7,8,9,11,12,13,14,15,16,17,18,19,20,21,22,23,24,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,46,47,48,49,50,51,54,55,56,57,58,59,62,63,64,65,66,69,70,72,73,75,76,77,78,79,82,83,84,85,86,87,88,90,91,92,93,94,95,96,97,98,99,100,101,102,103,104,105,106,107,108,109,110,111,112,113,114,115,116,117,118,119,120,122,124,126,127,128,129,130,132,133,134,135,136,137,138,139,140,141,142,143,144,145,146,147,148,149,150,151,152,153,154,155,156,157,158,159,160,161,162,163,164,165	146
		Grey	1,10,25,45,52,53,60,61,67,68,71,74,80,81,89,121,123,125,131	19

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Table 4.1.2 Concluded

5.	Flower colour	Purple	1,2,3,4,7,8,10,11,12,13,14,16,17,18,19,20,21,23,31,33,37,38,40,41,42,43,44,45,46,48,49,50,52,53,54,61,66,70,72,73,75,76,77,79,81,82,83,85,86,87,88,89,90,93,96,101,102,103,104,106,107,110,113,114,116,121,124,126,133,134,136,140,143, 148,149,150,151,155,156,157,159,161,163,164	84
		White	5,6,9,15,22,24,25,26,27,28,29,30,32,34,35,36,39,47,51,55,56,57,58,59,60,62,63,64,65,67,68,69,71,74,78,80,84,91,92,94,95,97,98,99,100,105,108,109,111,112,115,117,118,119,120,122,123,125,127,128,129,130,131,132,135,137,138,139,141,142,144,145,146,147,152,153,154,158,160,162,165	81
6.	Pod colour	Brown	2,3,4,5,6,7,8,9,11,12,13,14,15,16,17,18,19,20,21,22,23,24,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,46,47,48,49,50,51,54,55,56,57,58,59,62,63,64,65,66,69,70,72,73,75,76,77,78,79,82,83,84,85,86,87,88,90,91,92,93,94,95,96,97,98,99,100,101,102,103,104,105,106,107,108,109,110,111,112,113,114,115,116,117,118,119,120,122,124,126,127,128,129,130,132,134,135,136,137,138,139,140,141,142,143,144,145,146,147,148,149,150,151,152,153,154,155,156,157,158,159,160,161, 162,163,164	144
		Black	133,165	2
		Yellow	1,10,25,45,52,53,60,61,67,68,71,74,80,81,89,121,123,125,131	19
7.	Seed coat colour	Yellow	1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,92,93,94,95,96,97,98,99,101,102,103,104,105,106,107,108,109,110,111,112,113,114,115,116,117,118,119,120,121,122,123,124,125,126,127,128,129,130,131,132,134,135,136,137,138,139,140,141,142,143,144,145,146,147,148,149,150,151,152,153,154,155,156,157,158,159,160,161,162,163,164,165	161
		Black	133	1
		Brown	60,91,100	3
8.	Hilum colour	Black	3,4,16,20,21,29,30,31,33,40,41,43,44,49,54,62,65,67,68,69,72,75,80,82,83,93,94,95,97,98,104,107,108,109,114,124,125,128,133,135,136,137,139,140,141,144,146,152,157,159,163,164	52
		Brown	2,5,6,7,8,9,10,13,15,18,22,23,24,25,26,27,28,32,34,35,36,37,39,42,45,46,47,48,50,51,52,53,55,56,57,58,59,60,61,63,64,66,70,71,77,78,79,84,88,89,90,91,92,96,99,100,106,110,111,115,116,117,118,119,120,121,122,127,130,131,132,134,142,143,145,147,148,150,151,153,154,155,156,158, 160,161,165	87
		Yellow	1,11,12,14,17,19,38,73,74,76,81,85,86,87,101,102,103,105,112,113,123,126,129,138,149,162	26

in **Table 4.1.2** on the basis of National test guidelines for DUS testing in Soybean (**PVP and FRA, 2001 and Ramteke and Muralidharan, 2012**). The results obtained from the present study indicated a possibility of pubescence colour and pod colour showing linked inheritance. It was also found that the characters flower colour and hilum colour contributed more towards divergence than the other qualitative characters included in the present study.

4.2 Analysis of variance

Analysis of variance for fifteen quantitative characters revealed significant differences among the experimental material for all the characters studied. This suggested that there exists adequate amounts of genetic variability among the experimental material for all fifteen quantitative characters viz. plant height, days to 50% flowering, days to maturity, number of primary branches per plant, number of nodes per plant, number of pod bearing nodes per plant, number of pods per plant, number of seeds per pod, 100-seed weight, dry matter per plant, harvest index, seed yield efficiency, oil content, protein content and seed yield per plant, which were evaluated during the present study. Analysis of variance for all the characters evaluated in augmented block design-II is presented in **Table 4.2.1**.

Analysis of variance revealed highly significant differences among the checks with respect to all the characters under study except the number of primary branches per plant and number of nodes per plant, for which they only varied significantly. The variances (mean squares) of checks were found to be highly significant for plant height (52.56), days to 50% flowering (51.80), days to maturity (18.93), number of pod bearing nodes per plant (445.93), number of pods per plant (232.38), number of seeds per pod (0.06), 100-seed weight (0.33), dry matter weight per plant (338.03), harvest index (113.75), seed yield per plant (6.69), seed yield efficiency (0.10), oil content (0.64) and protein content (4.12), whereas the variances of checks were significant only for number of primary branches per plant (2.76) and number of nodes per plant (6.95). The presence of highly significant and significant variances for the checks for different characters indicated the presence of significant variation among the blocks for all the characters under study. Hence, the adjusted means for all the genotypes for different characters were estimated and used for further analysis to minimize the block variation effects.

The variances of genotypes were also recorded to be highly significant for all the

Table 4.2.1: Analysis of variance (ANOVA) for fifteen quantitative characters under study in soybean

Source of variation	d.f.	Mean Sum of Squares						
		Days to		Plant Height (cm)	Number of primary branches per plant	Number of nodes per plant	Number of pod bearing nodes per plant	Number of pods per plant
		50% Flowering	Maturity					
		1	2	3	4	5	6	7
Blocks	3	46.42**	15.01	700.00**	0.48	36.43**	224.32**	624.64**
Entries	164	18.32**	57.42**	203.17**	2.19	12.39**	71.43**	162.78**
Checks	4	51.80**	18.93*	52.56**	2.76*	6.95*	445.93**	232.38**
Genotypes	159	18.33**	34.61**	220.47**	1.32	9.56**	43.78**	142.19**
Checks vs. Genotype	1	-117.63	3837.51	-1944.08	138.38	485.35	2969.88	3158.38
Error	12	3.07	5.36	6.94	0.78	1.98	7.96	12.81
Total	179							

Least significant difference at 5%								
		1	2	3	4	5	6	7
Between checks		1.24	1.64	1.86	0.62	1.00	1.9948	2.5306
Between test entries		2.48	3.27	3.72	1.25	1.9916	3.9896	5.0613
Between entries of same block		2.71	3.59	4.08	1.37	2.1817	4.3704	5.5444
Between checks vs. genotype		2.14	2.84	3.23	1.08	1.7248	3.4551	4.3832

Contd....

* Significance at 5% level of probability

** Significance at 1% level of probability

Table 4.2.1 Concluded

Source of variation	d.f.	Mean Sum of Squares							
		Number of seeds per pod	100-seed weight (g)	Dry matter weight per plant (g)	Harvest Index (%)	Seed yield per plant (g)	Seed yield efficiency	Oil content (%)	Protein content (%)
		8	9	10	11	12	13	14	15
Blocks	3	0.25**	3.26**	102.25**	116.97**	24.72**	0.09**	24.46**	5.52**
Entries	164	0.04**	3.43**	107.16**	39.82**	13.49**	0.02**	4.83**	2.65**
Checks	4	0.06**	0.33**	338.03**	113.75**	6.69**	0.10**	0.64**	4.12**
Genotypes	159	0.04**	3.48**	88.13**	35.92**	10.09**	0.02**	4.52**	2.73**
Checks vs. Genotype	1	0.17	8.07	2209.51	363.04	581.66	0.16	71.64	-15.55
Error	12	0.002	0.02	3.59	3.02	0.25	0.004	0.06	0.09
Total	179								

Least significant difference at 5%									
		8	9	10	11	12	13	14	15
Between checks		0.0301	0.1115	1.3395	1.2279	0.3528	0.0452	0.1755	0.2154
Between test entries		0.0601	0.2230	2.6791	2.4558	0.7056	0.0903	0.3509	0.4309
Between entries of same block		0.0659	0.2442	2.9348	2.6901	0.7729	0.0990	0.3844	0.4720
Between checks vs. genotype		0.0521	0.1931	2.3201	2.1267	0.6111	0.0782	0.3039	0.3732

* Significance at 5% level of probability

** Significance at 1% level of probability

characters except number of primary branches per plant. The existence of variability for a particular trait in population provides an ample opportunity for improving the concerned trait through various breeding approaches. **Vavilov (1950)** stated that, the wider the range of variability, greater is the chance for improvement with respect to different traits through selection.

4.3 Mean performance and range of variation for fifteen quantitative characters

The mean performances of 160 genotypes and 5 checks for all characters and their range of variation for different quantitative traits were summarized in Table 4.3.1 and are discussed in detail in the ensuing pages. The mean values (adjusted) of 165 genotypes for different characters under study are presented in Appendix-II.

4.3.1 Days to 50% flowering

The range for days to 50% flowering varied from 35.85 (JS 20-25) to 62.65 days (EC 963805) with a mean value of 48.04 days. A total of 63 genotypes delayed in days to flowering, out of which 8 genotypes delayed significantly than the late flowering check [PS 1347 (49.75)], whereas 11 genotypes were numerically at par in terms of days to flowering with the earliest check and only JS 20-25 flowered significantly earlier than the earliest check [PS 1092 (41.00)].

4.3.2 Days to maturity

Days to maturity varied widely among the genotypes with a range from 89.30 (Cat 209) to 115.30 days (RPSP 935-E). A mean value of 100.38 days was observed for this character and all the genotypes were found to be earlier than the longest duration check [PS 1347 (117.50 days)]. Meanwhile, 129 genotypes matured significantly earlier and 24 genotypes matured at par in comparison with the earliest check [PS 1092(112.00 days)].

The interval from days to 50% flowering till maturity is referred to as the reproductive phase, which was shortest for the genotypes MACS 1394, JS 20-51 and AMS 77-3 (39.65 days each), followed by EC 16738 (40.65 days) and Shilajeet (43.65 days). This suggested that these genotypes were most suitable to those areas where terminal droughts during crop growth are a frequent problem. Whereas, the longest reproductive phase was observed in genotype JS 20-25 (71.65 days), followed by PS 1092 (71.00 days), and such genotypes were not recommended for areas susceptible to terminal drought as it may lead

to severe yield losses in soybean.

4.3.3 Plant height (cm)

Plant height showed a very large variation among the genotypes with a mean value of 58.55 cm. Jupiter (121.44cm) was the tallest, while Shilajeet (23.98 cm) was recorded to be the shortest of all genotypes. Overall, 35 genotypes were significantly taller and 28 genotypes were at par in height with the tallest check [SL 688 (61.50 cm)], whereas 27 genotypes were found to be significantly shorter and 26 genotypes at par in height with the shortest check [PS 1092 (51.85 cm)].

4.3.4 Number of primary branches per plant

The range for this character varied from 1.51 (JS 20-54) to 7.91 (PS 1225) with a mean value of 4.02 primary branches per plant. Only AMS 100-16-4-1-3 and PS 1225 were observed to be numerically superior but none was significant over the highest performing check [SL 688 (7.50)], whereas 43 genotypes were significantly inferior and 104 genotypes were numerically at par in comparison to the most inferior check [PS 1042 (5.40)].

4.3.5 Number of nodes per plant

The number of nodes per plant varied from 8.70 [G5P22 (PI)] to 26.10 (Kalitur). A mean value of 16.09 nodes per plant was observed for this character and 3 genotypes were found to be numerically superior but none was found to be significant over the best check [Bragg (23.50)], while 102 genotypes were significantly inferior and 43 genotypes were numerically at par when put against the most inferior checks [PS 1042 and PS 1092 (20.50)].

4.3.6 Number of pod bearing nodes per plant

A mean value of 23.34 was observed for this character with a range from 10.20 (PS 19) to 47.40 (Cat 902) pod bearing nodes per plant. All the genotypes were found to be inferior to the best check [PS 1042 (60.75)], while 68 genotypes were found to be numerically at par and 64 genotypes to be significantly inferior to the lowest check [PS 1092 (28.50)].

4.3.7 Number of pods per plant

Only AMS 100-16-4-1-3 was found to be significantly superior, while 3 other genotypes were found to be numerically at par in comparison with the best check [PS 1042 (79.50)]. Whereas, 55 genotypes were at par and 73 genotypes were significantly inferior to

the lowest performing check [Bragg (58.75)]. The mean value for this character was recorded to be 51.12, while the range from 24.45 (AMS 62) to 89.45 (AMS 100-16-4-1-3) pods per plant was observed among the genotypes.

4.3.8 Number of seeds per pod

The range varied from 1.85 (EC 14626) to 2.98 (AMS 42) seeds per pod with a mean value of 2.33 seeds per pod. Only AMS 42 was observed to be significantly superior, while 4 genotypes were at par with the best check [Bragg (2.73)], whereas 72 genotypes were significantly inferior and 50 genotypes were numerically at par in performance with the lowest check [SL 688 (2.42)]. This character showed narrow variation among the genotypes

4.3.9 100-seed weight (g)

The 100-seed weight exhibited a very high variability with a mean value of 8.78 g. Its range varied from 4.35 [Typical Bhatt (B)] to 15.43 g (EC 685243). In all, 34 genotypes were numerically superior out of which 25 genotypes were significantly superior over the highest performing check [Bragg (10.09)]. Meanwhile, 14 genotypes were numerically at par and 93 genotypes were significantly inferior to the lowest performing check [PS 1347 (9.31)] in terms of 100-seed weight.

4.3.10 Dry matter weight per plant (g)

The lowest and highest dry matter weight per plant was observed for Cat 746 (14.39 g), and JS 20-79 (61.93 g), respectively. Two genotypes i.e., AMS 100-16-4-1-3 and JS 20-79 were numerically superior, out of which only JS 20-79 was found to be significantly superior over the best check [PS 1042 (55.45 g)]. Whereas, 31 genotypes were at par and 72 genotypes were significantly inferior in weight to the lowest check [Bragg (33.00 g)]. A mean value of 31.29 g was observed for this character.

4.3.11 Harvest index (%)

The mean value of harvest index among the genotypes was recorded to be 32.24% with a range from 18.38 (Cat 902) to 46.51% (MAUS 102). Only 12 genotypes were numerically at par, while none was observed to be significant over the highest check [PS 1347 (43.65%)]. On the other hand, 35 genotypes were at par and 51 genotypes were significantly inferior to the lowest performing check [SL 688 (32.16%)].

4.3.12 Seed yield efficiency

The range varied from 0.21 (RKS 30) to 0.97 (MAUS 102) with a mean value of 0.49. Only PI 283327, IC 13051 and MAUS 102 were found to be numerically at par among which, only MAUS 102 was significant over the best check [Bragg (0.80)], while 70 genotypes were numerically at par and 10 genotypes were significantly inferior to the lowest performing check [SL 688 (0.46)].

4.4.13 Oil content (%)

Oil content showed a mean value of 17.82% and varied from 14.82 (AMS 50B) to 22.89% (AMS 38-24) which indicated a wide variability for this trait. Only 5 genotypes were numerically at par and 6 genotypes were significantly superior in oil content over the best check [PS 1092 (21.20)], whereas 12 genotypes were numerically at par and 127 genotypes were significantly lower in oil content than the lowest check [SL 688 (20.07)].

4.4.14 Protein content (%)

Moderate variability with a mean of 40.30% and a range of 35.21 (GP 67) to 43.84% (GP 305) was observed for this character. Overall, 31 genotypes were numerically at par, while 31 others were significantly superior in protein content over the best check [PS 1042 (40.88)], whereas 6 genotypes were numerically at par and 14 genotypes were significantly lower in protein content than the lowest check [SL 688 (38.48)].

4.3.15 Seed yield per plant (g)

Seed yield per plant also exhibited a moderate variability among the genotypes with a mean value of 9.96 g and its range varied from 4.63 (AMS 62) to 21.17 g (AMS 42). A total of 4 genotypes yielded significantly higher than the best check [PS 1042 (17.98)], whereas 11 genotypes yielded at par and 137 genotypes yielded significantly lower than the lowest check [Bragg (14.54)].

Similar findings were also reported by several earlier workers for different characters in soybean. **Karmakar and Bhatnagar (1996)** reported a range of 45.2-111.9 cm, while **Karnwal and Singh (2009)** recorded a span of 66.25-110.75 cm for plants height in their respective studies involving various soybean genotypes. **Ramteke et al. (2010)** reported a range of 5.67-21.33 and 3.67-8.67 for nodes per plant and number of branches per plant, respectively. **Srivastava and Jain (1994)** reported a range of 6.8-13.1 g for 100-seed weight, whereas **Wilson (2004)** observed a range of 34.1-56.8% and 8.1-27.9% for

Table 4.3.1: Mean performance, range of variation and superior genotypes over best check for fifteen quantitative characters in soybean

S.No.	Character	Genotype		Mean performance of check					Number of genotypes significantly superior over best check	Best 3 significantly superior genotypes	
		Mean	Range	SL 688	PS 1347	PS 1092	Bragg	PS 1042			
1	Days to 50% flowering	48.04	35.85-62.65	49.00	49.75	41.00	49.00	46.50	1	Early	JS 20-25
									8	Late	EC 963805, MACS 303 and T-49
2	Days to maturity	100.38	89.30-115.30	116.25	117.50	112.00	113.75	114.00	129	Early	Cat 209, JS 20-51 and AMS 77-3
									-	Late	-
3	Plant height(cm)	58.55	23.98-121.44	61.50	56.35	51.85	54.98	53.93	35	Jupiter, AMS 100-25-5 and Kalitur	
4	Number of primary branches per plant	4.02	1.51-7.91	7.50	7.00	7.25	6.50	5.40	-	-	
5	Number of nodes per plant	16.09	8.70-26.10	22.50	21.25	20.50	23.50	20.50	-	-	
6	Number of pod bearing nodes per plant	23.34	10.20-47.40	46.50	30.00	28.50	30.25	50.75	-	-	
7	Number of pods per plant	51.12	24.45-89.45	67.50	66.25	64.25	58.75	79.50	1	AMS 100-16-4-1-3	
8	Number of seeds per pod	2.33	1.85-2.98	2.42	2.61	2.57	2.73	2.44	1	AMS 42	
9	100-Seed weight (g)	8.78	4.35-15.43	9.91	9.31	9.69	10.09	9.76	25	EC 685243, AGS 751 and Cat 2755	
10	Dry matter weight per plant (g)	31.29	14.39-61.93	48.50	36.00	41.00	33.00	55.45	1	JS 20-79	
11	Harvest index (%)	32.24	18.38-46.51	32.16	43.65	38.30	42.81	33.06	-	-	
12	Seed yield efficiency	0.49	0.21-0.97	0.46	0.78	0.63	0.80	0.48	1	MAUS 102	
13	Oil content (%)	17.82	14.89-22.89	20.07	20.56	21.20	20.52	20.97	6	AMS 38-24, JS 20-23 and RVS 2002-7	
14	Protein content (%)	40.30	35.21-43.84	38.48	40.39	40.78	40.78	40.88	31	GP 305, Typical Bhatt (B) and EC 37937	
15	Seed yield per plant (g)	9.96	4.63-21.17	15.25	15.64	15.67	14.54	17.98	4	AMS 42, PS 1225 and AMS 100-16-4-1-3	

protein and oil contents, respectively. Similar variability for oil content was also reported by Dadson (1976); Maestri *et al.* (1998) and Malik *et al.* (2006).

4.4 Genetic divergence

The significance of genetic diversity and its role in plant breeding is evident from the results obtained in various crop species (Smartt, 1990; Ghafoor *et al.*, 2001; Upadhyaya *et al.*, 2002 and Upadhyaya, 2003). The ultimate aim of any crop improvement scheme is the development of superior genotypes, which can be utilized as cultivars. The success of any crop improvement programme depends on the magnitude of variability present in that particular crop. It is for this reason, crop germplasm is of keen interest in crop breeding as it acts like a natural reservoir for genetic variability. The knowledge of genetic divergence has been successfully exploited in different crop species for the selection of suitable parents for different breeding objectives, and hence the concept of ‘Genetic Divergence’ has its practical utility in differentiating well defined populations. In general, more diverse the parents, greater is the chance of obtaining heterotic combinations and a broad spectrum of variability in segregating generations (Arunachalam, 1981).

Mahalanobis D^2 statistic has been the most widely used statistical tool for estimating genetic diversity among the genotypes in crop breeding programmes. But its application gets crippled when a large number of entries were to be objectively evaluated in a breeding programme. Under these conditions, a method of numerical taxonomy known as Hierarchical Euclidean cluster analysis (Ward, 1963) has been found a successful tool for estimation of genetic diversity in crop breeding programmes. Therefore, in the present study Hierarchical Cluster Analysis (HCA) based on Euclidean distances was employed for estimating the genetic divergence among 165 genotypes of soybean and the results obtained from this study were discussed here under.

4.4.1 Cluster formation based on Hierarchical Cluster Analysis (HCA)

The experimental material for present study consisted of 160 genotypes of soybean obtained from ICAR-IISR, Indore and G.B.P.U.A.T, Pantnagar, which were evaluated in comparison with 5 checks viz. SL 688, Bragg, PS 1347, PS 1092 and PS 1042 using an augmented block design-II. The adjusted means of 165 genotypes were estimated and further subjected to Hierarchical Cluster Analysis (HCA), based on which the genotypes

Table 4.4.1.1: Distribution of 165 genotypes of soybean into different clusters using Hierarchical Cluster Analysis based on Euclidean distances

Cluster	Number of genotype(s)	Name of the genotype(s)
I	1	Kalitur
II	3	Jupiter, T-49 and AMS 100-25-5
III	9	Cat 209, JS 20-34, JS 20-38, G5P22 (PI), PS 2014, PS 564, Cat 746, MAUS 85 and EC 95291
IV	8	PS 1347 (C), PS 1092 (C), Bragg (C), MAUS 38, MACS 1394, Cat 133, GP 448 and PK 765
V	7	Typical Bhatt (B), Cat 307, PK 262, PS 1480, GP 67, RKS 30 and P RAB 1
VI	1	PS 19
VII	124	Shilajeet, AMS 38-24, EC 685343, EC 250607, Cat 135A, RVS 2006-19, EC 457174, MAUS 149, Cat 891, MACS 303, RVS 2002-6, JS 20-30, PP 6 (PI), Cat 195, MAUS 489, MAUS 164, G 620, Cat 142, MAUS 102, PI 283327, JS 20-53, AMS 62, IC 49685, JS 20-54, PK 416, GP 393, EC 396053, Cat 2705, Cat 2503, SL 983, Cat 783, AMS MB 5-19, K 88-262A, AMS 115, JS 20-25, RVS 2006-1, Cat 938, JS 20-60, JS 20-21, Cat 710, Chocolate Bold, MAUS 76, EC 251358, AGS 751, DT 21, Cat 118, IC 437079, RKS 27, JS 20-75, Cat 3284, Cat 2430, JS 20-27, Cat 340, Cat 886, Cat 780, JS 20-23, AMS 210-6, PK 327, Cat 2388, EC 116343, AMS 2005-19, Cat 2511, Cat 537, Cat 366, Cat 181, EC 963805, EC 325099, G 11, Cat 779, RPSP 935-E, GP 465, Himso 175, WT 150, Cat 148, Cat 3327, EC 14626, JS 20-31, F4P21, AMS 2005-24, EC 281462, EC 37937, EC 39362, EC 65772, RVS 2006-27, AMS 243-7-3, TGX 855-39E, AMS 77-3-6, JS 20-51, JS 20-52, AMS 77-3, JS 20-29, EC 250619, PS 1029, Cat 805, JS 20-41, Ankur, JS 20-61, EC 2581, AMS 2005-13, EC 457198, PS 1551, EC 100027, EC 457161, RVS 2002-7, EC 2581, Alankar, AMS 155 (A), SL (E) 1, Cat 103, AMS MB 5-18, AMS 59, AMS 25-5-1, Cat 50 (A), EC 172607, AMS 100, EC 118443, EC 33940, AMS 56, Cat 305, JS 82, EC 39491, GP 305, EC 250608 and EC 389148
VIII	4	Cat 902, PS 1042 (C), SL 688 (C) and MACS 993
IX	3	PS 1225, AMS 100-16-4-1-3 and AMS 42
X	5	AMS 13051, EC 16738, AMS 50B, JS 20-79 and AGS 129

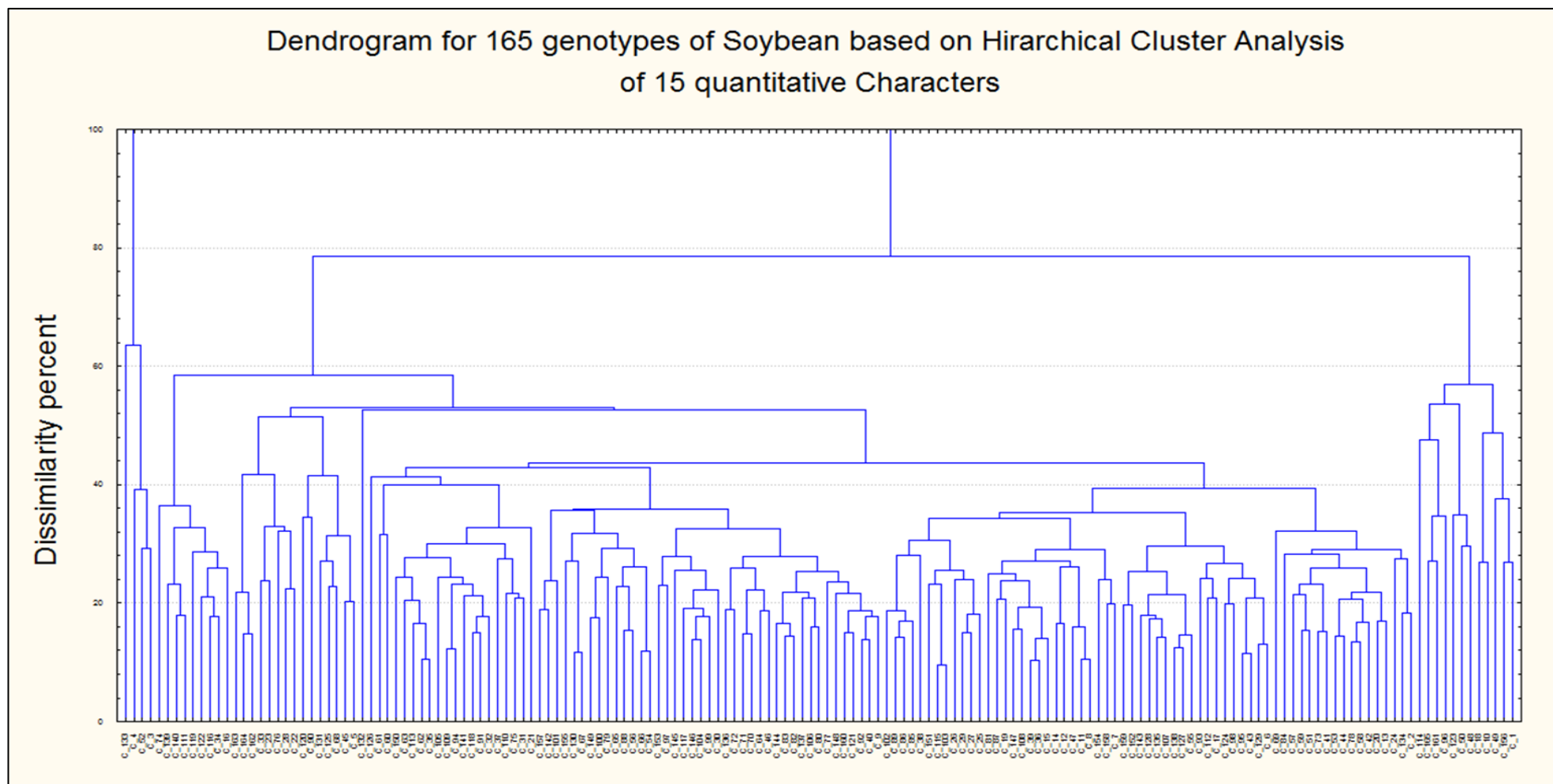


Figure 4.4.1.1: Tree diagram for 165 genotypes in soybean based on Unweighted Paired-group average Euclidean distances

The names C_1 to C_165 directly correspond to the genotypes from S.No. 1 to 165 as given in Table 4.1.1

were grouped into different clusters at 50% dissimilarity level.

The 165 genotypes including 5 checks were grouped into 10 clusters using Hierarchical Cluster Analysis based on Euclidean distances. The grouping of genotypes into different clusters is presented in **Table 4.4.1.1**. It can be seen from the results that Cluster VII was the largest (124 genotypes) followed by Cluster III (9 genotypes), Cluster IV (8 genotypes), Cluster V (7 genotypes), Cluster X (5 genotypes), Cluster VIII (4 genotypes), Clusters II and IX (3 genotypes each) and Clusters I and VI (1 genotype each) which were the smallest.

Kayande and Patil (2009) studied the clustering pattern among 50 genotypes of soybean grouped into 10 clusters and they reported high diversity among the clusters. Similar results were reported by **Chauhan and Singh, 1982; Mehetre et al., 1994; Yadav, 2005; Shadakshari et al., 2011 and Bekele et al., 2012**. The Dendrogram for 165 genotypes derived through HCA is presented in **Figure 4.4.1.1**. The genotypes in different clusters of dendrogram were denoted by their entry numbers which directly correspond to the names of genotypes given in **Table 4.1.1**.

A critical perusal of distribution pattern of genotypes into different clusters indicated that the genotypes from different geographic locations were included in the same cluster, whereas the genotypes from the same location were grouped into different clusters. Therefore, it could be inferred from the above that no parallelism existed between genetic diversity and geographical isolation. Similar observations were reported by **Chauhan, 1976; Ram et al., 1992; Kumar and Nadarajan, 1994; Sihag, 2004; Kadam, 2007 and Poornima Jency and Kalaimagal, 2015**.

4.4.2 Inter and Intra-cluster distance

Number of clusters refers to the number of groups into which the given genotypes were classified. The distance between two clusters is a measure of their degree of diversification. Hence, greater is the distance between two clusters, more will be the divergence between them and vice-versa. The genotypes that fall into the same cluster are more likely to be related with each other than with those belonging to a different cluster. In other words, all those genotypes that are grouped into one cluster are less divergent among themselves than with those which are placed into a different cluster. The intra and inter-cluster distances estimated for different clusters were presented in **Table 4.4.2.1** and also discussed below.

The highest intra-cluster distance among the given clusters was observed for Cluster X (27.10) followed by Cluster VIII (25.62), Cluster VII (25.15), Cluster II (23.09), Cluster IV (22.83), Cluster V (22.51), Cluster IX (21.33), whereas the lowest intra-cluster distance was recorded for Clusters I and VI (0.00) followed by Cluster III (19.65). Greater distance among the members of a cluster implied that considerable amount of variability still exists among the genotypes for the concerned characters under study. If the dissimilarity levels were further lowered, a more finer dissolution of the existing cluster could be obtained. On the contrary, clusters with lesser intra-cluster distance indicated that the genotypes included in those clusters were more closely related and hence should be less variable with respect to their mean values. Further, the mean values of these genotypes tend to be close to the cluster mean value and hence extraction of donors from these clusters will be easy.

The inter-cluster distance was recorded to be highest between the Clusters II and III (91.59) followed by Cluster I and IX (79.32), III and X (78.13), I and III (76.35), I and VIII (72.65) II and VI (72.28) and Clusters III and IX (71.29). Meanwhile, the lowest inter-cluster distance was observed between the Clusters IV and V (33.06) followed by Clusters IV and IX (33.66), VI and VII (33.90), IV and VIII (33.93), V and VII (34.05), IV and VIII (38.18) and Clusters VIII and IX (34.43).

The highest inter-cluster distance observed between Clusters II and III showed that these two clusters and also the members included within these clusters were distantly related to each other. The higher is the inter-cluster distance, more will be the diversity between the genotypes belonging to such clusters and vice-versa. This provides an ample opportunity for selection of suitable donors from these divergent clusters which could be used in hybridization programs for the development of superior genotypes in soybean. During hybridization, the most distantly related genotypes with desirable traits should be crossed in order to obtain a wide range of segregants among the progeny which may include a few transgressive segregants. Selection should be further practiced among such populations to identify superior segregants with desirable traits. Several authors suggested earlier that, crossing between genotypes obtained from divergent clusters with high inter-cluster distance would yield superior segregants for selection (**Ramgiry, 1999; Sharma, 2000 and Gawande et al., 2002**).

Ramgiry et al. (1998) classified 40 germplasm lines of soybean collected from India and abroad into 6 clusters. They noticed considerable amount of genetic diversity for yield

Table 4.4.2.1: Intra (diagonal) and Inter-cluster (off-diagonal) distances between clusters based on Hierarchical Cluster Analysis in soybean

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X
I	0.00	40.83	76.85	63.98	46.93	62.57	58.92	72.65	79.32	60.17
II		23.09	91.59	60.52	44.04	72.28	66.38	59.03	62.75	41.01
III			19.65	54.43	55.76	39.20	35.50	68.09	71.29	78.13
IV				22.83	33.06	37.90	34.18	33.93	33.66	38.27
V					22.51	40.49	34.05	38.18	42.33	36.71
VI						0.00	33.90	46.73	44.85	59.26
VII							25.15	48.34	54.70	52.39
VIII								25.62	34.43	37.85
IX									21.33	35.04
X										27.10

and yield attributes and also suggested inter-crossing between genotypes from diverse clusters to generate wide variability for effective selection in segregating generations to develop high yielding cultivars in soybean. Similarly, **Gaikwad *et al.* (2005)** also observed that the genotypes with greater variability were included in different clusters and crossing between those genotypes from such clusters would generate a broad spectrum of variability for yield enhancement in soybean.

4.4.3 Cluster mean values for different clusters

The cluster mean values for 15 quantitative characters were calculated and summarized in Table 4.4.3.1. A critical perusal into the results revealed that all the clusters exhibited varying differences for all the characters included in the study. This facilitates for identification of suitable donors for different traits, which could be further crossed as parents in crop breeding programs to obtain superior segregants with enhanced yield levels in soybean.

- a) Among all the 10 clusters obtained, the highest cluster mean value for plant height was recorded for Cluster II (112.76 cm), while the lowest cluster mean value was

recorded for Cluster III (35.72 cm). The mean plant heights for Clusters I, IV, V, VI, VII, VIII, IX and X were found to be 107.78, 59.43, 74.62, 40.58, 56.57, 59.50, 60.76 and 84.32 cm, respectively.

- b) The highest and lowest cluster mean values for days to 50% flowering were observed in Cluster II (54.05) and Cluster III (44.18), respectively. Further, the mean values of 50.85, 50.03, 52.34, 47.85, 47.54, 47.90, 49.52 and 51.93 were observed for Clusters I, IV, V, VI, VII, VIII IX and X, respectively.
- c) Cluster VII (112.51) showed the highest cluster mean value for days to maturity followed by Clusters I (112.50), II (111.30), VI (109.50), V (107.10), IV (105.09), IX (100.37), X (100.14), VII (99.07) and the lowest value of 97.90 in Cluster III.
- d) For the number of primary branches per plant, Cluster IX (7.52) exhibited the highest mean value, whereas Cluster III (2.83) showed the lowest mean value. Clusters I, II, IV, V, VI, VII, VIII and X recorded the mean values of 5.31, 4.63, 5.21, 4.51, 4.71, 3.77, 6.34 and 4.97 primary branches per plant, respectively.
- e) Of the 10 clusters, Cluster I included genotypes with the highest mean value for number of nodes per plant (26.10), whereas Cluster III consisted of genotypes with minimum number of nodes per plant (12.34). Clusters II, IV, V, VI, VII, VIII, IX and X included genotypes which exhibited mean values of 20.83, 18.87, 17.20, 16.90, 15.60, 20.10, 15.90 and 21.02 nodes per plant, respectively.
- f) The highest and lowest mean values for number of pod bearing nodes per plant were observed for Clusters VIII (45.21) and VI (10.20), respectively. The other Clusters X, II, IV, IX, V, I, VII, III and VI showed mean values of 37.40, 34.73, 31.42, 29.27, 26.11, 25.00, 21.69, 14.62 and 10.20 pod bearing nodes per plant, respectively.
- g) Cluster IX (82.12) exhibited the highest cluster mean value for number of pods per plant followed by Clusters X (76.41), VIII (73.78), IV (68.54), II (60.65), VI (56.45), V (55.54), VII (48.38), I (35.45) and Cluster III which exhibited the lowest mean value of 33.45 pods per plant.
- h) Lowest cluster mean value for the number of seeds per pod was recorded in Cluster III (2.24), whereas Clusters II and VI showed a mean value of 2.29 and the remaining Clusters VII, I, V, VIII, X, V and IX exhibited mean values of 2.32, 2.34, 2.36, 2.38, 2.40, 2.44 and 2.71 seeds per pod, respectively.

- i) For 100-seed weight, highest cluster mean value was recorded for Cluster VI (9.80 g) and lowest mean value for Cluster I (7.51 g). The rest exhibited mean values of 8.95 g (Cluster II), 9.03 g (Cluster III), 8.49 g (Cluster IV), 8.46 g (Cluster V), 8.83 g (Cluster VII), 8.34 g (Cluster VIII), 9.65 g (Cluster IX) and 7.83 g (Cluster X).
- j) Cluster IX exhibited the highest mean value for dry matter weight per plant (54.24 g) followed by Clusters VIII (48.43 g), II (47.32 g), X (46.60 g), VI (44.93 g), V (40.67 g), IV (32.39 g), VII (29.31 g), I (20.93 g) and Cluster III (20.77 g) which showed the least cluster mean value.
- k) Harvest index exhibited a highest cluster mean value of 42.33% (Cluster IX) and a lowest cluster mean value of 26.90% (Cluster VIII). The mean values for other clusters were found to be 29.08% (Cluster I), 27.07% (Cluster II), 29.31% (Cluster III), 38.92% (Cluster IV), 27.35% (Cluster V), 28.52% (Cluster VI) and 32.31% (Cluster VII) and 34.76% (Cluster X).
- l) In case of seed yield efficiency, Cluster IV (0.68) showed the highest cluster mean value followed by Clusters IX (0.64), X (0.58), VII (0.49), III (0.44), I and II (0.40 each), VI (0.39), VIII (0.38) and Cluster V with the lowest mean value of 0.37.
- m) Cluster VI (20.16%) exhibited the highest cluster mean value for oil content (%), whereas the Cluster IX (17.12%) recorded the lowest mean value. Others exhibited the values of 17.31% (Cluster I), 18.22% (Cluster II), 18.02% (Cluster III), 18.96% (Cluster IV), 18.09% (Cluster V), 17.67% (Cluster VII), 18.73% (Cluster VIII), and 17.93% (Cluster X).
- n) The highest cluster mean value for protein content (%) was recorded to be 40.81% (Cluster IX), while the lowest was observed for 38.84% (Cluster I). Mean values of 39.52% (Cluster II), 40.49% (Cluster III), 40.11% (Cluster IV), 38.93% (Cluster V), 39.30% (Cluster VI), 40.11% (Cluster VII), 39.72% (Cluster VIII) and 40.70% (Cluster X) were observed for the remaining clusters.
- o) The cluster mean value for seed yield per plant was found to be highest for Cluster IX (21.04 g) followed by Cluster X (15.91 g), Cluster VIII (13.70 g), Cluster IV (13.09 g), Cluster II (12.94 g), Cluster VI (12.87 g), Cluster V (11.13 g), Cluster VII (9.27 g), Cluster III (6.21 g) and Cluster I which showed the lowest mean seed yield of 5.87 g per plant.

In general, an overview of the above results showed that Cluster III included most of the genotypes which were earliest in flowering and maturity and hence, such genotypes could be used as donors in breeding for early maturing varieties. Cluster IX included the genotypes exhibiting highest mean values for yield and most of its attributes like number of primary branches per plant, number of pods per plant, number of seeds per pod, dry matter weight per plant and harvest index. Also this cluster included genotypes with high protein content. Hence, it could be considered as the most valuable cluster in terms of yield related traits. Cluster III included genotypes with short height and hence, these genotypes could be used as donors for breeding varieties with determinate growth habit. Clusters VIII, IV and I contained the genotypes having more number of pod bearing nodes per plant, high seed yield efficiency and more number of nodes per plant, respectively. Therefore, genotypes from these clusters can be included as donors in breeding programs for improvement of respective traits in soybean. Cluster VI included genotypes that were bold seeded as well as high in oil content and could act as superior donors for breeding varieties superior in terms of both these traits.

It can be concluded from all the above findings that the Cluster IX showed the highest cluster means for majority of characters under study followed by Cluster VI and Cluster VIII. This clearly indicated the presence of most promising genotypes within these clusters and hence, selection of such genotypes to be used as parents for hybridization should be highly rewarding to obtain desirable recombinants for yield and its attributes. This facilitates the simultaneous improvement of several characters in soybean by inter-crossing among superior genotypes selected as donors from different clusters, and the progeny if found superior could be released as new varieties, thereby ultimately resulting in enhanced yield levels in soybean. Similar findings were reported by **Sichhar *et al.* (1988)**; **Tyagi and Jyoti Sethi (2011)** and **Chavan *et al.* (2014)**, who suggested that distantly related parents in terms of their genetic diversity should be selected for hybridization to obtain superior recombinants for yield attributes. **Alpna *et al.* (2015)** also studied the genetic divergence among different genotypes in soybean and reported that 9 genotypes (Alankar, Kalitur, MACS 450 and *Glycine soja* derived pre-breeding lines) selected from superior clusters based on their genetic divergence demonstrated a great potential to recover superior recombinants for economic traits in soybean.

Table 4.4.3.1: Cluster mean values for fifteen quantitative characters among 165 genotypes of soybean

S. No.	Character	Cluster									
		I	II	III	IV	V	VI	VII	VIII	IX	X
1	Days to 50% flowering	50.85	54.05	44.18	50.03	52.34	47.85	47.54	49.70	49.52	51.93
2	Days to maturity	112.50	111.30	97.90	105.09	107.10	109.50	99.07	112.51	100.37	100.14
3	Plant height (cm)	107.78	112.26	35.72	59.43	74.62	40.58	56.57	59.50	60.76	84.32
4	Number of primary branches per plant	5.31	4.63	2.83	5.21	4.51	4.71	3.77	6.34	7.52	4.97
5	Number of nodes per plant	26.10	20.83	12.34	18.87	17.20	16.90	15.60	20.10	15.90	21.02
6	Number of pod bearing nodes per plant	25.00	34.73	14.62	31.42	26.11	10.20	21.69	45.21	29.27	37.40
7	Number of pods per plant	35.45	60.65	33.45	68.54	55.54	56.45	48.38	73.78	82.12	76.41
8	Number of seeds per pod	2.34	2.29	2.24	2.36	2.44	2.29	2.32	2.38	2.71	2.40
9	100-seed weight (g)	7.51	8.95	9.03	8.49	8.46	9.80	8.83	8.34	9.65	7.83
10	Dry matter weight per plant (g)	20.93	47.32	20.77	32.39	40.67	44.93	29.31	48.43	54.24	46.60
11	Harvest index (%)	29.08	27.07	29.31	38.92	27.35	28.52	32.31	26.90	42.33	34.76
12	Seed yield efficiency	0.40	0.40	0.44	0.68	0.37	0.39	0.49	0.38	0.64	0.58
13	Oil content (%)	17.31	18.22	18.02	18.96	18.09	20.16	17.67	18.73	17.12	17.93
14	Protein content (%)	38.84	39.52	40.49	40.11	38.93	39.30	40.41	39.72	40.81	40.70
15	Seed yield per plant (g)	5.87	12.94	6.21	13.09	11.13	12.87	9.27	13.70	21.04	15.91

4.4.4 Identification of suitable donors for different characters

Grain yield is a complex character since it is a resultant of interaction between several yield components. Therefore, a successful fabrication of any crop breeding programme is not only dependant on the selection of desirable parents as judged by their yield potential and combining abilities but also it necessitates the identification of principal yield contributing traits. There may not be any genetic factor directly controlling the yield *per se* but for their components, the multiplicative interaction of which ultimately results in increased yield levels. The improved genetic donors could be employed for contributing additional desirable traits into an otherwise well adapted and superior variety. Germplasm of a crop serves as a reservoir of valuable genes for which a careful screening and evaluation is obligatory. A critical analysis of means, variability and genetic diversity in the present investigation revealed that some genotypes of soybean, particularly those which are superior over the best check could be employed as donors for different yield contributing traits in order to breed high yielding varieties. The character-wise donors identified for yield and its components were presented in Table 4.4.4.1 and discussed below.

The genotypes Cat 209, JS 20-34 and JS 20-38 (Cluster III) and JS 20-35, EC 685243, AMS 38-24, EC 250607, RVS 2006-1 and Cat 2053 (Cluster VII) showed lowest mean values for days to flowering and bloomed quicker than the earliest flowering check (PS 1092). Similarly, the genotypes T-49 (Cluster II), EC 16738 (Cluster X) and Typical Bhatt (B), RKS 30 and P RAB 1 (Cluster V) were late in flowering with high cluster means and exceeded the best check for lateness (PS 1347). Therefore, these genotypes can be used as ideal donors in breeding for these two contrasting traits of this character.

Clusters VIII (112.51) and I (112.50) delayed maximum in maturity. But none of all evaluated genotypes exceeded the best check for lateness (PS 1347). However, since these clusters exhibited high inter-cluster distance, MACS 993 (VIII) and Kalitur (I) could be inter-crossed to obtain transgressive segregants for lateness. Meanwhile, Clusters III (97.90) and VII (99.07) included short duration genotypes among which G5P22 (PI), Cat 209, JS 20-34 and JS 20-38 (Cluster III) and EC 250607, EC 685243, EC 39491 (VII), Cat 2503, JS 20-51 and AMS 77-3 (Cluster VII) were found to be earliest in maturity than the best check (PS 1092) and hence, could be used as potential donors in breeding for earliness in soybean.

In case of plant height, Clusters III (35.72 cm) and VII (56.57 cm) included the shortest genotypes among which 7 genotypes viz. PS 1024, G5P22 (PI), JS 20-34, JS 20-38

and PS 564 (Cluster III) and Shilajeet (Cluster VII) were shorter than the best dwarf check i.e., PS 1092 (51.85 cm). They hence could be utilized as potential donors for breeding dwarf genotypes in soybean. Similarly, the genotypes Jupiter (II), AMS 10-25-5 (II) and Kalitur (I) were identified as superior donors for tallness as they were found to be superior to the best check for tallness (SL 688).

In case of number of primary branches per plant, 2 genotypes each from Clusters IX (PS 1225 and AMS 100-16-4-1-3), VII (EC 457198 and EC 2581) and VIII (MACS 993 and Cat 902) recorded higher number of primary branches per plant, but however only PS 1225 and AMS 100-16-4-1-3 were observed to be superior over the best check (SL 688). Also, high inter-cluster distances observed between these clusters suggested that it was possible to obtain superior recombinants for this character through hybridization.

The Clusters I (26.10), X (21.02) and II (20.83) possessed high cluster mean values for number of nodes per plant and only the genotypes Kalitur (I), Jupiter and T-49 (II) showed higher number of nodes than the best check (Bragg). Number of pod bearing nodes per plant were observed to be high for genotypes Cat 902 (Cluster VIII), AMS 100-25-5 (Cluster II) and IC 13051 (Cluster X) but none among the given genotypes was found to be superior over the best check in this category (PS 1042). A high inter-cluster distance observed between these clusters indicated that there exists an ample scope to recover transgressive segregants for this character through hybridization between distantly related donors.

The genotypes AMS 100-16-4-1-3 and PS 1225 (Cluster IX), MACS 993 (Cluster VIII), AMS 50B and JS 20-79 (Cluster X) showed higher number of pods per plant and of these all except AMS 50B were superior to the best check (PS 1042). The number of seeds per pod were more among the genotypes AMS 42 (Cluster IX), PS 1480, PK 262 and Cat 307 (Cluster V), JS 20-79 (Cluster X), EC 250619 and JS 20-73 (Cluster VII). Among these, only JS 20-79, AMS 42, EC 250619 and JS 20-73 were superior over the best check (Bragg). Here, the inter-cluster distances and means for the above clusters were moderate for number of seeds per pod, but they included such genotypes which performed better than the best check. Hence, these genotypes could be used in the improvement of concerned characters in soybean.

In case of 100-seed weight, 27 genotypes from Cluster VII (including PS 1551, EC 457198, RVS 2002-7, EC 39491, JS 20-29, AMS 77-3, AMS77-3-6, EC 37937, RKS 27,

Table 4.4.4.1: List of suitable donors for yield and its components identified in the present study among 165 genotypes of soybean

S.No.	Character		Donor
1	Days to 50% flowering	Early	JS 20-34 (III), JS 20-38 (III), Cat 209 (III), JS 20-35 (VII) and RVS 2006-1 (VII)
		Late	T-49 (II), Typical Bhatt (B) (II), RKS 30 (V), P RAB 1 (V) and EC 16738 (X)
2	Days to maturity	Early	G5P22 (PI) (III), Cat 209(III), EC 250607 (VII), EC 39491 (VII), JS 20-51 (VII) and AMS 77-3 (VII)
		Late	MACS 993 (VIII) and Kalitur (I)
3	Plant height (cm)	Dwarfness	Shilajeet (VII), PS 1024 (III), G5P22 (PI) (III) and PS 19 (VI)
		Tallness	Jupiter (II), AMS 100-25-5 (II) and Kalitur (I)
4	Number of primary branches per plant		PS 1225 (IX), AMS 100-16-4-1-3 (IX) and Cat 902 (VIII)
5	Number of nodes per plant		Kalitur (I), Jupiter (II) and T-49 (II)
6	Number of pod bearing nodes per plant		Cat 902 (VIII), AMS 100-25-5 (II) and IC 13051 (X)
7	Number of pods per plant		AMS 100-16-4-1-3 (IX), PS 1225 (IX), MACS 993 (VIII) and JS 20-79 (X)
8	Number of seeds per pod		JS 20-79 (X), AMS 42 (IX), EC 250619 (VIII) and JS 20-73 (VII)
9	100-seed weight (g)		AGS 751 (VII), Cat 2755 (VII), AMS 38-24 (VII), PK 262 (V), EC 685243 (VII) and EC 457174 (VII)
10	Dry matter weight per plant (g)		AMS 100-16-4-1-3 (IX), JS 20-79 (X), AMS 50B (X) and MACS 993 (VIII)
11	Harvest index (%)		Cat 118 (VII), AGS 751 (VII), DT 21 (VII), SL (E)1 (VII) and AMS 59 (VII),
12	Seed yield efficiency		IC 13051 (X), MAUS 102 (VII), MACS 1394 (IV), PS 1225 (IX) and PI 283327 (VII)
13	Oil content (%)		JS 20-23 (VII), SL (E)1 (VII), RVS 2002-7 (VII), Jupiter (II), GP 393 (VII) and PS 1480 (V)
14	Protein content (%)		GP 305 (VII), EC 37937 (VII), Cat 2503 (VII), Typical Bhatt (B) (V), Cat 209 (III) and AMS 50B (X)
15	Seed yield per plant (g)		PS 1225 (IX), AMS 42 (IX) and JS 20-79 (X)

AGS 751, Cat 2755, Cat 118, PK 416, AMS 38-24, EC 685243, EC 457174 and Cat 135A), 2 genotypes from Cluster V (PK 262 and PS 1480), 2 genotypes from Cluster III (EC 95291 and JS 20-34) and one genotype from Cluster II (Jupiter) was found to be bold seeded and had higher 100-seed weight than the best check (Bragg). Although, these clusters exhibited lower mean values but the genotypes included in them were selected on the basis of their high means *per se* and inter-cluster distances.

The genotypes MACS 993 (Cluster VIII), AMS 42 and AMS 100-16-4-1-3 (Cluster IX), AMS 50B, AGS 129 and JS 20-79 (Cluster X) produced high dry matter weight per plant, and among these, only AMS 100-16-4-1-3 and JS 20-79 were found to be superior over the best check (PS 1042). One genotype each from Clusters IV (Cat 133), IX (AMS 42) and X (IC 13051) along with 12 genotypes from Cluster VII (EC 685243, AMS 100, MAUS 102, AMS 115, PI 283327, Cat 118, AGS 751, DT 21, SL (E) 1, AMS 59, Cat 50 (A) and EC 118443) showed high harvest index values and all these genotypes except Cat 133 were superior to the best check (PS 1347). However, these clusters showed moderate inter-cluster distances indicating genetic relation between such genotypes to some extent and hence, variability can be incorporated by crossing these genotypes with superior genotypes from unrelated clusters.

Seed yield efficiency was found high among the genotypes MAUS 38 and MACS 1394 (Cluster IV), PS 1225 and AMS 42 (Cluster IX), IC 13051 (Cluster X), MAUS 102 and PI 283327 (Cluster VII). Also, the genotypes IC 13051, MAUS 102 and PI 283327 were found to be superior to the best check (PS 1347). Moderate to high inter-cluster distance between these clusters indicated that seed yield efficiency could be improved through hybridization among genotypes included within these clusters.

One genotype each from Cluster II (Jupiter) and VI (PS 19), 2 genotypes from Cluster V (PS 1480, GP 67) and 9 genotypes from Cluster VII (AMS 38-24, RVS 2002-6, JS 20-30, PK 416, GP 393, RVS 2006-1, JS 20-23, RVS 2002-7, SL (E) 1) were found to possess high oil contents which were higher than the best check for high oil content (PS 1092). Hence, an improvement of oil content in soybean could be achieved through selection within these genotypes or by including them in genetic crosses to recover transgressive segregants. The genotypes Cat 209 and JS 20-38 (Cluster III), Typical Bhatt (B) (V), AMS 50B and AGS 129 (X), GP 305, EC 37937, EC 65772, Cat 148, Cat 886, Cat 340, JS 20-60, JS 20-21, Cat 2503, Cat 891, EC 250607, Cat 135A and RVS 2006-19 (Cluster VII)

contained high protein contents and were superior to the best check for protein content (PS 1042). The clusters exhibited high inter-cluster distances which indicated that the genotypes within these clusters could be utilized as suitable parents in crossing programs to recover high protein segregants in soybean. It was observed from the results that genotypes like P RAB 1 (20.40% and 40.03%), AMS 2005-13 (20.61% and 40.84%) and JS 20-30 (21.36% and 39.66%) were found to possess high oil as well as adequate protein content, and hence could be used in crossing programmes for simultaneous improvement of both these traits.

Seed yield per plant was observed to be high among the genotypes PS 1225 and AMS 42 (Cluster IX), JS 20-79 and AGS 129 (Cluster X) for which these clusters exhibited high mean values of 21.04 g and 15.91 g respectively. All these genotypes except AGS 129 were also superior over the best check (PS 1042) for seed yield per plant. Although, these clusters showed moderate inter-cluster distance, the genotypes from these clusters were selected based on the high cluster means and high *per se* performance. Hence, these genotypes could be included as potential donors in genetic crosses to obtain better segregants.

In general, it could be concluded based on inter-cluster distance, cluster mean values and *per se* performance, the most desirable genotypes identified were PS 1225, Jupiter, JS 20-79, Cat 209, SL (E) 1 and AMS 10-16-4-1-3 which could be used as superior donors in hybridization programs, and the potential parental combinations that could be considered for enhancing the overall yield levels in soybean were, PS 1225 x Jupiter, PS 1225 x JS 20-79, PS 1225 x Cat 209, PS 1225 x SL (E) 1, PS 1225 x AMS 100-16-4-1-3, Jupiter x JS 20-79, Jupiter x Cat 209, Jupiter x AMS 100-16-4-1-3, JS 20-79 x Cat 209, JS 20-79 x SL (E) 1, JS 20-79 x AMS 100-16-4-1-3, Cat 209 x SL (E) 1, Cat 209 x AMS 100-16-4-1-3, SL (E) 1 x AMS 100-16-4-1-3, while the crosses Jupiter x SL (E) 1 and Cat 209 x AMS 50B would be promising to recover superior segregants for oil and protein contents, respectively.

4.5 Genetic variability parameters

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 the 15 quantitative characters are summarized in Table 4.5.1. 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 consideration.

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)

4.5.1 Phenotypic coefficient of variation (PCV)

The estimates of Phenotypic coefficient of variance (PCV) revealed moderate to high values for majority of the characters included with the highest value of PCV (%) being recorded seed yield per plant (30.94%) followed by dry matter weight per plant (28.92%), number of primary branches per plant (28.15%) and number of pod bearing nodes per plant (27.72%), seed yield efficiency (26.85%), plant height (24.11%), number of pods per plant (22.50%) and 100-seed weight (20.28%). The characters number of nodes per plant (19.99%), harvest index (17.85%) and oil content (11.40%) exhibited moderate values of PCV (%), whereas the lowest estimate of PCV (%) were recorded for protein content (3.91%) followed by days to maturity (5.64%), number of seeds per pod (7.74%) and days to 50% flowering (8.54%).

4.5.2 Genotypic coefficient of variation (GCV)

The estimates of genotypic coefficients of variance (GCV) exhibited a similar trend of distribution like phenotypic coefficients of variation (PCV) with majority of characters being included under moderate to high categories. Highest value of GCV (%) was observed for seed yield per plant (30.51%) followed by dry matter weight per plant (28.26%), number of pod bearing nodes per plant (24.84%), plant height (23.68%), seed yield efficiency (23.38%), number of pods per plant (21.36%) and 100-seed weight (20.19%). Moderate values of GCV (%) were observed for number of nodes per plant (17.95%), number of primary branches per plant (17.72%), harvest index (17.01%) and oil content (11.32%) meanwhile, days to 50% flowering (7.73%), number of seeds per pod (7.52), days to maturity (5.14%) and protein content (3.83%) exhibited the lowest values for GCV (%).

4.5.3 Environmental coefficient of variation (ECV)

It could be observed from the results obtained 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 number of primary branches per plant (21.87%) followed by seed yield efficiency (13.21%) and number of pod bearing nodes per plant (12.32%), whereas, the lowest values of ECV were recorded for

protein content (0.76%) followed by oil content (1.40%) and 100-seed weight (1.80%). 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.

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 number of primary branches per plant, seed yield efficiency and number of pod bearing nodes per plant showed a greater contribution of GCV (%) values towards PCV (%) values with a negligible impact of ECV (%). 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)** also reported high estimates of PCV and GCV in comparison to ECV. They reported a near equal and high estimates of PCV and GCV for plant height, number of primary branches and pods per plant, 100-seed weight, biological yield and seed yield per plant and reported moderate estimates of PCV and GCV for days to 50% flowering, days to maturity and number of seeds per pod. Similar results were reported by **Pushpa reni and Koteshwara rao (2013) and Baraskar et al. (2014)**. 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**).

4.5.4 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 programs 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)

A critical perusal of heritability estimates given in the Table 4.5.1 revealed that 100-seed weight recorded highest heritability value (99.80%) followed by oil content (98.50%)

Table 4.5.1: PCV, GCV, ECV, heritability, genetic advance and genetic advance as per cent of mean for different characters under study in soybean

S.No.	Character	PCV (%)	GCV (%)	ECV (%)	$h^2(b)$ (%)	GA (%)	GA as % of mean
1	Days to 50% flowering	8.54	7.73	3.64	81.80	6.92	14.39
2	Days to maturity	5.64	5.14	2.32	83.10	9.66	9.66
3	Plant height (cm)	24.11	23.68	4.49	96.50	28.11	47.93
4	Number of primary branches per plant	28.15	17.72	21.87	39.60	0.93	22.98
5	Number of nodes per plant	19.99	17.95	8.80	80.60	5.32	33.20
6	Number of pod bearing nodes per plant	27.72	24.84	12.32	80.30	10.50	45.83
7	Number of pods per plant	22.50	21.36	7.07	90.10	21.14	41.77
8	Number of seeds per pod	7.74	7.52	1.83	94.40	0.35	15.04
9	100-seed weight (g)	20.28	20.19	1.80	99.20	3.62	41.44
10	Dry matter weight per plant (g)	28.92	28.26	6.13	95.50	17.59	56.89
11	Harvest index (%)	17.85	17.01	5.42	90.08	10.70	42.78
12	Seed yield efficiency	26.85	23.38	13.21	75.80	0.20	41.94
13	Oil content (%)	11.40	11.32	1.40	98.50	4.10	23.14
14	Protein content (%)	3.91	3.83	0.76	96.30	3.12	7.74
15	Seed yield per plant (g)	30.94	30.51	5.11	97.30	6.06	61.99

and seed yield per plant (97.30%). High heritability values were also observed for plant height (96.50%), protein content (96.30%), dry matter weight per plant (95.50%), number of seeds per pod (94.40%), number of pods per plant (90.10%), harvest index (90.08%), days to maturity (83.10%), days to 50% flowering (81.80%), number of nodes per plant (80.60%), number of pod bearing nodes per plant (80.30%) and seed yield efficiency (75.80%). However, moderate heritability was observed for number of primary branches per plant (39.60%).

The estimates of genetic advance (%) were found to be highest and lowest for plant height (28.11%) and seed yield efficiency (0.20%), respectively. The values of genetic advance for the remaining characters were recorded as number of pods per plant (21.14%), dry matter weight per plant (17.59%), harvest index (10.70%), number of pod bearing nodes per plant (10.50%), days to maturity (9.66%), days to 50% flowering (6.92%), seed yield per plant (6.06%), number of nodes per plant (5.32%), oil content (4.10%), 100-seed weight (3.62%), protein content (3.12%), number of primary branches per plant (0.93%) and number of seeds per pod (0.30%).

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)

The estimates of genetic advance expressed as per cent of mean were observed to be highest for seed yield per plant (61.99%) followed by dry matter weight per plant (56.89%), plant height (47.93%), number of pod bearing nodes per plant (45.83%), harvest index (42.78%), seed yield efficiency (41.94%), number of pods per plant (41.77%), 100-seed weight (41.44%), number of nodes per plant (33.20%), oil content (23.14%) and number of primary branches per plant (22.98%). 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 moderate genetic advance as percent of mean were observed for number of seeds per pod (15.04%) and days to 50% flowering (14.39%), whereas days to maturity (9.66%) and protein content (7.74%) showed low estimates of genetic advance as per cent mean.

Majority of the characters under study including plant height (cm), number of nodes

per plant, number of pod bearing nodes per plant, number of pods per plant, 100-seed weight (g), dry matter weight per plant (g), harvest index (%), seed yield efficiency, oil content (%) and seed yield per plant (g) exhibited high values of heritability along with high estimates of genetic advance as per cent mean. 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 **Agrawal *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, number of seeds per pod, hundred seed weight 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)** and **Amrita *et al.* (2014)**.

High heritability coupled with moderate genetic advance as per cent mean was recorded for days to 50% flowering and number of seeds per pod. **Datt Shiv *et al.* (2011)** also reported high heritability and moderate genetic advance for days to 50% percent flowering. Moderate heritability coupled with high genetic advance as per cent mean was observed for number of primary branches per plant, which indicate the role of additive gene effects in the expression of such characters.

High heritability coupled with low genetic advance as per cent mean was observed for days to maturity and protein content 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. **Ramteke *et al.* (2010)** reported a high heritability and low genetic advance for protein content in soybean and suspected the influence of non-additive genetic effects for which he suggested heterosis breeding accompanied by population improvement strategies for the improvement of protein content in soybean.

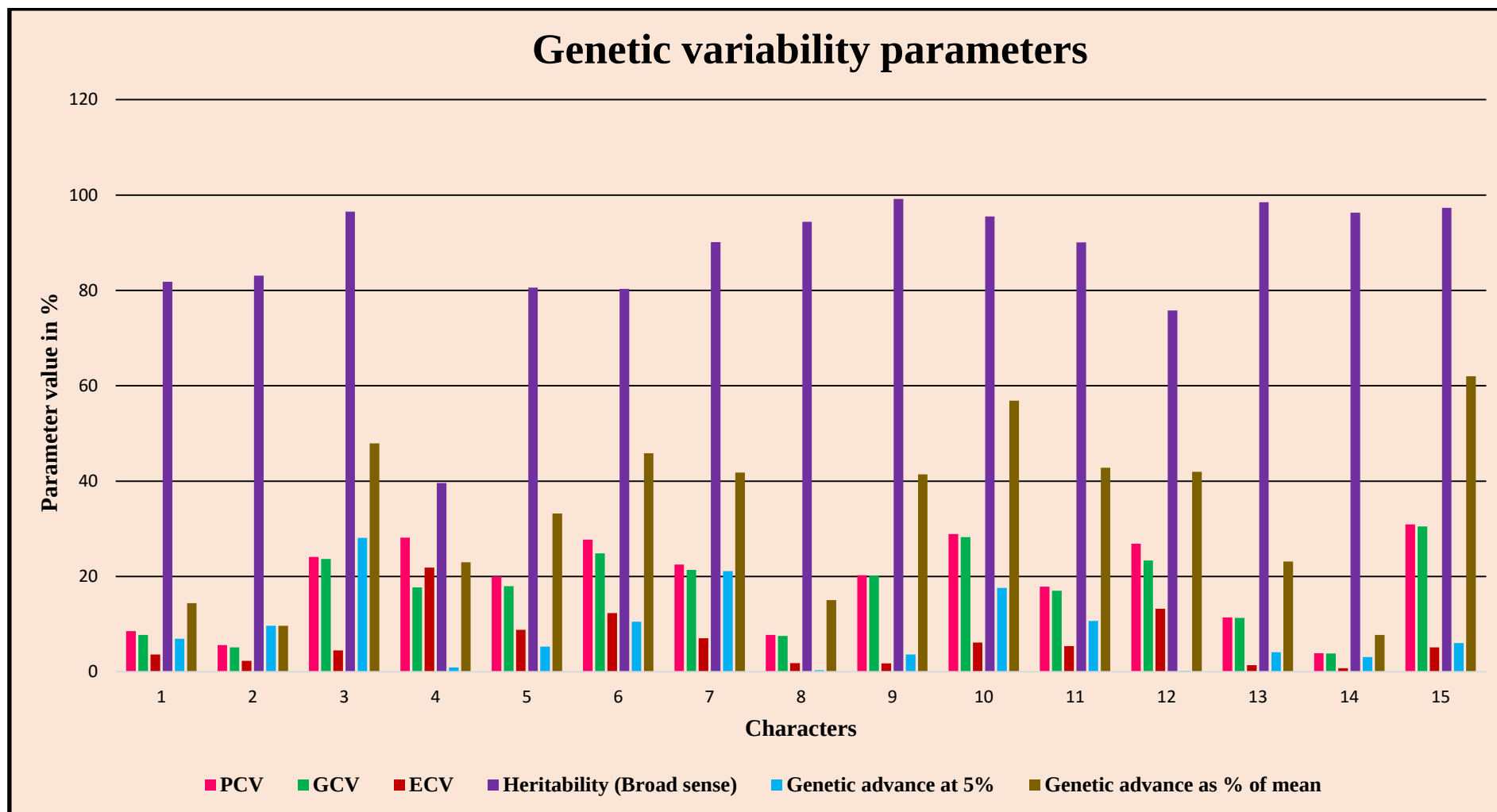


Figure 4.5.1: Histogram of Genetic variability parameters for different characters under study in soybean

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) and Jain and Ramgiry (2000). Datt Shiv *et al.* (2011)** reported high GCV accompanied with high heritability and genetic gain for number of pods per plant, moderate GCV coupled with high heritability and moderate genetic gain for days to 50% flowering and plant height, moderate GCV together with high heritability and low genetic gain for primary branches per plant, 100-seed weight and seed yield per plant, moderate GCV accompanied by moderate heritability and low genetic advance for seeds per pod.

4.6 Inter-character association (correlation) analysis

Seed yield in soybean is an extremely complex trait and is the resultant of expression and interaction between numerous plant growth components. Hence, a direct selection of genotypes for higher yield may not be much rewarding. It is well documented that seed yield is dependent on a number of yield attributes that are relatively less complex, simply inherited and are also interlinked in their action. Therefore, selection practiced for one such character may simultaneously bring about the changes in other related characters. Hence, the characters which exhibit a close association among themselves and also with seed yield, are easy to select with, facilitating not only the improvement of concerned characters but also seed yields ultimately. This information regarding the magnitude and direction of association between characters may be useful in the prediction of correlated response to directional selection in the construction of selection indices and also in the detection of few such characters which have no value in themselves but can act as indicators of desirable traits under consideration (**Johnson *et al.*, 1955**). Correlation is of high practical utility in plant breeding as it allows for simultaneous improvement of several characters that are interlinked. Correlation, therefore plays an important role in selecting the marker trait associated with higher manifestation of seed yield and also in bringing about the desired change in a particular character without provoking the others much, due to the absence of undesirable linkages. The results obtained from correlation analysis were presented in **Table 4.6.1** and also were discussed below.

Seed yield per plant showed a highly significant and positive correlation with most of the characters including dry matter weight per plant (0.785), number of pods per plant (0.728), number of primary branches per plant (0.610), number of pod bearing nodes per plant (0.542), 100-seed weight (0.416), seed yield efficiency (0.388), harvest index (0.339),

number of seeds per pod (0.309), number of nodes per plant (0.294), oil content (0.230) and plant height (0.215), This infers that a selection in positive direction for any of these characters could ultimately enhance the seed yield in soybean. However, the rest all showed non-significant positive interactions with seed yield per plant except protein content which showed a non-significant negative correlation.

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. These results reported were in agreement with that obtained during the present study. **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. 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) and Nagarajan et al. (2015).**

The two nutritional traits viz. oil content and protein content exhibited a highly significant and negative correlation with each other (-0.513), thereby suggesting that a positive selection for either of the two would have a resultant negative impact on the other. **Leffel and Rhodes (1993)** reported from a study that high-protein lines were inferior in terms of seed yield and oil concentration in soybean. **Schwender et al. (2003)** reported a relationship between oil and protein contents and they observed that a reduction in total oil content by 1% will lead to a 2% increase in total protein content. The results obtained in the present study were comparable with **Manjaya et al. (2007)** who evaluated 55 genotypes of soybean and reported a negative correlation between oil and protein contents. **Sharma et al. (2008)** also reported a negative correlation between oil and protein content based on the study of 74 genotypes of soybean. Several workers have reported similar findings including

Table 4.6.1: Correlation coefficients for fifteen quantitative characters in soybean

Character	DTF	DTM	PH (cm)	NBP	NNP	NPB	NPP	NSP	HSW (g)	DWP (g)	HI (%)	SYE	OC (%)	PC (%)	SYP (g)
DTF	1.000	0.394**	0.393**	0.173*	0.365**	0.294**	0.302**	-0.040	-0.246**	0.221**	-0.253**	-0.185*	0.017	-0.187*	0.111
DTM		1.000	0.226**	0.222**	0.291**	0.241**	0.136	0.100	-0.00001	0.231**	-0.124	-0.108	0.200**	-0.197*	0.140
PH (cm)			1.000	0.243**	0.474**	0.438**	0.346**	0.015	-0.135	0.318**	-0.033	-0.076	-0.049	-0.134	0.215**
NBP				1.000	0.325**	0.538**	0.582**	0.259**	0.111	0.527**	0.113	0.136	0.019	-0.005	0.610**
NNP					1.000	0.449**	0.313**	0.060	-0.118	0.363**	-0.202**	-0.064	-0.021	-0.095	0.294**
NPB						1.000	0.735**	0.078	-0.126	0.561**	-0.026	0.041	0.060	-0.090	0.542**
NPP							1.000	0.061	-0.153	0.679**	0.079	0.132	-0.010	0.008	0.728**
NSP								1.000	0.070	0.310**	0.098	-0.049	0.167*	-0.100	0.309**
HSW (g)									1.000	0.210**	0.360**	0.379**	0.274**	-0.146	0.416**
DWP (g)										1.000	-0.195*	-0.202**	0.143	-0.095	0.785**
HI (%)											1.000	0.880**	0.236**	-0.042	0.339**
SYE												1.000	0.170*	-0.045	0.388**
OC (%)													1.000	-0.513**	0.230**
PC (%)														1.000	-0.084
SYP (g)															1.000

** Significance at 1% level of probability; * Significance at 5% level of probability

Note: DTF= Days to 50% flowering; DTM= Days to maturity; PH= Plant Height; NBP= Number of primary branches per plant; NNP= Number of nodes per plant; NPB= Number of pod bearing nodes per plant; NPP= Number of pods per plant; NSP= Number of seeds per pod; HSW= Hundred seed weight; DWP= Dry matter weight per plant; HI= Harvest Index; SYE= Seed yield efficiency; OC= Oil content; PC= Protein content and SYP= Seed yield per plant.

Thorat *et al.* (2001); Ganesamurthy and Seshadri (2004); Malik *et al.* (2007); Ramteke *et al.* (2010) and Chandel *et al.* (2014).

Also, protein content exhibited a non-significant and negative correlation with seed yield as found in the present study. This observation was similar to **Salimi *et al.* (2013)** who also reported a negative and non-significant correlation between seed yield and protein content in soybean. Similar finding was also reported by **Patil *et al.* (2011)**. Highly significant and positive correlation was observed during the present study between 100-seed weight and oil content (0.274). This finding was similar with that of **Sharma *et al.* (1983)** who also observed a positive correlation between 100-seed weight and oil content. Also 100-seed weight exhibited a highly significant and positive correlation with harvest index (**Dubey *et al.*, 2015**), dry matter weight per plant and seed yield efficiency.

Number of pods per plant showed a highly significant and positive correlations with days to flowering, plant height, number of primary branches per plant, number of nodes per plant, number of pod bearing nodes per plant and dry matter weight per plant. Similar findings were reported by **Shrivastava *et al.* (1998); Pooran Chand (1999); Chamundeswari and Aher (2003); Sirohi *et al.* (2007) and Malek *et al.* (2014)**. In the present study, dry matter weight per plant also showed a highly significant and positive correlations with days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of nodes per plant, number of pod bearing nodes per plant, number of pods per plant, number of seeds per pod and 100-seed weight (**Jain *et al.*, 2015**), while exhibited strong negative correlation with harvest index (**Bhushan *et al.*, 2006**) and seed yield efficiency. **Shruti *et al.* (2015)** reported a strong positive correlation of dry matter yield with days to 50% flowering, plant height, branches per plant and 100-seed weight.

Highly significant and positive correlations were also observed between characters like plant height, number of primary branches per plant, nodes per plant and number of pod bearing nodes per plant (**Rajanna *et al.*, 2000; Ganeshmurthy and Seshadri, 2004; Nag *et al.*, 2007 and Showkat and Tyagi, 2010**) indicating that selection of any one among these characters would bring about a positive response among all others.

Therefore, it could be concluded from the present findings that plant height, number of primary branches per plant, number of nodes per plant, number of pod bearing nodes per plant, number of pods per plant, number of seeds per pod, 100-seed weight, dry matter weight per plant, harvest index and seed yield efficiency are the important attributes that

contributed towards higher yield. Hence, more emphasis should be given on these characters during selection for improving seed yields in soybean.

4.7 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 coefficients does not provide a reliable estimates 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. The results of various causes influencing seed yield per plant (direct and indirect effects) were summarized in the Table 4.7.1. The path coefficient is free of unit, and the concept of path correlation coefficient was originally developed by **Wright (1921)** but the technique was used by **Dewey and Lu (1959)**. The path coefficient analysis was carried out by taking seed yield per plant as a dependent variable and rest all characters as independent variables.

An overview of the path coefficient analysis indicated that, dry matter weight per plant exhibited the highest positive direct effect (0.757) on seed yield per plant, followed by seed yield efficiency (0.514) and number of pods per plant (0.147). Also, positive direct effects on seed yield were observed for 100-seed weight (0.108), number of seed per pod (0.057), number of primary branches per plant (0.052) and oil content (0.013). However, highest negative direct effect on seed yield per plant was exhibited by number of pod bearing nodes per plant (-0.048) followed by harvest index (-0.044), plant height (-0.027), days to maturity (-0.007) and days to 50% flowering (-0.003). Also, a low residual effect (0.024) observed on seed yield per plant indicated that the traits under study were adequate to study the effect on seed yield.

Also, strong positive correlations with seed yield were observed for seed yield efficiency, number of pods per plant, 100-seed weight, number of seeds per pod, number of primary branches per plant and oil content. The positive correlations of these characters with seed yield could be attributed primarily due to the direct effects exhibited by these characters on seed yield.

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**), number of pod clusters per plant, 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, 100-seed weight and oil content (**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**).

Number of pod bearing nodes per plant showed negative direct effects (-0.048) but its strong positive correlation with seed yield could be due to the indirect effects through dry matter weight per plant (0.415). Similarly for harvest index (-0.044) through seed yield efficiency (0.432) and for plant height (-0.027), days to maturity (-0.007) and days to 50% flowering (-0.003) through dry matter weight per plant (0.260, 0.169 and 0.136, respectively). These findings were similar to that of **Ganeshmurthy and Seshadri (2004) and Iqbal et al. (2010)** who reported negative direct effects for plant height and **Jain et al. (2015)** who reported negative direct effects for plant height and days to 50% flowering. Protein content, although, had direct positive effects (0.008) on seed yield per plant but it exhibited non-significant negative correlation with seed yield which could be attributed to the indirect negative effects through dry matter weight per plant (-0.086).

Therefore, it can be summarized from the present findings of path coefficient analysis that dry matter weight per plant, seed yield efficiency and number of pods per plant contributed maximum towards seed yield per plant through both direct and indirect effects, whereas number of pod bearing nodes per plant exhibited maximum direct as well as indirect effects on seed yield per plant.

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, 100-seed weight, dry matter weight per plant, seed yield efficiency and oil content 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.

Table 4.7.1: Path coefficient analysis showing direct and indirect effects of different quantitative characters on seed yield in soybean

Character	Correlation with SYP	Direct effects	Indirect effects via													
			DTF	DTM	PH (cm)	NBP	NNP	NPB	NPP	NSP	HSW (g)	DWP (g)	HI (%)	SYE	OC (%)	PC (%)
DTF	0.111	-0.003	-	-0.003	-0.011	0.009	0.003	-0.014	0.045	-0.002	-0.027	0.136	0.009	-0.030	0.0002	-0.002
DTM	0.140	-0.007	-0.001	-	-0.006	0.012	0.002	-0.012	0.020	0.006	0.00001	0.169	0.005	-0.050	0.003	-0.002
PH (cm)	0.215**	-0.027	-0.001	-0.001	-	0.013	0.003	-0.021	0.051	0.001	-0.015	0.230	0.0002	-0.016	-0.001	-0.001
NBP	0.610**	0.052	-0.0005	-0.001	-0.007	-	0.002	-0.026	0.086	0.015	0.012	0.402	-0.005	0.080	0.0003	-0.00004
NNP	0.294**	0.007	-0.001	-0.002	-0.013	0.017	-	-0.021	0.046	0.003	-0.013	0.258	0.008	0.005	-0.0003	-0.001
NPB	0.542**	-0.048	-0.001	-0.002	-0.012	0.028	0.003	-	0.108	0.004	-0.014	0.415	-0.0002	0.059	0.001	-0.001
NPP	0.728**	0.147	-0.001	-0.001	-0.009	0.030	0.002	-0.035	-	0.004	-0.016	0.510	-0.005	0.103	-0.0001	0.0001
NSP	0.309**	0.057	0.0001	-0.001	-0.0004	0.013	0.0004	-0.004	0.009	-	0.008	0.220	-0.007	0.012	0.002	-0.001
HSW (g)	0.416**	0.108	0.001	0.00001	0.004	0.006	-0.001	0.006	-0.022	0.004	-	0.203	-0.012	0.117	0.004	-0.001
DWP (g)	0.785**	0.757	-0.0005	-0.001	-0.008	0.028	0.002	-0.026	0.099	0.017	0.029	-	0.007	-0.094	0.002	-0.001
HI (%)	0.339**	-0.044	0.001	0.001	0.0001	0.006	-0.001	-0.0002	0.016	0.009	0.030	-0.116	-	0.432	0.003	-0.00004
SYE	0.388**	0.514	0.0002	0.001	0.001	0.008	0.0001	-0.006	0.029	0.001	0.025	-0.138	-0.037	-	0.002	0.0002
OC (%)	0.230**	0.013	-0.0001	-0.001	0.001	0.001	-0.0002	-0.003	-0.001	0.010	0.030	0.123	-0.010	0.073	-	-0.004
PC (%)	-0.084	0.008	0.001	0.001	0.004	-0.0003	-0.001	0.004	0.001	-0.006	-0.016	-0.086	0.000	0.012	-0.007	-

Residual effects = 0.024

Note: DTF= Days to 50% flowering; DTM= Days to maturity; PH= Plant Height; NBP= Number of primary branches per plant; NNP= Number of nodes per plant; NPB= Number of pod bearing nodes per plant; NPP= Number of pods per plant; NSP= Number of seeds per pod; HSW= Hundred seed weight; DWP= Dry matter weight per plant; HI= Harvest Index; SYE= Seed yield efficiency; OC= Oil content; PC= Protein content and SYP= Seed yield per plant.

4.8 Screening for disease reaction

All the 165 genotypes included in the present study were screened against three important diseases of soybean prevalent at this experiment station i.e., Yellow mosaic, Bacterial pustule and Rhizoctonia aerial blight. Disease rating of genotypes based on a 0-9 point scale of uniform method of disease rating was presented in Table 4.8.1 and also discussed in detail in the following section. Also, the results obtained were summarized in **Table 4.8.2**.

4.8.1 Yellow mosaic virus (YMV)

Yellow mosaic in soybean is caused by Mungbean Yellow Mosaic Virus (MYMV), belonging to the family *Geminiviridae* and Genus *Begomovirus* and is transmitted by white fly (*Bemisia tabaci*). It causes yellow mosaic disease in a number of leguminous crops in India and South-east Asia and was first described by **Nariani (1960)**. The most seriously affected leguminous crops are mung bean, black gram and soybean. In severe cases, yield losses may range from 70-80% (**Nene, 1972**). Since the application of plant protection chemicals to control the vector adds to the cost of cultivation and also it may have harmful effects on health due to the chemical residues in seeds. Hence, development of resistant varieties offers an ideal method of controlling this disease which is cost-effective as well as it renders the grain healthy for human consumption.

Earlier studies showed that the genotype UPSM-534 to be immune to this disease (**Singh et al., 1974**) and the resistance in this genotype is governed by two recessive genes viz. *rym*¹ and *rym*². The inheritance pattern of resistance follows the ratio 15:1 (susceptible: resistant) in the crosses where UPSM-534 is used as a donor (**Singh and Malick, 1978**). **Bhattacharya et al. (1999)** studied the inheritance of resistance for YMV in another resistant genotype *Glycine soja* and reported that the resistance was governed by a single dominant gene.

The results obtained from screening for disease resistance as presented in Table 4.8.2 showed that a disease rating of 1 was given for 33 genotypes, which indicated that up to 1% plants in each of these genotype were infected by YMV. Disease rating of 3 was noted for 20 genotypes indicating that about 1.1 to 10% plants among such infected genotypes showed symptoms for the disease. Similarly, ratings of 5, 7 and 9 were recorded for 39, 41 and 32 genotypes, respectively, indicating 10.1 to 25%, 25.1 to 50% and more than 50% infected

plants, respectively, among such infected genotypes. None among all the evaluated genotypes was found immune (disease rating of 0). A highly susceptible variety, JS 335 (with a disease rating of 7) was planted in infector rows on both the sides of the experimental block to apply a uniform pressure of disease inoculum on the experimental material.

4.8.2 Bacterial pustule (BP)

Bacterial pustule is an important bacterial disease of soybean caused by gram-negative aerobic bacterium, *Xanthomonas axonopodis* pv. *glycines* and it causes premature defoliation with reduced seed size. The results obtained in the present study showed that none of the genotypes was assigned a disease rating of 0, indicating no immune reaction for any genotype. Whereas, disease rating of 1 was noted for 163 genotypes, which shows that about 1% of leaf area is infected with bacterial lesions among such genotypes. No genotypes were assigned a rating of 3 and 9, while a disease rating of 5 and 7 was recorded for one genotype each (EC 398148 and EC 39362), respectively indicating 10.1 to 25% and 25.1 to 50% of infected leaf area with lesions, respectively, resulting in little and conspicuous damage by the disease among the concerned genotypes.

4.8.3 Rhizoctonia aerial blight (RAB)

Rhizoctonia aerial blight is a fungal disease in soybean caused by a Basidiomycetes fungus, *Rhizoctonia solani* and can cause extensive yield losses (40-50%) under favourable conditions. The present revealed that none of the genotypes was rated as immune (disease rating of 0) for this disease. Only 2 genotypes (PS 1225 and PS 1480) were assigned a rating of 1, which showed only 1% infected lesions on the leaf area. A rating of 3 was noted for 79 genotypes which showed no spot on stem but 1.1 to 10% leaf area covered with lesions, 59 genotypes were given a rating of 5 that showed 10.1 to 25% infected lesions on leaves with little overall damage, 21 genotypes were found to be susceptible which were given a rating of 7 in which 25.1 to 50% of leaf area was infected with lesions and suffered conspicuous damage by the disease. Whereas, a disease rating of 9 was recorded for 4 genotypes [AMS 155 (A), TGX 855-39E, AMS 62 and AMS 210-6] that showed more than 50% damage, with all the infected plants being succumbed to death by the disease.

Hence, it can be concluded from the present study that, only 2 genotypes (PS 1225 and PS 1480) showed a disease rating of 1 and were classified as highly resistant for all the three diseases i.e., YMV, BP and RAB. This indicated that these genotypes should give high

Table 4.8.1: Disease reaction scored against YMV, RAB and BP in 165 genotypes of soybean

S.No.	Genotype	Disease reaction		
		YMV	BP	RAB
1	AGS 129	9	1	3
2	EC 389148	3	5	5
3	Jupiter	5	1	3
4	T-49	5	1	3
5	P RAB 1	1	1	3
6	AMS 155 (A)	9	1	9
7	TGX 855-39E	9	1	9
8	AMS 77-3-6	7	1	5
9	AMS 2005-19	9	1	5
10	EC 16738	9	1	5
11	EC 37937	9	1	5
12	EC 39362	5	7	5
13	EC 39491	5	1	7
14	EC 65772	7	1	7
15	RVS 2006-27	9	1	5
16	EC 95291	3	1	5
17	EC 100027	7	1	7
18	IC 13051	9	1	7
19	EC 14626	7	1	5
20	JS 82	7	1	3
21	PI 283327	7	1	3
22	PK 765	7	1	7
23	MACS 993	7	1	3
24	GP 305	9	1	3
25	RPSP 935-E	7	1	7
26	GP 465	7	1	5
27	Himso 175	9	1	7
28	GP 448	9	1	7
29	WT 150	7	1	5
30	MAUS 76	7	1	5
31	MAUS 102	7	1	5
32	MAUS 489	7	1	5
33	MAUS 38	5	1	5

S.No.	Genotype	Disease reaction		
		YMV	BP	RAB
34	MAUS 85	7	1	5
35	MAUS 149	3	1	3
36	AMS 2005-24	9	1	5
37	MAUS 164	5	1	3
38	EC 963805	9	1	5
39	EC 281462	7	1	5
40	EC 116343	7	1	5
41	EC 172607	9	1	7
42	EC 33940	5	1	3
43	EC 2581	3	1	3
44	EC 118443	5	1	3
45	RKS 30	7	1	3
46	RKS 27	5	1	3
47	AMS 243-7-3	5	1	3
48	AMS 42	5	1	3
49	AMS 50B	3	1	3
50	Kalitur	7	1	5
51	AMS -25-5-1	7	1	5
52	AMS 100-25-5	7	1	5
53	AMS 100	7	1	3
54	AMS 115	7	1	3
55	AMS 2005-13	9	1	5
56	AMS MB 5-19	9	1	5
57	AMS MB 5-18	9	1	5
58	AMS 56	9	1	5
59	AMS 59	9	1	5
60	AMS 38-24	3	1	3
61	EC 685243	1	1	3
62	RVS 2006-19	3	1	5
63	EC 457174	1	1	3
64	IC 437079	1	1	3
65	SL 983	1	1	3
66	K 88-262A	1	1	3

S.No.	Genotype	Disease reaction		
		YMV	BP	RAB
67	GP 393	1	1	3
68	GP 67	1	1	3
69	SL(E) 1	1	1	3
70	AGS 751	1	1	3
71	DT 21	1	1	3
72	Cat. 118	5	1	3
73	Cat. 50 (A)	7	1	3
74	Cat. 209	7	1	3
75	Cat. 142	5	1	3
76	Cat. 133	5	1	3
77	Cat. 886	7	1	5
78	Cat. 305	7	1	7
79	Cat. 2503	3	1	7
80	Cat. 780	5	1	5
81	Cat. 148	9	1	7
82	Cat. 3284	9	1	5
83	Cat. 2430	9	1	7
84	Cat.103	9	1	7
85	Cat. 537	7	1	5
86	Cat. 366	5	1	3
87	Cat. 3327	5	1	3
88	Cat. 783	3	1	3
89	Cat. 181	1	1	7
90	Cat. 307	5	1	7
91	Cat. 195	5	1	3
92	Cat. 2388	9	1	5
93	EC 2581	5	1	3
94	RVS 2002-6	7	1	5
95	RVS 2002-7	3	1	3
96	MACS 993	7	1	3
97	RVS 2006-1	3	1	3
98	EC 457161	1	1	3
99	Chocolate Bold	5	1	3

Contd....

Table 4.8.1 Concluded

S.No.	Genotype	Disease reaction		
		YMV	BP	RAB
100	Cat. 2755	3	1	5
101	IC 49685	5	1	3
102	Cat 2511	5	1	3
103	Cat. 779	7	1	3
104	Cat. 710	3	1	5
105	Cat. 891	1	1	3
106	Cat. 340	5	1	5
107	Cat. 805	7	1	5
108	F4P21	5	1	5
109	MACS 303	5	1	5
110	G 620	7	1	5
111	G5P22 (PI)	5	1	5
112	EC 457198	3	1	5
113	Cat. 135A	5	1	5
114	Cat. 902	3	1	3
115	G 11	5	1	7
116	Cat. 746	7	1	5
117	Cat. 938	5	1	3
118	PP 6 (PI)	1	1	3
119	PS 1024	1	1	3
120	Typical Bhatt (B)	7	1	3
121	PK 327	3	1	3
122	PS 564	1	1	3
123	PS 1225	1	1	1
124	PS 1551	1	1	3
125	PS 1480	1	1	1
126	Shilajeet	1	1	3
127	Ankur	1	1	3
128	PS 1029	1	1	3
129	Alankar	1	1	3
130	PK 416	1	1	3
131	PK 262	1	1	3
132	PS 19	1	1	3

S.No.	Genotype	Disease reaction		
		YMV	BP	RAB
133	AMS 100-16-4-1-3	3	1	3
134	EC 250608	5	1	5
135	JS 20-41	3	1	5
136	EC 251358	7	1	3
137	JS 20-27	5	1	5
138	JS 20-61	7	1	3
139	JS 20-34	3	1	7
140	JS 20-38	5	1	7
141	JS 20-30	5	1	3
142	AMS 62	9	1	9
143	EC 250619	9	1	7
144	JS 20-75	9	1	5
145	JS 20-60	9	1	5
146	JS 20-21	5	1	5
147	JS 20-31	5	1	5
148	JS 20-23	7	1	5
149	EC 396053	9	1	5
150	EC 250607	9	1	7
151	EC 325099	9	1	5
152	JS 20-29	1	1	5
153	JS 20-25	7	1	3
154	JS 20-51	5	1	3
155	JS 20-54	7	1	3
156	JS 20-79	5	1	3
157	JS 20-53	3	1	5
158	JS 20-52	1	1	3
159	AMS 77-3	7	1	5
160	AMS 210-6	9	1	9
161	SL 688 (C)	5	1	3
162	PS 1347 (C)	1	1	3
163	PS 1092 (C)	1	1	3
164	Bragg (C)	1	1	3
165	PS 1042 (C)	1	1	3

Note:

YMV = Yellow Mosaic Virus

BP = Bacterial Pustule

RAB = Rhizoctonia Aerial Blight

Table 4.8.2: Summary of Disease reaction studies against YMV, BP and RAB among 165 genotypes of soybean

Yellow Mosaic Virus (YMV)		Bacterial Pustule (BP)		Rhizoctonia Aerial Blight (RAB)	
Disease reaction score	No. of genotypes	Disease reaction score	No. of genotypes	Disease reaction score	No. of genotypes
0	0	0	0	0	0
1	33	1	163	1	2
3	20	3	0	3	79
5	39	5	1	5	59
7	41	7	1	7	21
9	32	9	0	9	4
Total	165	Total	165	Total	165

and stable seed yields since they only suffered a very little plant damage by the disease. 31 genotypes showed a disease rating of 1 for YMV and BP and were found to be highly resistant for these two diseases, also suggesting a little damage among such genotypes and should also be comparatively stable in yield performance. The rest of all genotypes suffered considerably to major damage due to one or the other among the three diseases and hence, showed moderate to high losses in terms of overall seed yield. Among all the genotypes evaluated AMS 62, AMS 210-6, EC 250607, EC 250619, AMS 155 (A), TGX 855-39E, IC13051, Himso 175, GP 448, EC 172607, Cat 148, Cat 103, Cat 2430 were found to be highly susceptible to YMV and RAB but highly resistant to BP. **Singh *et al.* (1974)** screened 1014 and 3047 accessions of soybean collected from different parts of the globe for rust and YMV resistance and they reported a highly immune genotype PI 171443 (UPSM-534) for YMV. **Sharma *et al.* (1993)** screened 20 genotypes against Bacterial pustule and reported that 2 genotypes (P- 169-3 and P-4-2) showed complete resistance whereas, 4 genotypes (Bragg, Kalitur, EC 34160 and PK 472) showed moderate resistance to this disease. **Suryadi *et al.* (2012)** reported 43 resistant, 41 moderately resistant, 14 moderately susceptible and 2 susceptible genotypes, while screening 100 genotypes for resistance to bacterial pustule. **Kumar *et al.* (2014)** screened 500 genotypes against YMV and reported 21 genotypes including PS 1042, UPSM 534 and PK 1347 showed stable resistance against YMV consecutively for three years. **Baruah *et al.* (2014)** evaluated 44 genotypes of soybean against Yellow mosaic virus (YMV) resistance and reported that one genotype (JS 335) was highly susceptible for YMV, while 2 genotypes (DS 9712 and DS 9814) were found to be highly resistant for the disease. **Kumar *et al.* (2016)** screened 42 accessions against the

aerial blight caused by *Rhizoctonia solani* and reported 2 accessions (SL 752 and RKS 48) to be absolutely resistant and 6 accessions to be highly resistant to the pathogen. Similar studies were reported by **Talukdar *et al.* (2013)** and **Ingle *et al.* (2016)** in soybean.

A variable expression for disease reaction in terms of susceptibility and resistance among the experimental material for three different diseases viz. YMV, BP and RAB was confirmed from the above findings. Therefore, it can be affirmed from the present study that there exists considerable amounts of genetic variability among the experimental material for resistance towards these three diseases. Also, it can be concluded from the present study that the genotypes PS 1225 and PS 1480 which manifested high resistance against all three diseases could be used as promising donors in breeding for resistant varieties which offers a cheap and stable source of resistance as well as prevent yield losses in soybean.

4.9 Bio-chemical profiling of genotypes

Based on the estimates of protein content among the 165 genotypes, 11 genotypes were randomly selected to study the diversity in protein content using SDS-PAGE. These genotypes were arbitrarily classified into three different categories based on their protein content:

- a) Typical Bhatt (B), EC 389148, PS 1092, Cat 2503 and EC 39491 (> 42% protein)
- b) RVS 2002-7, RVS 2002-6 and PS 1042 (40-42% protein)
- c) SL (E) 1, PS 1024 and PK 416 (<40% protein)

The total seed protein content was extracted from 11 genotypes of soybean as per the procedures given in methodology section 3.5 and further quantified using **Bradford (1976)** method. Equal amount of protein i.e., 20 µg was loaded into each well and further subjected to gel electrophoresis.

A medium range marker (97.4kDa, 66.0kDa, 43.0kDa, 29.0kDa, 20.1kDa and 14.3kDa) was used along with a 15% SDS-PAGE gel (**Laemmli, 1970**) which is capable of resolving polypeptides and proteins ranging from 3 kDa to 100 kDa. The protein profile of 11 genotypes obtained through SDS-PAGE detected a total of 18 bands ranging from 10kDa to 100kDa. About 10 major bands were detected in all the genotypes approximately of molecular weights 83.19, 78.62, 74.34, 57.49, 53.91, 43.74, 38.74, 21.23, 15.67 and 14.43 kDa. The rest of the bands were found to be polymorphic with majority of them being minor

bands. However, two major bands also showed polymorphism with the band of approximate molecular weight 33.23 kDa absent in Typical Bhatt (B) and the band at 19.59 kDa showing low expression in PS 1024.

A total of 5 out of the 11 genotypes evaluated were found to show variable expression in polypeptide bands with a few bands absent in certain genotypes. The band with an approximate molecular weight of 62.3 kDa was not detected in the genotypes EC 389148, EC 39491 and Typical Bhatt (B) but was found in rest all genotypes as detected by Coomassie brilliant blue staining. Cat 2503 did not showed a band at 64.0 kDa region which was found among the other genotypes. Although, there existed significant differences among the 11 selected genotypes in terms of their protein contents, the results obtained from SDS=PAGE revealed that only a low level of polymorphism was observed among the genotypes using 1-Dimensional SDS-PAGE. Typical Bhatt (B) and PS 1024 could be differentiated from the rest of the genotypes, but however, the protein profiles showed only minute qualitative differences among the remaining 9 genotypes which could not be used for their identification. However, the banding pattern of 11 genotypes obtained in the present study could be used as a general bio-chemical fingerprint of the concerned genotypes.

Bonfitto *et al.* (1999) also reported low level of polymorphism among melon genotypes using SDS-PAGE and he attributed this to the conservative nature of seed protein. Low polymorphism among the protein profiles of soybean was also reported by **Adjukovic *et al.* (2007)** who evaluated 20 genotypes of soybean and found similarity in their polypeptide banding pattern. **Iqbal *et al.* (2005)**. Even though SDS-PAGE was reported by many workers (**Jha and Ohri, 1996; Mennella *et al.*, 1999 and Emre *et al.*, 2007**) as an ideal tool to differentiate between genotypes of a particular crop with respect to their protein content, however few studies do indicate that cultivar identification was not possible with the SDS-PAGE method (**Ahmad and Slinkard, 1992 and De Vries, 1996**).

Hence, it can be concluded from the present findings that in order to further differentiate the genotypes at their polypeptide level, 2-Dimensional electrophoresis is further suggested along with marker technology for accurate detection of polymorphism among the concerned genotypes. Similar conclusions were also given by **Alege *et al.* (2014)** while studying the protein profiles of members of Fabaceae and **Iqbal *et al.* (2005)** who reported low level of polymorphism using SDS-PAGE while working with chick pea.

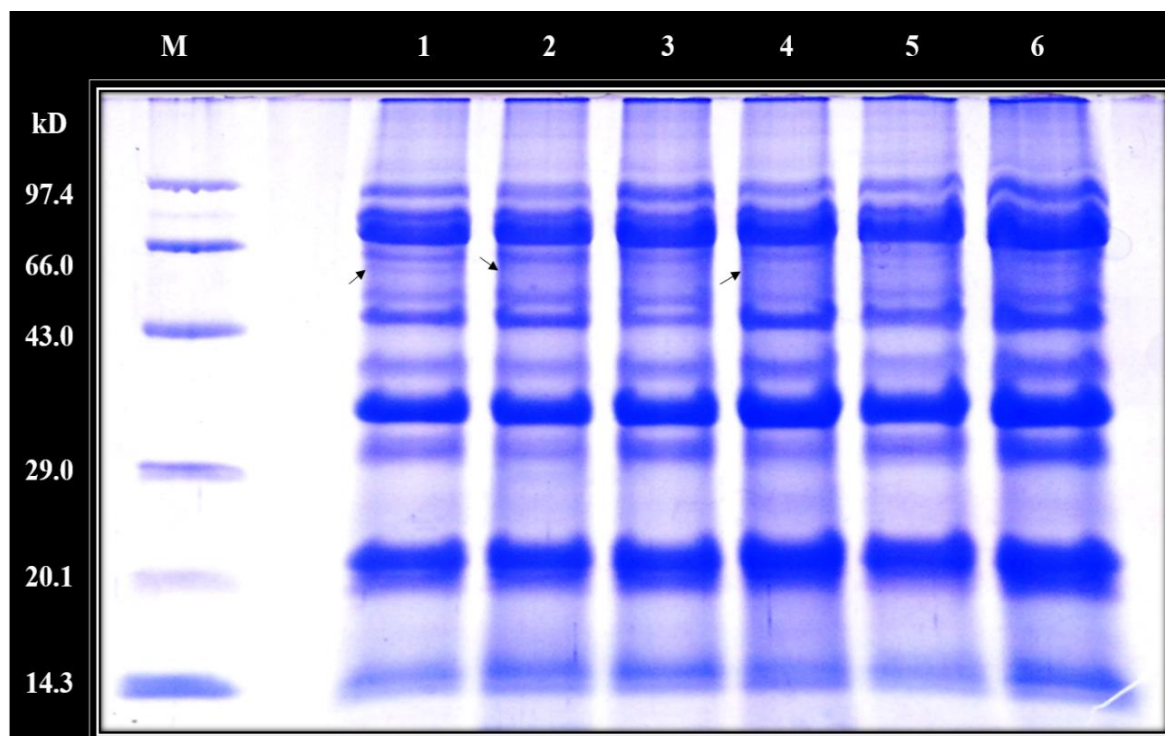


Figure 4.9.1: SDS-PAGE of total seed protein in 6 genotypes of soybean
 Sequence: M-Marker, 1-PS 1092, 2- EC 389148, 3-RVS 2002-7, 4-EC 39491, 5-PS 1042, 6-RVS 2002-6

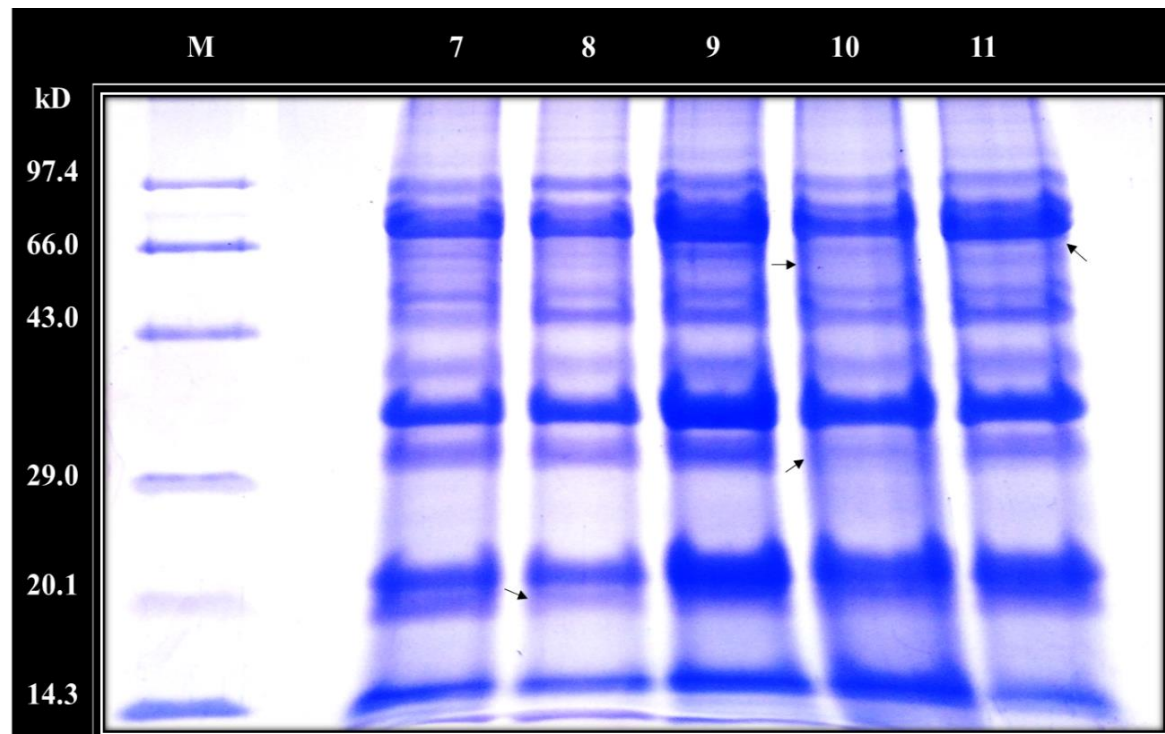


Figure: 4.9.2: SDS-PAGE of total seed protein in 5 genotypes of soybean
 Sequence: M-Marker, 7-SL (E) 1, 8- PS 1024, 9-PK 416, 10-Typical Bhatt (B), 11-Cat 2503

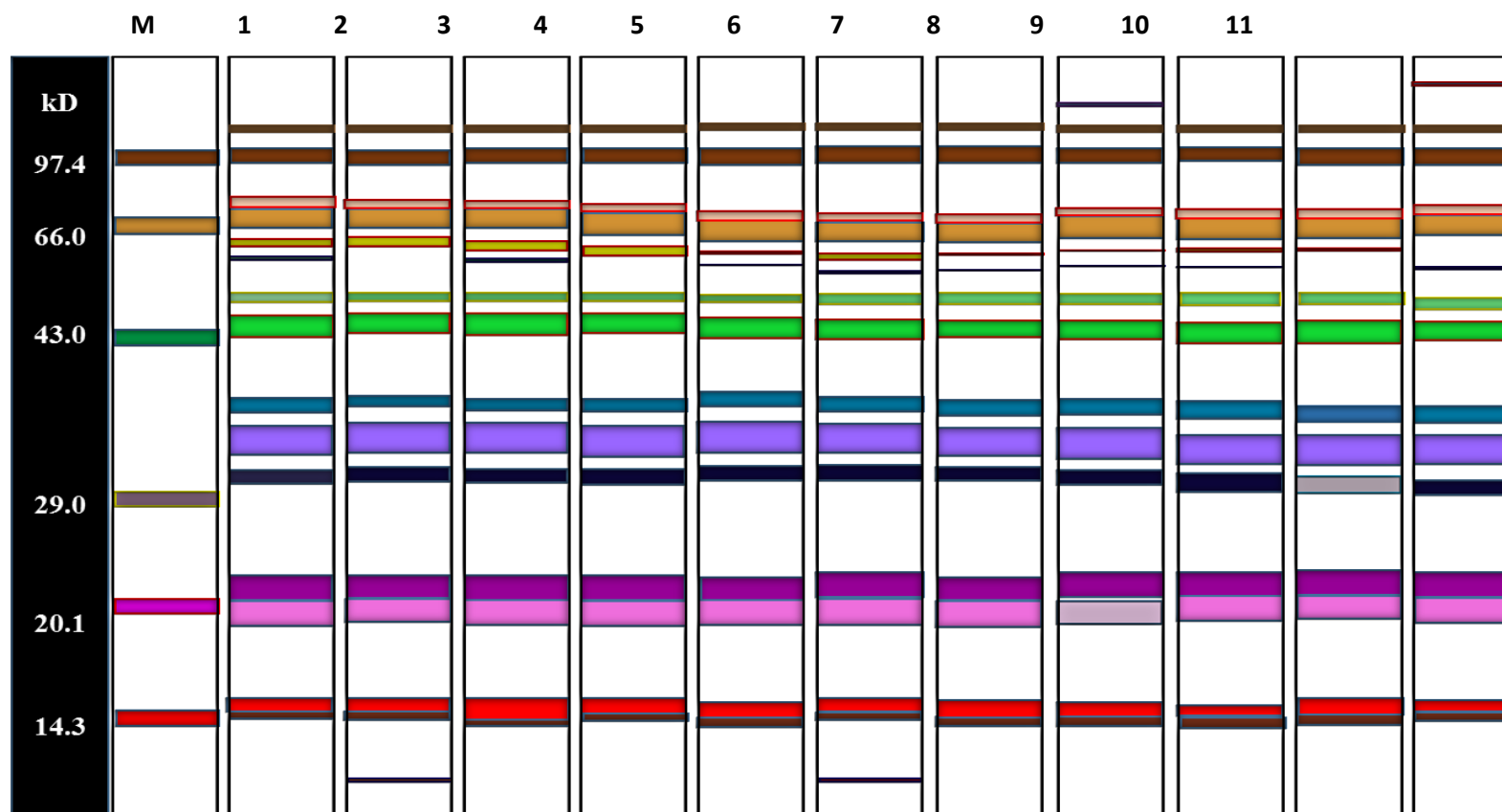


Figure 4.9.3: Pictorial representation of banding pattern in protein profile of eleven genotypes of soybean obtained through SDS-PAGE
Sequence: M-Marker, 1-PS 1092, 2- EC 389148, 3-RVS 2002-7, 4-EC 39491, 5-PS 1042, 6-RVS 2002-6, 7-SL (E) 1, 8- PS 1024, 9-PK 416, 10-Typical Bhatt (B) and 11-Cat 2503.

Breeding Implications

In the light of the results presented and discussed above, based on the inter-cluster distance, cluster mean values and *per se* performance, the genotypes PS 1225, AMS 100-16-4-1-3, JS 20-79, Jupiter, Cat 209, SL (E) 1 and AMS 50B could be used as potential donors in the following parental combinations i.e., PS 1225 x Jupiter, PS 1225 x JS 20-79, PS 1225 x Cat 209, PS 1225 x SL (E) 1, PS 1225 x AMS 100-16-4-1-3, Jupiter x JS 20-79, Jupiter x Cat 209, Jupiter x AMS 100-16-4-1-3, JS 20-79 x Cat 209, JS 20-79 x SL (E) 1, JS 20-79 x AMS 100-16-4-1-3, Cat 209 x SL (E) 1, Cat 209 x AMS 100-16-4-1-3, SL (E) 1 x AMS 100-16-4-1-3 to improve the yield attributes, while the parental combinations Jupiter x SL (E) 1 and Cat 209 x AMS 50B could be exploited to obtain superior segregants for oil and protein contents, respectively. These combinations are expected to result in maximum hybrid vigour and highest number of useful segregants for yield improvement during the process of selection in soybean. Also, the two highly resistant genotypes viz. PS 1225 and PS 1480 identified during the present study could be used as donors in breeding for resistant varieties against YMV, BP and RAB which could reduce potential yield losses in soybean. Also, it could be suggested that, number of primary branches per plant, number of nodes per plant, number of pods per plant, number of seeds per pod, 100-seed weight, dry matter weight per plant, seed yield efficiency and oil content should be given the prime consideration for yield improvement in soybean.

Branching ability should be considered as an important trait when selecting varieties of high yield potential for tropical and sub-tropical environments. Poor plant stand is commonly observed in soybean fields of tropical and sub-tropical areas, and, therefore, it may be desirable to breed soybean varieties for more branching ability. High branching varieties may have the ability to compensate for poor plant stand by producing more branches per plant under low plant competition. The present study suggests that the plants with intermediate height (75-90 cm), with 8-10 branches per plant, determinate growth habit, narrow leaves and seed size in the range of 12-15g per 100-seeds seem to be the ideal types for tropical regions.

A decorative border resembling a scroll, with a green line and grey circular accents at the corners and along the left edge.

SUMMARY AND CONCLUSIONS

The present investigation entitled, “Studies on genetic parameters for quantitative and qualitative traits in soybean [*Glycine max* (L.) Merrill]” was conducted with 165 genotypes of soybean (including 5 checks) at N.E. Borlaug Crop Research Centre, G. B. Pant University of Agriculture and Technology, Pantnagar, during *Kharif, 2014*. The experimental material was planted in an augmented design-II with 4 blocks, each consisting of 40 test entries and 5 checks (SL 688, PS 1347, PS 1092, Bragg, and PS 1042) planted randomly and in which only checks were repeated in each block.

The objectives of the present study were to estimate the genetic divergence and genetic variability, study the inter-character correlation and their direct and indirect effects on seed yield, identify suitable donors for yield attributes, screen the genotypes against resistance to YMV, BP and RAB and to study the protein profiles of selected genotypes using SDS-PAGE to evaluate the diversity in protein content in soybean.

The data were recorded for twenty three quantitative as well as qualitative characters which included morphological, derived and nutritional traits, during the present study. The data pertaining to the metric characters were subjected to statistical analyses to derive information on genetic diversity, variability, heritability, expected genetic advance, correlation co-efficients and their direct and indirect effects. The major findings of the present investigation were summarized below.

- ❖ A total of 8 qualitative characters were taken up for the present study. All the 165 genotypes were classified into different groups with respect to each qualitative trait under study. The genotypes were categorized into different groups as i) Germination: good (156), fair (5) and poor (4). ii) Leaf colour: green (152), dark green (13). iii) Leaf shape: pointed ovate (157), lanceolate (6) and round ovate (2). iv) Pubescence colour: tawny (146) and grey (19). v) Flower colour: purple (84) and white (81). vi) Pod colour: brown (144), yellow (19) and black (2). vii) Seed coat colour: yellow (161), brown (3) and black (1). viii) Hilum colour: brown (87), black (52) and yellow (26).
- ❖ The analysis of variance revealed significant differences among genotypes for most of the characters under study. which showed the existence of significant amounts of variability among the experimental material and hence, a greater scope for

improvement of concerned characters through selection.

- ❖ A moderate to wide range of mean values among the genotypes for different characters like days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of nodes per plant, number of pod bearing nodes per plant, number of pods per plant, number of seeds per pod, 100-seed weight, dry matter per plant, harvest index, seed yield efficiency, oil and protein contents and seed yield per plant also indicated a wide variability among the experimental material and thereby offered a promising scope for the improvement of different yield attributes in soybean.
- ❖ Genetic diversity analysis revealed that the entire experimental material under study could be grouped into 10 clusters. Cluster VII was found to be largest which included 124 genotypes followed by Clusters III (9), IV (8), V (7), X (5), VIII (4), II and IX (3) with the least number of genotypes included in Clusters I and VI (1). The distribution pattern of 165 genotypes into different clusters indicated no parallelism between geographical isolation and genetic diversity.
- ❖ The maximum and minimum intra-cluster distance was observed within the Cluster X (27.10) and Clusters I and VI (0.00), respectively. Whereas, highest inter-cluster distance was observed between Clusters II and III (91.59) followed by Clusters I and IX (79.32) and III and X (78.13), indicating that genetic crosses between genotypes obtained from these clusters would manifest high heterosis and also generate high variability among the segregating generations, which further facilitates selection for the improvement of concerned characters in soybean. However, least inter-cluster distance was observed between Clusters IV and V (33.06).
- ❖ On the basis of genetic divergence analysis, cluster mean values and *per se* performance, the following genotypes were found most desirable to be exploited as superior donors in hybridization programs for the improvement of different yield attributes in soybean. They include, JS 20-34, JS 20-38, Cat 209, JS 20-35 and RVS 2006-1 (early flowering), T-49, Typical Bhatt (B), RKS 30, P RAB 1 and EC 16738 (late flowering), G5P22 (PI), Cat 209, EC 250607, EC 39491, JS 20-51 and AMS 77-3 (early maturity), MACS 993 and Kalitur (late maturity), Shilajeet, PS 1024, G5P22 (PI) and PS 19 (dwarf plant type), Jupiter, AMS 100-25-5 and Kalitur (tall plant type), PS 1225, AMS 100-16-4-1-3 and Cat 902 (number of primary branches

per plant), Kalitur, Jupiter and T-49 (number of nodes per plant), Cat 902, AMS 100-25-5 and IC 13051 (number of pod bearing nodes per plant), AMS 100-16-4-1-3, PS 1225, MACS 993 and JS 20-79 (number of pods per plant), AMS 42, EC 250619 and JS 20-73 (number of seeds per pod), JS 20-79, AGS 751, Cat 2755, AMS 38-24, PK 262, EC 685243 and EC 457174 (100-seed weight), AMS 100-16-4-1-3, JS 20-79, AMS 50B and MACS 993 (dry matter weight per plant), Cat 118, AGS 751, DT 21, SL (E)1 and AMS 59 (harvest index), IC 13051, MAUS 102, MACS 1394, PS 1225 and PI 283327 (seed yield efficiency), JS 20-23, SL (E)1, RVS 2002-7, Jupiter, GP 393 and PS 1480 (oil content), GP 305, EC 37937, Cat 2503, Typical Bhatt (B), Cat 209 and AMS 50B (protein content), PS 1225, AMS 42 and JS 20-79 (seed yield per plant). These genotypes were also found superior to the best check for majority of the characters.

- ❖ The magnitudes of PCV were higher than that of GCV for all the characters under study. ECV showed a meagre contribution towards PCV for majority of the characters. PCV and GCV together with genetic advance as per cent of mean were observed to be highest for seed yield per plant followed by dry matter weight per plant, whereas the lowest values for PCV and GCV were observed for protein content followed by number of seeds per pod. The highest and lowest values of ECV were observed for number of primary branches per plant and protein content, respectively.
- ❖ Higher magnitudes coupled with a greater correspondence of the values of GCV with PCV for characters like plant height, number of nodes per plant, number of pod bearing nodes per plant, number of pods per plant, 100-seed weight, dry matter weight per plant, harvest index, seed yield efficiency and seed yield per plant revealed the existence of high variability and hence, improvement of such characters through selection based on phenotype should be rewarding.
- ❖ High estimates of heritability were observed for majority of the characters included in the present study, except number of primary branches per plant which showed only moderate heritability. Highest value of heritability was observed for 100-seed weight, followed by oil content, seed yield per plant, plant height, protein content, dry matter weight per plant, number of seeds per pod, number of pods per plant, harvest index, days to maturity, days to 50% flowering, number of nodes per plant,

number of pod bearing nodes per plant and seed yield efficiency which suggested that, selection of these characters based on phenotype performance should be effective.

- ❖ The estimates of genetic advance (%) were found to be highest and lowest for plant height (28.11%) and seed yield efficiency (0.20%), respectively. The estimates of genetic advance for the remaining characters were found to be, number of pods per plant (21.14%), dry matter weight per plant (17.59%), harvest index (10.70%), number of pod bearing nodes per plant (10.50%), days to maturity (9.66%), days to 50% flowering (6.92%), seed yield per plant (6.06%), number of nodes per plant (5.32%), oil content (4.10%), 100-seed weight (3.62%), protein content (3.12%), number of primary branches per plant (0.93%) and number of seeds per pod (0.30%).
- ❖ High estimates of heritability coupled with high genetic advance as per cent of mean were recorded for characters like plant height, number of nodes per plant, number of pod bearing nodes per plant, number of pods per plant, 100-seed weight, dry matter weight per plant, harvest index, seed yield efficiency, oil content and seed yield per plant, which clearly indicated a preponderance of additive gene effects in the expression of such characters. Hence, selection for these characters in early segregating generations should be rewardable. High values of GCV coupled with high heritability and genetic gain were observed for plant height, number of pod bearing nodes per plant, number of nodes per plant, number of pods per plant, 100-seed weight, dry matter weight per plant, seed yield efficiency and seed yield per plant.
- ❖ Moderate GCV together with high heritability and genetic advance as per cent of mean was reported for number of nodes per plant, harvest index and oil content. Low GCV coupled with high heritability and moderate genetic advance as per cent mean was reported for days to 50% flowering and number of seeds per pod whereas, moderate levels of GCV and heritability accompanied by high genetic advance as per cent mean were observed for number of primary branches per plant, all of which indicated additive gene action. However, low GCV coupled with high heritability and low genetic advance as per cent mean was recorded for days to maturity and protein content, which indicated an influence of dominant effects on the expression of such characters and hence, progeny testing or heterosis breeding could be utilized

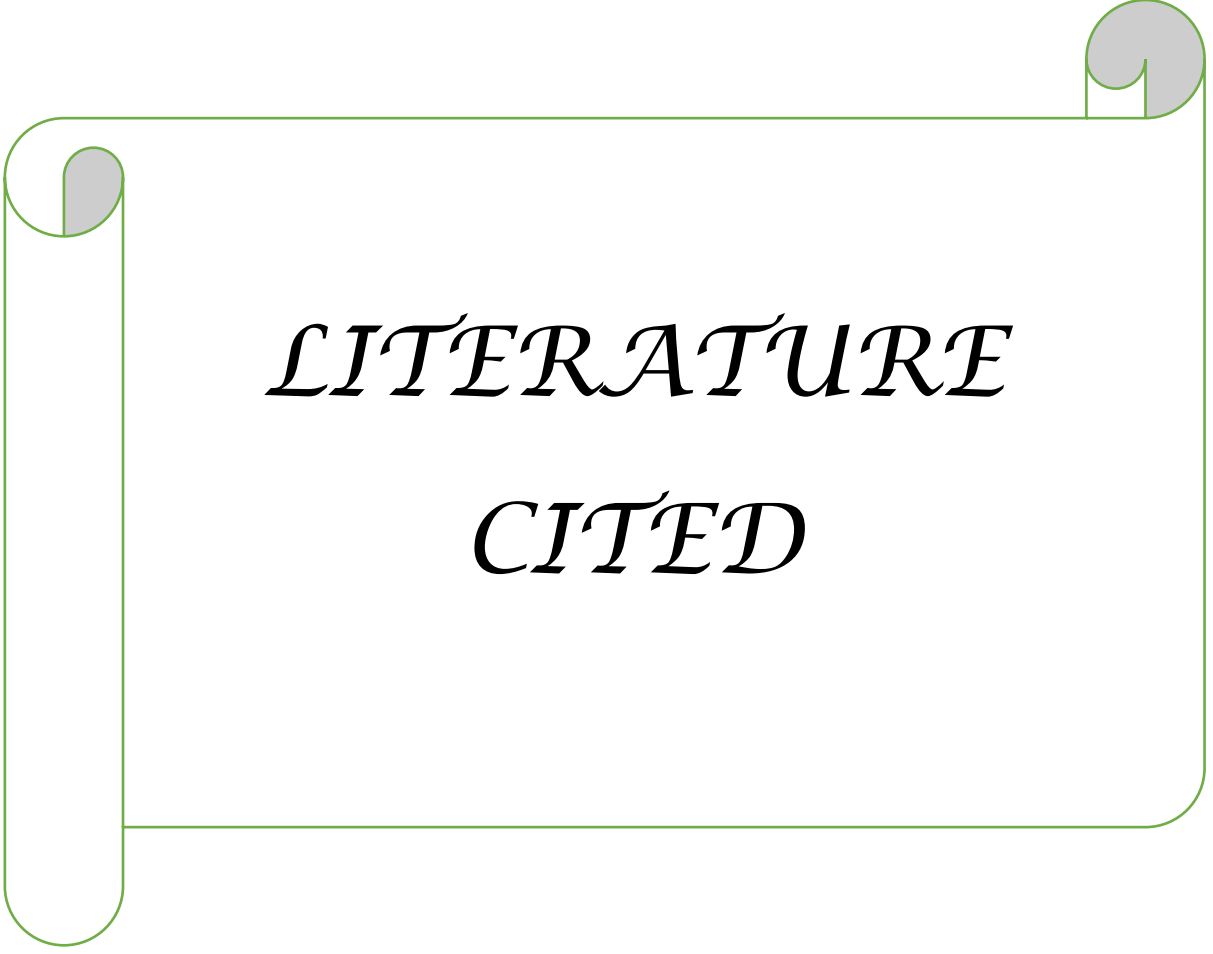
for the improvement of these characters.

- ❖ Most of the characters under study exhibited a highly significant and positive correlation with seed yield per plant. Protein content exhibited a non-significant negative correlation with seed yield whereas, protein and oil contents showed highly significant and negative correlation with each other. The oil content showed highly significant positive correlation with 100-seed weight. Highly significant and positive correlations were also observed between the characters like plant height, number of primary branches per plant, nodes per plant, number of pods per plant and number of pod bearing nodes per plant. 100-seed weight, harvest index and seed yield efficiency also exhibited a strong positive correlation among themselves.
- ❖ Path coefficient analysis revealed that dry matter weight per plant (0.757) exhibited the highest positive direct effect on seed yield per plant followed by seed yield efficiency (0.514), number of pods per plant (0.147), 100-seed weight (0.108), number of seed per pod (0.057), number of primary branches per plant (0.052) and oil content (0.013). Whereas, highest negative direct effects on seed yield were exhibited by number of pod bearing nodes per plant (-0.048) followed by harvest index (-0.044) and plant height (-0.027). The characters dry matter weight per plant, seed yield efficiency and number of pods per plant exhibited highest direct as well as indirect positive effects, while the number of pod bearing nodes per plant exerted maximum direct as well as indirect negative effects on seed yield per plant.
- ❖ Screening of the experimental material under study against three important diseases of soybean widely prevalent in the *tarai* region i.e., YMV, BP and RAB showed that none of the genotypes was immune to any of the three diseases. Only two genotypes (PS 1225 and PS 1480) showed a disease rating of 1 and classified as highly resistant for all the three diseases studied (YMV, BP and RAB), while 31 genotypes were found to be highly resistant to YMV and BP. The rest all genotypes were found to be susceptible to one or the other of these three concerned diseases.
- ❖ Bio-chemical profiling through one-dimensional SDS-PAGE of 11 genotypes selected on the basis of their protein content estimates revealed a low level of polymorphism among the genotypes with reference to their total seed protein content. Although, the protein profiles revealed a few qualitative difference with respect to the absence of specific bands in certain genotypes, they were not suitable

enough to identify the concerned genotypes. Hence, in order to further differentiate between the genotypes at their genotype level, two-dimensional electrophoresis and molecular techniques based on DNA markers were further suggested to obtain more accurate results.

In the context of all the above findings, it can be summarized that adequate amounts of genetic diversity and variability for yield and its contributing characters existed among the experimental material (160 genotypes + 5 checks) taken up for the present study. Although, genetic diversity analysis, screening for resistance to disease reaction and biochemical profiling differentiated the genotypes from each other and grouped them in different groups, molecular markers could also be included in analysis to further differentiate the individual genotypes. High inter-cluster distance between certain clusters obtained through genetic diversity analysis indicated that hybridization between superior genotypes obtained from these clusters would be highly promising to bring about yield improvement in soybean.

On the basis of genetic diversity analysis, the genotypes PS 1225, AMS 100-16-4-1-3, JS 20-79, Jupiter, Cat 209, SL (E) 1 and AMS 50B were identified as superior donors for yield contributing traits, whereas the studies on genetic variability, correlation and path coefficient analysis showed that the number of primary branches per plant, number of nodes per plant, number of pods per plant, number of seeds per pod, 100-seed weight, dry matter weight per plant, seed yield efficiency and oil content were the most important yield attributes to be emphasized during selection programs for improving the overall yield levels in soybean.



LITERATURE CITED

LITERATURE CITED

- Aditya, J.P., Bhartiya, P. and Bhartiya, A. 2011.** Genetic variability, heritability and character association for yield and component characters in soybean [*G. max* (L.) Merrill]. *Journal of Central European Agriculture*. 12(1): 27-34.
- Adsul, H.R. and Monpara, B.A. 2014.** Genetic variability and selection indices for improving seed yield in soybean (*Glycine max* L. Merrill). *Electronic Journal of Plant Breeding*. 5(4): 807-811.
- Agrawal, A.P., Patil, S.A. and Salimath, P.M. 2001.** Variability, heritability and genetic advance of some quantitative characters over the seasons in soybean. *Madras Agricultural Journal*. 88(1-3): 36-40.
- Ahmad F. and Slinkard, A.E. 1992,** Genetic relationships in the genus *Cicer* L. as revealed by polyacrylamide gel electrophoresis of seed storage proteins. *Theor. Appl. Genet.*, 84: 688-692.
- Ajdukovic, K.T., Djordjevic, V., Vidic, M. and Vujakovic, M. 2010.** Subunit composition of seed storage proteins in high-protein soybean genotypes. *Pesq. agropec. bras.*, 45(7): 721-729.
- Alege, G.O., Ngozi, A.E. and Sunday, C.E. 2014.** Seed protein electrophoresis of some members of the family Fabaceae. *African journal of biotechnology*. 13(36): 3730-3735.
- Ali, A., Khan, S.A., Khan, E., Ali, N., Hussain, I. and Ahmad, F. 2015.** Genetic studies among diverse soybean [*Glycine max* (L.) Merrill] genotypes for variability and correlation at Swat. *Int. J. Biosci.*, 6(4): 165-169.
- All India Coordinated Research Project on soybean. 2016.** Proceedings and technical programme (2016-17). In: 46th annual group meeting, Dharwad. April 5-7, 2016. University of Agricultural Sciences, Dharwad. pp. 47-48.
- Alpna., Pushpendra., Singh, K., Gupta, M.K. and Bhareti, P. 2015.** Morphological Characterization and Genetic Divergence Study in Soybean. *Soybean Research*. 13(2): 1-8.

- Aminifar, J., Mohsenabadi, G., Biglouei, M.H. and Samiezadeh, H. 2015.** Investigation of relationship between yield and dependent traits on yield in two group maturity of soybean by path analysis. *Sci. Agri.*, 12(2): 89-92.
- Amrita, B., Shrivastava, A.N., Bisen, R. and Mishra, S. 2014.** Genetic variability, association and path analyses in advanced generation fixed lines of soybean [*Glycine max* (L.) Merrill]. *Soybean Research*. 12(1): 20-27.
- Aondover, S., Lekan, B.L. and Terkimbi, V. 2013.** Correlation, path coefficient and principal component analysis of seed yield in soybean genotypes. *International Journal of Advanced Research*. 1(7): 1-5.
- Arefrad, M., Jelodar N.B., Nematzadeh, G., Karimi, M. and Kazemitabar, S.K. 2014.** Assessment of seed storage protein composition of six Iranian adopted soybean cultivars [*Glycine max* (L.) Merrill.]. *Journal of Plant Molecular Breeding*. 2(1): 29-44.
- Arshad, M., Ali, N. and Ghafoor, A. 2006.** Character correlation and path coefficient in soybean [*Glycine max* (L.) Merrill]. *Pak. J. Botany.*, 38(1): 121-130.
- Arunachalan, V. 1981.** Genetic divergence in plant breeding. *Indin J. Genet. Pl. Breed.* 41: 226-236.
- Attia, S.A.A. 2014.** Correlation coefficient analysis for quantitative and resistance characters with fingerprinting in ten soybeans *Glycine max* (L.) Genotypes based on DNA polymorphism. *Middle East Journal of Applied Sciences*. 4(2): 318-325.
- Badaya, V.K., Gill, B.S., Kaur, J. and Dhakad, U.K. 2015.** Assessment of genetic diversity and path coefficient in reproductive phases and quality traits and their correlation with seed yield in soybean [*Glycine max* (L.) Merrill]. *The Ecoscan*. 7: 209-213.
- Balasubramaniyan, P. and Palaniappan, S.P. 2003.** Principles and practices of agronomy. Jodhpur, Agrbios (India). pp. 45-46.
- Balla, M.Y. and Elrayah, I.S. 2010.** Genetic variability of soybean for yield and yield components under irrigation conditions of Gzeira, Sudan. *In: Second RUFUROM*

biennial regional conference on “Building capacity for food security in Africa”, Enebbe, September 2010. Uganda. pp. 983-986.

Baraskar, V.V., Kachhadia, V.H., Vachhani, J.H., Barad, H.R., Patel, M.B. and Darwankar, M.S. 2014. Genetic variability, heritability and genetic advance in soybean [*Glycine max* (L.) Merrill]. *Electronic Journal of Plant Breeding*. 5(4): 802-806.

Baraskar, V.V., Vachhani, J.H., Kachhadia, V.H., Patel, M.B. and Barad, H.R. 2015. Correlation and path analysis for seed yield in soybean [*Glycine max* (L.) Merrill]. *Electronic Journal of Plant Breeding*. 6(2): 570-573.

Barbarino, E., and Lourenço, S.O. 2009. Comparison of CHN analysis and Hach acid digestion to quantify total nitrogen in marine organisms. *Limnol. Oceanogr.: Methods.*, 7(11): 751-760.

Barh, A., Pushpendra., Khulbe, R.K. and Joshi, M. 2014. Bhat: A new source of genetic divergence for soybean improvement. *African Journal of Agricultural Research*. 9(1): 119-124.

Barrett, B.A. and Kidwell, K.K. 1998. AFLP-based genetic diversity assessment among wheat cultivars from the Pacific Northwest. *Crop Sci.*, 38: 1261-1271.

Baruah, S., Sarma, M.K., Baishya, D., Sharma, A.A., Borah, R. and Bhuyan, J. 2014. Genetic variation for seed yield and Yellow Mosaic Virus Resistance in Soybean [*Glycine max* (L.) Merrill]. *International Journal of Scientific and Research Publications*. 4(9): 1-10.

Bekele, A., Alemaw, G. and Zeleke, H. 2012. Genetic divergence among soybean (*Glycine max* (L.) Merrill) introductions in Ethiopia based on agronomic traits. *Journal of Biology, Agriculture and Healthcare*. 2(6): 6-12.

Bhartiya, A., Aditya, J.P., Singh, G., Gupta, A., Agarwal, P.K. and Bhat, J.C. 2011. Assessment of genetic variability of agronomic characters in indigenous and exotic collection of black soybean (*Glycine max* (L.) Merrill.). *SABRAO Journal of Breeding and Genetics*. 43(1): 81-90.

- Bhattacharya, P.K., Kole, P.C., and Ram, H.H. 1999.** Inheritance of resistance to yellow mosaic virus in interspecific crosses of soybean. *Euphytica*. 108(3): 157-159.
- Bhushan, B., Sharma, S.P. and Sharma, V. 2006.** Correlation and path coefficient analysis of soybean [*Glycine max* (L.) Merrill]. *Crop Improv.*, 33(2): 190-93.
- Bonato, A.L.V., Calvo, E.S., Geraldi, I.O. and Arias, C.A.A. 2006.** Genetic similarity among soybean (*Glycine max* (L) Merrill) cultivars released in Brazil using AFLP markers. *Genetics and Molecular Biology*. 29: 692-704.
- Bonfitto, R., Galleschi, L., Macchia, M., Saviozzim, F. and Navari-Izzo, F. 1999.** Identification of melon cultivars by gel and capillary electrophoresis. *Seed Sci. Tech.*, 27: 779-83.
- Bradford, M.M. 1976.** A rapid and sensitive method for the quantitation of microgram quantities of protein utilizing the principle of protein-dye binding. *Analytical Biochemistry*. 72: 248-254.
- Bretting, P.K. and Widrlechner, M.P. 1995.** Genetic markers and plant genetic resource management. In: J. Janick. ed. *Plant Breeding Reviews*. 13. New York, John Wiley & Sons, Inc. pp. 11-87.
- Brown, A.D.H. 1978.** Isozymes, plant population genetic structure and genetic conservation. *Theor. Appl. Genet.*, 52: 145-147.
- Burton, G.W. and De Vane, E.H. 1953.** Estimations of heritability in tall festca (*Festuca arundinacea*) from replicated clonal materials. *Agron. J.*, 45: 487-488.
- Bushehri, S.A.A., Mishani, C.A., Samadi, B.Y. and Tabatabaei, B.E.S. 2000.** Variety specific electrophoretic profiles of soybean cultivars. *Iranian J. Agric. Sci.*, 31(1): 55-61.
- Chamundeswari, N., and Aher, R.P. 2003.** Character association and component analysis in soybean. *Annals of Biology*. 19: 199-203.
- Chandel, K., Sood, O.P., Sood, V.K. and Gartan, S.L. 2005.** Character associations and path analysis studies in cultivated soybean (*Glycine max*) genotypes restructured through introgression of *G.soja* chromatin. *Crop Res. Hisar.*, 29(3): 469-473.

- Chandel, K.K., Patel, N.B. and Patel, J.B. 2014.** Correlation coefficients and path analysis in soybean (*Glycine max* L. Merrill). *AGRES – An International e-Journal*. 3(1): 25-31.
- Chandrawat, K.S., Baig, K.S., Sarang, D.H., Dumai P.K., Dhone, P.U. and Kumar, A. 2015.** Association analysis for yield contributing and quality parameters in soybean. *The Ecoscan*. 7: 113-118.
- Chaudhary, J. and Dantu, P.K. 2011.** Phylogenetic relationships within selected Indian soybean (*Glycine max* (L.) Merr.) varieties based on SDS-PAGE of seed proteins. *Journal of proteins and proteomics*. 2(1): 23-29.
- Chaudhary, D.N. and Singh, B. 1974.** Correlation and path coefficient analysis of yield components of soybean. *Indian J. Agric.Sci.*, 44: 487-490.
- Chauhan, V.S. 1976.** Studies on heterosis, combining ability and genetic variability in relation to genetic divergence in soybean. Thesis, Ph.D. G. B. Pant University of Agriculture and Technology, Pantnagar, 176 p.
- Chauhan, V.S. and Singh, B.B. 1982.** Heterosis and genetic variability in relation to genetic divergence in soybean. *Indian J. Genet.*, 42: 324-328.
- Chavan, R.B., Pulate, S.C. and Thakare, D.S. 2014.** Assessment of existing genetic variability and diversity in soybean. *Biolife*. 2(3): 949-955.
- Chen, L.F.O., Yun, W.C., Kou, H.Y. and Chen, M.H. 1994.** Polymorphic distinction of soybean by molecular markers. *Soybean Genetics Newsletter*. 21: 70-75.
- Chung, G. and Singh, R.J. 2008.** Broadening the genetic base of soybean: a multidisciplinary approach. *Critical Reviews in Plant Science*. 27: 295-341.
- Comstock, R.E. and Robinson, H.F. 1948.** The component of genetic variance in population of biparental progenies and their use in estimating the average degree of dominance. *Biometrics*. 4: 254-266.
- Dadson, R.B. 1976.** Screening and evaluation of soybean cultivars at Legon. In: Doku, E.V. ed. Proc. Of the Joint University of Ghana Council for Scientific and Industrial Research Symposium on Grain Legumes. Ghana. pp. 71–77.

- Das, M.L., Ratuman, A. and Miah, A.J. 1989.** Correlation, path coefficient and regression studies in soybean. *Bangladesh J. of Agric. Research.*, 14(1): 27-29.
- Das, S. and Mukarjee, K.K. 1995.** Comparative study on seed proteins of Ipomea. *Seed Sci. & Technol.*, 23: 501-509.
- Das, S.P., Harer, P.N. and Biradar, A.B. 2001.** Genetic divergence and selection of genotypes in soybean. *J. Mah. Agric. Univ.*, 25(3): 250-252.
- Datt Shiv., Sharma, P.R., Kumar, M. and Gupta, A.K. 2011.** Genetic Variability and Trait Relationships among Yield and Other Quantitative Traits in Soybean [*Glycine max* (L.) Merrill]. *VEGETOS*. 24(2): 117-120.
- De Sousa, L.R., Hamawaki, O.T., Batista, R.O., Bertan, I., Nogueira, A.P.O., Romanato, F.N. and Hamawaki, R.L. 2015.** Genetic variability among soybean biparental crosses evaluated by multivariate analysis. *Biosci. J., Uberlândia.*, 31(5): 1404-1412.
- De-Vries, I.M. 1996.** Characterization and identification of *Lactuca sativa* cultivars and wild relatives with SDS-electrophoresis (*Lactuca* sect. *Lactuca*, *Compositae*) *GRACE*. 43: 193-202.
- Dewey, J.R. and Lu, K.H. 1959.** A correlation and path co-efficient analysis of components of crested wheat seed production. *Agron. J.*, 51: 515-518.
- Dilnesaw, Z., Abadi, S., Merkeb, F., Dechassa, N. and Zelek, H. 2014.** Genetic variability and character association of twenty soybean (*Glycine max* L. Merrill) genotypes for biological nitrogen fixation and related traits in Pawe district Metekel zone Northwestern Ethiopia. *Global advanced research journal of food science and technology*. 3(5): 135-140.
- Dong, Y.S., Zhuang, B.C., Zhao, L.M., Sun, H. and He, M.Y. 2001.** The genetic diversity of annual wild soybeans growing in china. *Theor. Appl. Genet.*, 103(1): 98 -103.
- Dubey, N., Shrivasthava, A.N., Avinash, H.A. and Jaiwar, S. 2015.** Genetic variability, correlation and path analysis for yield and yield contributing characters in soybean (*Glycine max* L.). *Electronic Journal of Plant Breeding*. 6(1): 318-325.

- El-Badaway, M.E.M. and Mehasen, S.A.S. 2012.** Correlation and path coefficient analysis for yield and yield components of soybean genotypes under different planting density. *Asian Journal of Crop Science*. 4(4): 150-158.
- El-Mohsen, A.A.A., Mahmoud, G.O. and Safina, S.A. 2013.** Agronomical evaluation of six soybean cultivars using correlation and regression analysis under different irrigation regime conditions. *Journal of Plant Breeding and Crop Science*. 5(5): 91-102.
- Emre, I., Balik, D.T., Genç, H. and Şahin, A. 2010.** Total seed storage protein patterns of some *Lathyrus* species growing in Turkey using SDS-PAGE. *Pak. J. Bot.*, 42(5): 3157-3163.
- Emre, I., Turguk-Balik, T. and Sahin, A. 2007,** Electrophoretic analysis of total protein profiles of some *Lathyrus* L. (Sect. *Cicerula*) grown in Turkey. *Pak. J. Biol. Sci.*, 10: 2890-2894.
- Federer, W.T. 1956.** Augmented. (or Hoonuiaku) design. *Hawai. Plant.Rec.*, 55: 191-208.
- Federer, W.T. 1961.** Augmented designs with one way elimination of heterogeneity. *Biometrics*. 17: 447-473.
- Federer, W.T. and Raghavarao, D. 1975.** On augmented designs. *Biometrics*. 31(1): 29-35.
- Fisher, R.A. 1918.** The correlations between relatives on the supposition of Mendelian inheritance. *Trans. Roy. Soc. Edin.* 52: 399-433.
- Frankel, O.H., Brown, A.D.H. and Burdon, J.J. 1995.** The conservation of plant biodiversity. Cambridge. UK. Cambridge Uni. Press. 299 p.
- Fu, Y.B. 2006.** Impact of plant breeding on genetic diversity of agricultural crops: searching for molecular evidence. *Plant Genetic Resources*. 4: 71-78.
- Gaikwad, S.R., Bangar, N.D. and Chavan, B.H. 2005.** Genetic diversity studies in soybean. *Journal of Maharashtra Agricultural Universities*. 30(3): 281-284.

- Gaikwad, S.R., Bangar, N.D. and Chavan, B.H. 2007.** Correlation and path coefficient analysis in soybean. *Journal of Maharashtra Agricultural University*. 32(2): 276-277.
- Ganesamurthy, K. and Seshadri, P. 2004.** Genetic variability, character association and path coefficient analysis in soybean. *Madras Agric. J.*, 91(1-3): 61-65.
- Gawande, P., Patil, S. and Joshi, S. 2001.** Selection of superior germplasm lines for soybean based on morphological characters for hybridization. *J. of Physiological Res.*, 14(2): 125-130.
- Gawande, P.P., Patil, S., Kumari, M. and Bailkiwad, V.J. 2002.** Selection of superior germplasm lines of soybean [*Glycine max* (L.) Merrill] for breeding. *J. Soils & crops.*, 12(2): 236-240.
- Gepts, P. 1989.** Genetic diversity of seed storage proteins in plants. *In*: A.H.D. Brown, M.T. Clegg, A.L. Kahler and B.S. Weir. eds. *Plant Population Genetics, Breeding and Genetic Resources*. Sunderland, Massachusetts. Sinauer Associates Inc., pp. 64-82.
- Ghafoor, A., Ahmad, Z. and Afzal, M. 2005.** Use of SDS-PAGE markers for determining quantitative traits loci in Black gram [*Vigna mungo* (L.) Hepper] germplasm. *Pak. J. Bot.*, 37(2): 263-269.
- Ghafoor, A., Sharif, A., Ahmad, Z., Zahid, M.A. and Rabbani, M.A. 2001.** Genetic diversity in black gram (*Vigna mungo* L. Hepper). *Field Crops Res.*, 69: 183-190.
- Ghatge, R.D. and Kadu, R.N. 1993.** Genetic variability and heritability studies in soybean. *Advances Pl. Sci.*, 6: 224-8.
- Ghodrati, G. 2013.** Study of genetic variation and broad sense heritability for some qualitative and quantitative traits in soybean (*Glycine max* L.) genotypes. *Current Opinion in Agriculture*. 2(1): 31–35.
- Gibson, L. and Benson, G. 2005.** Origin, History, and Uses of Soybean (*Glycine max*). Department of Agronomy, Iowa State University.
- Gireesh, C., Husain, S.M., Bhojraj, N.K. and Yatish, K.R. 2012.** Studies on variability, character association and path coefficient analysis for yield and its attributing traits

in exotic lines of soybean (*Glycine max* (L.) Merrill). *Bhartiya Krishi Anusandhan Patrika*. 27(1): 35-39.

Gohil, V.N., Mehta, D.R. and Pandya, H.M. 2007. Genetic divergence in soybean (*Glycine max* (L.) Merrill). *Legume Research*. 30(3): 224-226.

Gohil, V.N., Pandya, H.M. and Mehta, D.R. 2003. Genetic association and path analysis for seed yield, its components and quality attributes in soybean. *GAU Research Journal*. 28(1-20): 9-11.

Guedira, G.L.B., Thompson, J.A., Nelson, R.L. and Warburton, M.L. 2000. Evaluation of genetic diversity of soybean introductions and North American ancestors using RAPD and SSR markers. *Crop Science*. 40: 815–823.

Gupta, A.K. and Punetha, H. 2007. Genetic Variability Studied for Quantitative Traits In Soybean [*Glycine max* (L.) Merrill]. *Agricultural Science Digest*. 27(2): 140-141.

Haghi, Y., Boroomandan, P., Moradin, M., Hassankhali, M., Farhadi, P., Farsaei, F. and Dabiri, S. 2012. Correlation and path analysis for yield, oil and protein content of soybean (*Glycine max* L.) Genotypes under different levels of nitrogen starter and plant density. *Biharean biologist*. 6(1): 32-37.

Hakima, L., Suyamtob. and Paturohmana, E. 2014. Genetic variability, heritability and expected genetic advances of quantitative characters in F₂ progenies of soybean crosses. *Indones. J. Agric. Sci.*, 15(1): 11-16.

Han, O., Abe, J. and Shimamoto, Y. 1999. Genetic diversity of soybean landraces in Korea. *Korean J. Crop Sci.*, 44: 256-262.

Hanson, C.H., Robinson, H.F. and Comstock, R.E. 1956. Biometric studies of yield segregating population in Korean lespedeza. *Agron. J.*, 48: 268-272.

Hasler, C.M. 1998. Functional foods: their role in disease prevention and health promotion. *Food Technology*. 52: 63-70.

Hayman, B.D. and Mather. 1955. The description of genetic interaction in continuous variation. *Biometrics*. 11: 68-82.

- Hill A., Kurki A. and Morris M. 2006.** Biodiesel: The Sustainability Dimensions. Butte, MT: National Center for Appropriate Technology, ATTRA Publication. pp. 4-5.
- Hirata, T., Abe, J. and Shimamoto, Y. 1999.** Genetic structure of the Japanese soybean population. *Genet. Resour. Crop Evol.*, 46: 441-453.
- Hiromoto, D.M. and Vello, N.A. 1986.** The genetic base of Brazilian soybean (*Glycine max* (L.) Merrill) cultivars. *Brazilian Journal of Genetics*. 9: 295-306.
- <http://www.iita.org/soybean>. IITA: Research to Nourish Africa. 29/05/2016.
- <http://www.soyatech.com>. Soya tech: Growing opportunities™. 24/05/2016.
- Hyten, D., Song, Q., Zhu, Y., Choi, I.K.Y., Nelson, R.L., Costa, J.M., Specht, J.E., Shoemaker, R.C. and Cregan, P.B. 2006.** Impacts of genetic bottlenecks on soybean genome diversity. *Proceedings of the National Academy of Sciences of the United States of America*. 103: 232-241.
- Indian Council of Agricultural Research – Indian Institute of Soybean Research. 2016.** AICRP on Soybean. Director's Report and Summary Tables of Experiments (2015-16). Indore. pp. i-ii.
- Ingle, Y.V., Chandankar, G.D., Patil, P.V. and Patil, C.U. 2016.** Evaluation of advance lines of soybean for resistance to major diseases under natural field condition. *Indian J. Agric. Res.*, 50(1): 84-87.
- Iqbal, S., Mahmood, T., Tahira., Ali, M., Anwar, M. and Sarwar, M. 2003.** Path coefficient analysis in different genotypes of soybean [*Glycine max* (L.) Merrill]. *Pak. J. Biol. Sci.*, 6: 1085-1087.
- Iqbal, S.M., Ghafoor, A. and Ayub, N. 2005.** Relationship between SDS-PAGE markers and *Ascochyta* blight in chickpea. *Pak. J. Bot.*, 37(1): 87-96.
- Iqbal, Z., Arshad, M., Ashraf, M., Mahmood, T. and Waheed, A. 2008.** Evaluation of soybean [*Glycine max* (L.) Merrill] germplasm for some important morphological traits using multivariate analysis. *Pak. J. Bot.*, 40(6): 2323-2328.

- Iqbal, Z., Arshad, M., Ashraf, M., Naeem, R., Malik, M.F. and Waheed, A. 2010.** Genetic divergence and correlation studies of soybean (*Glycine max* (L.) Merrill) genotypes. *Pakistan J. Bot.*, 42(2): 971-976.
- Jadhav, A.S., Jadhav, P.J. and Bachchhav, S.M. 1995.** Correlation and path coefficient analysis in soybean. *Journal of Maharashtra Agricultural Universities*. 54(4): 418-424.
- Jadhav, D.J., Deosarkar, D.B. and Jawale, L.N. 2002.** Correlation and path coefficient analysis in seed quality characters of soybean. *J. of Maharashtra Agric. Universities.*, 26(3): 325-326.
- Jagtap, D.R. and Mehetre, S.S. 1994.** Genetic variability in some quantitative characters of soybean. *Annals Agric. Res.*, 15: 45-49.
- Jain, P.K. and Ramgiry, S.R. 2000.** Genetic variability of metric traits in Indian germplasm of soybean [*Glycine max* (L.) Merrill]. *Adv. Pl. Sci.*, 13(1): 127-131.
- Jain, S., Srivastava, S.C., Singh, S.K., Indapurkar, Y.M. and Singh, B.K. 2015.** Studies on genetic variability, character association and path analysis for yield and its contributing traits in soybean [*Glycine max* (L.) Merrill]. *Legume Research*. 38(2): 182-184.
- Jha, S.S. and Ohri, D. 1996.** Phylogenetic relationships of *Cajanus cajan* (L.) Millsp. (pigeon pea) and its wild relatives based on seed protein profiles. *Genet. Resour. Crop Evol.*, 43: 275-281.
- Jimenez, R.R. and Ladho, J.K. 1993.** Automated elemental analysis: A rapid and reliable but expensive measurement of total carbon and nitrogen in plant and soil samples. *Communications in Soil Science and Plant Analysis*. 24(15-16): 1897-1924
- Johansson, W.L. 1909.** Elements des exatistes exblich Keitslehire: Gustum Fisher.
- Johnson, H.W., Robinson, H.F. and Comstock, R.E. 1955.** Estimation of genetic and environmental variability in soybean. *Agron. J.*, 47(7): 314-317.
- Joshi, A. B. and Dhawan, N. L. 1966.** Genetic improvement of yield with special reference to self-fertilizing crops. *Indian J. Genet.*, 26A: 101-113.

- Kachhadia, V.H., Baraskar, V.V., Vachhani, J.H., Patel, M.B. and Barad. H.R. 2015.** Genetic divergence in soybean [*Glycine max* (L.) Merrill.]. *Electronic Journal of Plant Breeding*. 5(3): 563-566.
- Kadam, D.D. 2007.** Genetic architecture on finger millet [*Elusine corcana* (L.) Gaertn]. *International Journal of Agricultural Sciences*. 3(2): 104-107.
- Karmakar, P.G. and Bhatnagar, P.S. 1996.** Genetic improvement of soybean varieties released in India from 1969 to 1993. *Euphytica*. 90: 95-103.
- Karnwal, M.K. and Singh, K. 2009.** Studies on genetic variability, character association and path coefficient for seed yield and its contributing traits in soybean [*Glycine max* (L.) Merrill]. *Legume Res.*, 32(1): 70-73.
- Kayande, N.V. and Patil, S.P. 2009.** Genetic divergence in soybean [*Glycine max* (L.) Merrill]. *International Journal of Plant Sciences Muzaffarnagar*. 4(1): 218-220.
- Khan, M.A. 1992.** Seed-protein electrophoretic pattern in *Brachypodium* P. Beauv. species. *Ann. Bot.*, 70: 61-68.
- Koladiya, P.B., Saravaiya, S.N., Patel, D.A., Chaudhari, K.N. and Patel, B.N. 2012.** Correlation and path coefficient analysis for yield and yield contributing traits in Soybean (*Glycine max* (L.) Merrill). *Vegetable Science*. 39(1): 95-97.
- Kumar, A., Lal, G.M. and Mishra, P.K. 2014.** Genetic variability and character association for yield and its components in soybean. *Annals of Plant and Soil Research*. 16(1): 48-52.
- Kumar, A., Pandey, A. and Pattanayak, A. 2015.** Assessment of genotypic variation in soybean (*Glycine max*). *Legume Research*. 38(2): 174-177.
- Kumar, B., Talukdar, A., Verma, K., Girmilla, G., Bala, I., Lal, S.K., Singh, K.P. and Sapra, R.L. 2014.** Screening of soybean [*Glycine max* (L.) Merr.] genotypes for yellow mosaic virus (YMV) disease resistance and their molecular characterization using RGA and SSRs markers. *Australian Journal of Crop Science*. 8(1): 27-34.
- Kumar, T., Dantre, R.K. and Verma, K.P. 2016.** Studies on aerial blight of soybean caused by *Rhizoctonia solani*. *Journal of Plant Development Sciences*. 8(3): 143-147.

- Kumar. and Nadarajan, N. 1994.** Genetic divergence studies in soybean {*Glycine max* (L.) Merrill.}. *Indian J. Genet. Pl. Breed.* 54(3): 242-24.
- Laemmli, U.K. 1970.** Cleavage of structural proteins during the assembly of the head of bacteriophage T4. *Nature.* 227: 680-685.
- Leffel, R.C. and Rhodes, W.K. 1993.** Agronomic performance and economic value of high-seed protein soybean. *J. Prod. Agric.*, 6(3): 365-368.
- Li, C.D. 1956.** The concept of path coefficient and its impact on population genetics. *Biometrics.* 12: 190-210.
- Li, Y.S., Du, M., Zhang, Q.Y., Hashemi, M., Liu, X.B. and Hebert, S.J. 2013.** Correlation and path coefficient analysis for yield components of vegetable soybean in North-east China. *Legume Research.* 36(4): 284-288.
- Liggins, J., Bluck, L.J.C., Runswiick, S., Atkinson, C., Coward, W.A. and Bingham, S.A. 2000.** Daidzein and genistein contents of vegetables. *British Journal of Nutrition.* 84(5): 717-725.
- Liu, S., Zhou, R., Tian, S. and Gai, J. 2007.** A study on subunit groups of soybean protein extracts under SDS-PAGE. *J. Am. Oil Chem. Soc.*, 84: 793-801.
- Lush, J.L. 1949.** Heritability of quantitative characters in farm animals. *In: Proceedings of the Eighth International Congress of Genetics.* Lund: Berlingska Boktryckeriet. 1949. *Hereditas, Suppl. Vol.* pp. 357-375.
- Machikowa, T. and Laosuwan, P. 2011.** Path coefficient analysis for yield of early maturing soybean. *Songklanakarin J. Sci. Technol.*, 33(4): 365-368.
- Maestri, D.M., Labuckas, D.O., Guzman, C.A. and Giorda, L.M. 1998.** Correlation between seed size, protein and oil contents and fatty acid composition in soybean genotypes. *Grasas Aceites.* 49: 450–453.
- Mahbub, M.M., Rahman, M.M., Hossain, M.S., Mahmud, F. and Kabir, M.M.M. 2015.** Genetic Variability, Correlation and Path Analysis for Yield and Yield Components in Soybean. *American-Eurasian J. Agric. & Environ. Sci.*, 15(2): 231-236.

- Mahbub, M.M., Rahman, M.M., Hossain, M.S., Nahar, L. and Shirazy, B.J. 2016.** Morphophysiological Variation in Soybean (*Glycine max* (L.) Merrill). *American-Eurasian J. Agric. & Environ. Sci.*, 16 (2): 234-238.
- Malek, M.A., Rafii, M.Y., Afroz, M.S.S., Nath, U.K. and Mondal, M.M.A. 2014.** Morphological characterization and assessment of genetic variability, character association, and divergence in soybean mutants. *The Scientific World Journal*. 2014: 12.
- Malik, M.F.A., Qureshi, A.S., Ashraf, M. and Ghafoor, A. 2006.** Genetic variability of the main yield related characters in soybean. *Int. J. Agric. Biol.*, 8(6): 815-819.
- Malik, M.F.A., Qureshi, A.S., Ashraf, M. and Ghafoor, A. 2007.** Assessment of genetic variability, correlation and path analyses for yield and its components in soybean. *Pak. J. Bot.*, 39(2): 405-413.
- Malik, M.F.A., Qureshi, A.S., Ashraf, M., Khan, M.R. and Javed, A. 2009.** Evaluation of genetic diversity in soybean (*Glycine max*) lines using seed protein electrophoresis. *Australian Journal of Crop Science*. 3(2): 107-112.
- Manjaya, J.G., Gopalkrishna, T., Pawar, S.E. and Bapat V.A. 2007.** Genetic variability for trypsin inhibitor content with oil and protein. *Indian Journal of Genetics*. 67(1): 51-55.
- Martin, M.S. 2000.** Crop strength through diversity. *Nature*. 406: 681-682.
- Masoomah, J., Mehran, G. and Fatemeh, J. 2015.** Seed storage protein electrophoresis for identification of some Groundnut (*Arachis hypogaea* L.) cultivars. *International Research Journal of Applied and Basic Sciences*. 9(10): 1718-1721.
- Mehetre, S.S., Mahajan, C.R., Patil, P.A. and Hajare, D.N. 1994.** Genetic divergence in soybean [*Glycine max* (L.) Merrill.]. *Indian J. Genet. Pl. Breed.* 54(1): 83-88.
- Mennella, G., Onofaro, S.V., Tonini, A. and Magnifico, V. 1999.** Seed storage protein characterization of Solanum species and of cultivars and androgenetic lines of *S. melongena* L. by SDS-PAGE and AE-HPLC. *Seed Sci. Technol.*, 27: 23-35.

- Mielenz, J.R., Bardsley, J.S. and Wyman, C.E. 2009.** Fermentation of soybean hulls to ethanol while preserving protein value. *Bioresource Technology*. 100(14): 3532-3539.
- Moe, S. and Girdthai, T. 2013.** Relationships of soybean [*Glycine max* (L.) Merrill] accessions based on physiological and agro-morphological traits. *International Journal of Chemical, Environmental & Biological Sciences*. 1(2): 375-379.
- Moll, R.H., Salhuana, W.S. and Robinson, H.F. 1962.** Heterosis and genetic diversity in variety crosses of maize. *Crop. Sci.*, 2: 197-198.
- Mundewadikar, D.M. and Deshmukh, P.R. 2014.** Genetic Variability and Diversity Studies in Soybean [*Glycine max* (L.) Merrill] using RAPD Marker. *International Journal of Scientific and Research Publications*. 4(9): 1-4.
- Nag, S.K., Yadav, R.K., Sahu, L., Salam, J.L., Soni, D.K. and Ranjan, S.K. 2007.** Study of correlation and path coefficient analysis for yield and its attributes in soybean (*Glycine max* (L.) Merrill). *Plant Archi.*, 7(1): 175-178.
- Nagarajan, D., Kalaimagal, T. and Murugan, E. 2015.** Correlation and path coefficient analysis for yield and yield attributes in soybean, *Glycine max* L. (Merr). *International Journal of Farm Sciences*. 5(3): 28-34.
- Nariani, T.K. 1960.** Yellow mosaic of green gram [(*Phaseolus aureus* (L.))]. *Indian Phytopath.*, 13: 24.
- Nene, Y.L. 1972.** A survey of the viral diseases of pulse crops in India. G B Pant Univ. Agric. Tech., Pantnagar, *India J. Res. Bull.*, 4: 191.
- Niles, H.F. 1922.** Correlation, causation and Wrights' theory of path-coefficient. *Genetics*. 7: 255-258.
- Oz, M., Karasu, A.A., Goksoy, T. and Turan, Z.M. 2009.** Interrelationships of Agronomical Characteristics in Soybean (*Glycine max*) Grown in Different Environments. *International Journal of Agriculture & Biology*. 11(1): 85-88.
- Patil, S.S., Naik, M.R., Patil, P.P. and Shinde, D.A. 2011.** Genetic variability, correlation and path analysis in soybean. *Legume Res.*, 34(1): 36-40.

- Patil, S.S., Patil, P.P., Lodam, V.A. and Chaudhari, M.H. 2014.** Character association and genetic diversity in soybean to formulate a sound breeding program – A review. *Trends in Biosciences*. 7(7): 508-511.
- Pawar, K.K., Yadav, S.K., Jarman, M. and Singh, A.K. 2013.** Assessment of Divergence in Soybean (*Glycine Max* L. Merrill) Germplasm for Yield Attributing Traits. *International Journal of Scientific Research*. 2(10): 1-2.
- Peterson, R.G. 1985.** Augmented design for preliminary yield trial (revised). *Rachis*. 4: 27-32.
- Pooran Chand. 1999.** Association analysis of yield and its components in soybean. *Madras Agric J.*, 86: 378-381.
- Poornima Jency, J. and Kalaimagal, T. 2015.** Genetic diversity in soybean [*Glycine max* (L.) merill] based on morphological characters. *Journal of Food Legumes*. 28(2): 125-127.
- Priolli, R.H.G., Mendes-Junior, C.T., Arantes, N.E. and Contel, E.P.B. 2002.** Characterization of Brazilian soybean cultivars using microsatellite markers. *Genetics and Molecular Biology*. 25: 185-193.
- Promin, L., Khoyumthem, P., Nanita Devi, H., Sharma, P.R. and Paul Amitiva. 2014.** Genetic divergence studies in soybean [*Glycine max* (L.) Merill.]. *Soybean Research (Special Issue Number 2)*: 75-80.
- Pushpa Reni, Y. and Koteswara Rao, Y. 2013.** Genetic variability in soybean [*Glycine max* (L) Merrill]. *International Journal of Plant, Animal and Environmental Sciences*. 3(4): 35-38.
- Pushpendra. and Ram, H.H. 1987.** Genetic components of variation for certain yield contributing traits in soybean. *Indian J. Agric. Sci.*, 57(4): 221-224.
- Rajanna, M.P., Viswanatha, S.R., Kulkarni, R.S. and Ramesh, S. 2000.** Correlation and path analysis in soybean (*Glycine max* (L.) Merrill). *Crop Res.(Hisar)*., 20(2): 244-247.
- Rajarathinam, S., Muppudathi, N. and Pandian, R.S. 1996.** Variability and character association in soybean during rabi season. *Madras Agric. J.*, 83(12): 776-777.

- Rajput, R.L., Srivastava, U.K. and Pandey, R.N. 2000.** Correlation studies in soybean (*Glycine max*. (L) Merrill.). *Advances-in-Agric.-Res.-in-India*. 10: 57-60.
- Ram, H., Singh, K. and Pushpendra. 1992.** Genetic divergence in the elite germplasm of soybean. *Narendra Deva J. Agric. Res.*, 7(1): 156-163.
- Ram, J. and Panwar, D.V.S. 1970.** Intraspecific divergence in rice {*Oryza sativa* (L.)}. *Indian J. Genet.*, 30: 1-10.
- Ramgiry, S.R. 1999.** Genetic divergence in Soybean. *Madras Agric. J.*, 85 (3-4): 167-170.
- Ramgiry, S.R., Raha, P. and Tiwari, V.N. 1998.** Genetic analysis of yield and quality attributes in soybean (*Glycine max* (L.) Merrill). *Adv. Plant Sci.*, 11: 83-86.
- Ramteke, R., Kumar, V., Murlidharan, P. and Agarwal, D.K. 2010.** Study on genetic variability and traits interrelationship among released soybean varieties of India [*Glycine max* (L.) Merrill]. *Electronic Journal of Plant Breeding*. 1(6): 1483-1487.
- Ramteke. R. and Murlidharan, P. 2012.** Characterization of soybean (*Glycine max*) varieties as per DUS guidelines. *Indian Journal of Agricultural Sciences*. 82(7): 572–577.
- Ranganna, S. 1977.** Handbook of analysis and quality control for fruit and vegetable products. New Delhi, Tata McGraw-Hill. 1112 p.
- Ranganna, S. 1977.** Manual of analysis of fruit and vegetable products. New Delhi, Tata McGraw-Hill. pp. 8-9.
- Rao, M.S.S., Bhagsari, A.S., and Muhammad, A.I. 1998.** Yield, protein and oil quality of soybean genotypes selected for tofu production. *Pl. Food Hum. Nutr.*, 52: 241-251.
- Rao, R., Vaglio, M.D., Urzo, M.P.D., Monti, L. and Vaglio, M.D. 1992.** Identification of *Vigna spp.* through specific seed storage polypeptides. *Euphytica*. 62: 39-43.
- Rasaily, S.K., Desai, N.D. and Kukadia, M.U. 1986.** Genetic variability in soybean (*Glycine max* L. Merrill). *Gujrat Agric. University Res. J.*, 11: 57-60.
- Raut, V.M. 2003.** Qualitative genetics of soybean- a review. *Soybean Research*. 1: 1–28.

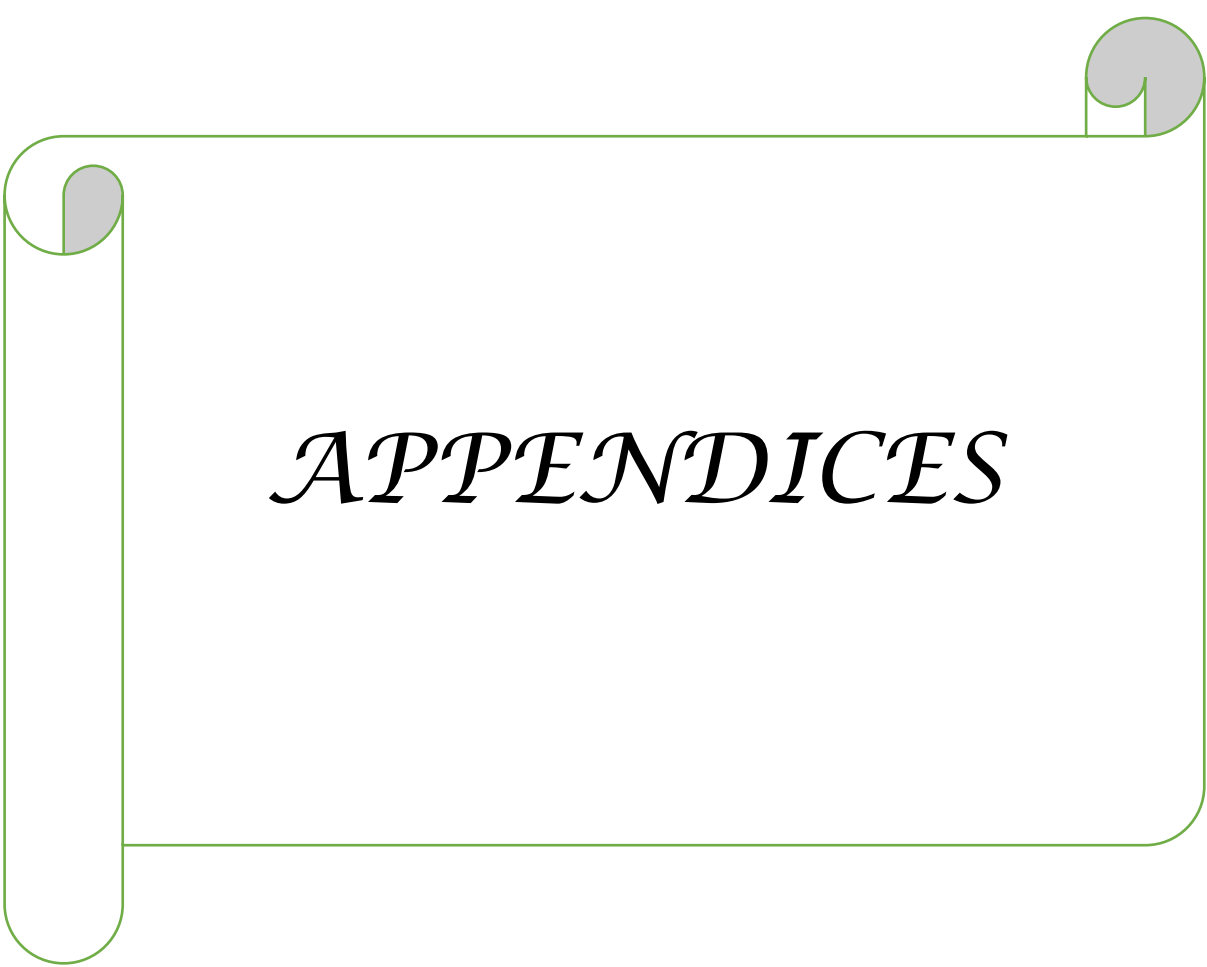
- Registrar (PVP and FRA). 2009.** Guidelines for the conduct of test for distinctiveness, uniformity and stability (DUS) on Soybean [*Glycine max* (L.) Merrill]. *Plant Variety Journal of India* 3(10): 289–298.
- Riaz, M.N. 2006.** Soy Applications in Food. Boca Raton. CRC Press. Florida.
- Robinson, H.F., Comstock, R.E., and Harvey, P.H. 1949.** Estimates of heritability and the degree of dominance in corn. *Agron. J.*, 41: 353-359.
- Rodrigues, B., Serafim, F., Nogueira, A.P.O., Hamawaki, O.T., De Sousa, L.B. and Hamawaki, R.L. 2015.** Correlations between traits in soybean (*Glycine max* L.) naturally infected with Asian rust (*Phakopsora pachyrhizi*). *Genet. Mol. Res.*, 14 (4): 17718-17729.
- Salimi, S. and Moradi, S. 2012.** Effect the correlation, regression and path analysis in soybean genotypes (*Glycine Max* L.) under moisture and normal condition. *Int. J. Agron. Plant Prod.*, 3(10): 447-454.
- Salimi, S., Lahiji, H.S., Abadi, G.M., Salimi, S. and Moradi, S. 2012.** Genetic diversity in soybean genotypes under drought stress condition using factor analysis and cluster analysis. *World Applied Sciences Journal*. 16(4): 474-478.
- Salimi, S., Moradi, S., Nezhad, K.A. and Ahmed, J.O. 2013.** Effect quantitative traits in soybean genotypes (*Glycine max* L.) under drought stress condition. *International Journal of Agriculture and Crop Sciences*. 5(5): 544-548.
- Sandoval, M.P., Carter, T.E., Webb, D.M. and Burton, J.W. 1997.** RFLP genetic similarity and coefficient of parentage as genetic variance predictors for soybean yield. *Crop Sci.*, 37: 698-703.
- Sarutayophat, T. 2012.** Correlation and path coefficient analysis for yield and its components in vegetable soybean. *Songklanakarin J. Sci. Technol.*, 34(3): 273-277.
- Schwender, J., Ohlrogge, J.B. and Hill, S.Y. 2003.** A flux model of glycolysis and the oxidative pentosephosphate pathway in developing *Brassica napus* embryos. *J. Biol. Chem.*, 278: 29442–29453.
- Searle, S. R. 1961.** Phenotypic, genotypic and environmental correlation. *Biometrics*. 17: 475-480.

- Shadakshari, T.V., Kalaimagal, T., Senthil, N., Boranayaka, M.B., Kambegowda, R. and Rajesha, G. 2011.** Genetic diversity studies in soybean (*Glycine max* (L.) Merrill) based on morphological characters. *Asian J. of Bio Sci.*, 6(1): 7-11.
- Sharma, B., Singh, B.V., Singh, K., Pushpendra., Gupta, A.K. and Gupta, M.K. 2006.** Genetic divergence in Indian varieties of soybean [*Glycine max* (L.) Merrill.]. *Soybean Research*. 3: 9-16.
- Sharma, S., Saxena, A.K., Gill, B.S. and Dhillon, S.K. 2008.** Identification of soybean genotypes with superior quality traits and their correlation with oil and protein. *Indian Journal of Genetics*. 68(3): 265-268.
- Sharma, S.M., Rao, S.K. and Goswami, U. 1983.** Genetic variation, correlation and regression analysis and their implications in selection of exotic soybean. *Mysore J. Agric. Sci.*, 17: 26-30.
- Sharma, S.R. 2000.** Genetic divergence in soybean. *J. Oilseed Res.*, 17(1): 17-19.
- Sharma, A., Nair, P.M. and Pawar, S.E. 1993.** Identification of soybean strains resistant to *Xanthomonas campestris* pv. *glycines*. *Euphytica*. 67: 95-99.
- Showkat, M. and Tyagi, S.D. 2010.** Correlation and path coefficient analysis of some quantitative traits in soybean (*Glycine max* L. Merrill.). *Res. J. Agric. Sci.*, 1(2): 102-106.
- Shrivastava, M.K., Shukla, R.S. and Singh, C.B. 1998.** Relationship between yield and its components in diverse genotypes of soybean. *Adv. in Plant Sciences.*, 11: 193-98.
- Shruti, K., Basavaraja, G.T., Shobha, I. and Vijayakumar, A.G. 2015.** Correlation and path coefficient analysis for yield and its components in soybean (*Glycine max* L. Merrill). *The Bioscan*. 10(4): 2065-2067.
- Sichkar, V.I., Grigoryan, E.M. and Lugovoi, A.P. 1988.** Multivariate analysis of Mahalanobis distance parameters for economically useful characters in different groups of soybean. *Tsitologiya I Genetica*. 22(3): 37-43.
- Sihag, R., Hooda, J.S., Vashistha, R.D. and Malik, B.P.S. 2004.** Genetic divergence in soybean [*Glycine max* (L.) Merrill.]. *Annals of Biology*. 20(1): 17-21.

- Singh, B.B. and Malick, A.S. 1978.** Inheritance of resistance to yellow mosaic in soybean. *Indian J. Genet.*, 38: 258-261.
- Singh, B.B., Gupta, S.C. and Singh, B.D. 1974a.** Sources of field resistance to rust and yellow mosaic diseases of soybean. *Indian J. Genet.*, 34: 400-404.
- Singh, I., Phul, P.S., Singh, T.P., Gupta, R.P. and Sharma, S.R. 1995.** Genetic variability and response of soybean genotypes to *Bradyrhizobium japonicum* inoculation. *J. Res. Punjab Agri. Univ.*, 32(3): 245-252.
- Singh, R.J. and Hymowitz, T. 1999.** Soybean genetic resources and crop improvement. *Genome*. 42(4): 605-616.
- Singh, R.K. and Chaudhary, B.D. 1977.** Biometrical methods in quantitative genetic analysis. New Delhi-Ludhiana, India. Kalyani publishers. 318 p.
- Sirohi, S.P.S., Malik, S., Singh, S.P., Yadav, R., and Meenakshi. 2007.** Genetic variability, correlations and path coefficient analysis for seed yield and its components in soybean [*Glycine max* (L.) Merrill]. *Progr. Agric.*, 7(1/2): 119-123.
- Sivasubramanian, S. and Menon, P.M. 1973.** Genotypic and phenotypic variability in rice. *Madras Agric. J.*, 60(9-13): 1093-1096.
- Skaloud, V. and Kovacik, A. 1994.** Findings on sunflower self-fertility in connection with line hybridization. *Helia*. 17(20): 13- 20.
- Smartt, J. 1990.** Evolution of genetic resources. In: *Grain legumes*, ed. J. Smartt. Cambridge, Cambridge University Press. pp. 140-175.
- Snedecor, G. W and Cochran, W.G. 1967.** Statistical methods. 6th ed. New Delhi. Oxford and IBH Pub. Co.
- Sonwane, J.K., Kashid, N.V., Kamble, M.S. and Ahire, R.K. 2006.** Study of yield, yield attributes and grain protein of soybean genotypes. *Indian Journal of Agricultural Research*. 40(2): 92-97.
- Srivastava, A.N. and Jain, J.K. 1994.** Variability and coheritability estimates for physiological and economic attributes in soybean. *Indian J. Genet.*, 54(2): 179-183.

- Sureshrao, S.S., Singh, V.J., Srihima, G. and Rangare, N. R. 2014.** Assessment of genetic variability of the main yield related characters in soybean. *International Journal of Food, Agriculture and Veterinary Sciences*. 4(2): 69-74.
- Suryadi, Y., Suhendar, M.A., Akhdiya, A., Manzila, I. and Wawan. 2012.** Evaluation of soybean germplasm for its resistance to several foliar pathogens in Indonesia. *Journal of Agricultural Technology*. 8(2): 751-763.
- Talukdar, A., Harish, G.D., Shivakumar, M., Kumar, B., Verma, K., Lal, S.K., Sapra, R.L. and Singh, K.P. 2013.** Genetics of yellow mosaic virus (YMV) resistance in cultivated soybean [*Glycine max* (L.) Merr.]. *Legume Res.*, 36(3): 263-267.
- Thakur, D.K., Nag, S.N., Gendley, T.K. and Patel, R.K. 2015.** Character association and path coefficient analysis for seed yield and its contributing traits in soybean [*Glycine max* (L.) Merrill]. *The Bioscan*. 10(4): 1947-1950.
- Thompson, J.A., Nelson, R.L. and Vodkin, L.O. 1998.** Identification of diverse soybean germplasm using RAPD markers. *Crop Sci.*, 38: 1348-1355.
- Thorat, A., Narkhede, M.N. and Khorgade, P.W. 2001.** Correlation studies in soybean (*Glycine max* (L.) Merril). *Annals of Plant Physio.*, 13(2): 195-198.
- Tiwari, S.P. 2001.** Introduction, diversity and enhancement of soybean genetic resources in India – A status report. Rome, Italy. Consultancy report for the IPGRI. pp. 1-67.
- Turkey, H. B. 1954.** Causation, segregation and path-analysis. *In: Statistics and Mathematics in Biology*. Ames, Iowa. Iowa State College Press.
- Tyagi, S.D. and Sethi, J. 2011.** Genetic Diversity Pattern in Soybean [*Glycine max* (L.) Merrill]. *Research Journal of Agricultural Sciences*. 2(2): 288-290.
- Upadhyaya, H.D. 2003.** Phenotypic diversity in groundnut (*Arachis hypogaea* L.) core collection assessed by morphological and agronomical evaluations. *Genet. Res. Crop Evol.*, 50: 539-550.
- Upadhyaya, H.D., Ortiz, R., Bramel, P.J. and Singh, S. 2002.** Phenotypic diversity for morphological and agronomic characteristics in chickpea core collection. *Euphytica*. 123(3): 333-342.
- Vavilov, N.I. 1926.** Studies on the origin of cultivated plants. *Bull. Appl. Bot.*, 16: 2.

- Ward, J.H. 1963.** Hierarchical grouping to optimize an objective function. *Journal of the American statistical Association*. 58(301): 236-244.
- Wilson, R.F. 2004.** Seed composition. In: H.R. Boerma and J.E. Specht, eds, Soybeans: Improvement, Production, and Uses, Vol 3. Madison, WI. American Society of Agronomy, Crop Science Society of America, and Soil Science Society of America. pp. 621–677.
- Wright, S. 1921.** Correlation of causation. *Journal of Agricultural Research*. 20: 202-209.
- Yadav, N.S. 2005.** Estimation of genetic diversity and characters association for yield and its components in elite lines of soybean [*Glycine max* (L.) Merrill]. Thesis, M.Sc. G.B. Pant University of Agriculture and Technology, Pantnagar. pp. 1-124.
- Yadav, S.P. and Sharma, S.P. 2001.** Variation for hilum colour and its stability during four crop seasons in soybean (*Glycine max*). *Indian Journal of Agricultural Sciences*. 71(1): 23-26.
- Zarkadas, C.G., Gagnon, C., Gleddie, S., Khanizadeh, S., Cober, E.R. and Guillemette, R.J.D. 2007.** Assessment of the protein quality of fourteen soybean [*Glycine max* (L.) Merr.] cultivars using amino acid analysis and two-dimensional electrophoresis. *Food Research International*. 40: 29-146.
- Zhu, J.C., 1992.** Study on the heritability, genetic advance and correlation of primary agronomic traits of spring soybean varieties sown in spring and autumn. *Soybean Sci.*, 11: 322-8.



APPENDICES

Appendix I

Standard Meteorological Week's average weather data for 2014 at G.B. Pant University of Agriculture & Technology

Standard Metro. Week No.(2014)	Temperature (°C)		Relative Humidity (%)		Rainfall (mm)	No. of Rainy Days	Sun-Shine Hrs.	Wind Velocity (km/hr.)	Evap. (mm)
	Max.	Min.	0712 am	1412 pm					
22	37.4	25.4	68.0	38.0	21.2	1	9.5	8.1	8.5
23	41.0	26.6	65.0	34.0	0.0	0	11.4	6.9	8.1
24	38.3	25.7	71.0	45.0	23.6	1	6.5	9.4	9.6
25	35.0	25.7	83.0	55.0	67.0	1	5.9	9.0	5.5
26	36.9	26.6	78.0	53.0	2.8	2	7.2	5.4	6.9
27	32.3	25.4	88.0	67.0	50.8	4	2.4	5.2	4.5
28	33.5	26.9	87.7	71.0	50.6	2	3.1	6.1	5.2
29	30.5	25.6	92.0	80.0	265.6	6	2.1	7.6	4.5
30	32.5	26.2	88.0	67.0	15.8	3	4.7	6.6	4.0
31	33.5	25.8	90.0	67.0	72.0	5	6.1	5.3	4.0
32	33.3	26.3	88.0	68.0	34.4	3	7.9	6.7	4.8
33	32.3	25.6	89.0	71.0	27.0	2	4.8	6.5	3.9
34	34.2	25.9	90.0	64.0	0.0	0	7.1	4.5	6.6
35	33.9	25.7	86.0	62.0	1.2	1	7.5	5.3	5.8
36	33.2	25.1	85.0	63.0	1.2	1	8.7	7.3	5.4
37	32.0	23.5	92.0	67.0	5.4	4	5.4	4.6	3.9
38	33.2	23.3	89.0	63.0	29.4	1	8.3	4.0	5.5
39	32.7	21.3	89.0	58.0	1.0	1	8.3	5.2	4.7
40	32.0	22.3	90.0	60.0	5.6	2	4.9	2.8	3.2
41	32.7	17.9	87.0	55.0	1.6	2	9.2	3.7	3.7
42	26.9	15.5	91.0	51.0	8.2	1	7.5	3.2	3.1
43	30.9	16.6	85.0	55.0	0.0	0	5.3	1.7	2.5
44	28.5	13.1	91.0	46.0	0.0	0	4.3	1.8	2.6
45	29.2	12.8	91.0	46.0	0.0	0	8.2	2.7	2.5
46	27.9	9.5	94.0	34.0	0.0	0	7.7	2.7	2.9
47	26.3	8.6	92.0	38.0	0.0	0	8.0	2.0	2.4
48	26.2	8.7	92.0	41.0	0.0	0	7.9	2.3	2.3
49	24.3	9.9	94.0	49.0	0.0	0	4.9	2.0	1.8
50	20.8	8.2	91.0	57.0	40.1	2	4.3	5.3	2.1
51	16.8	7.4	96.0	78.0	0.0	0	4.1	3.9	1.2
52	18.5	4.9	95.0	57.0	0.0	0	5.2	3.4	1.1

Appendix II

Adjusted mean values of soybean genotypes for yield and yield contributing traits

S.No.	Genotype	Character evaluated														
		DTF	DTM	PH (cm)	NBP	NNP	NPB	NPP	NSP	HSW (g)	DWP (g)	HI (%)	SYE	OC (%)	PC (%)	SYP (g)
1	AGS 129	51.65	97.30	78.04	4.03	22.70	38.00	72.05	2.52	8.16	28.91	50.89	0.51	17.45	41.14	15.98
2	EC 389148	40.65	93.30	69.34	4.03	14.70	29.40	57.05	2.31	6.90	32.34	23.29	0.58	16.05	42.50	8.78
3	Jupiter	51.65	109.30	121.44	3.03	24.70	32.20	65.05	2.24	10.20	28.74	50.29	0.50	22.00	38.54	15.72
4	T-49	59.65	114.30	105.04	5.03	23.70	31.80	53.45	2.14	7.83	22.81	40.29	0.40	15.30	39.28	10.40
5	P RAB 1	56.65	113.30	69.24	3.03	17.70	26.20	51.05	2.29	9.06	26.04	39.29	0.45	20.40	40.03	11.46
6	AMS 155 (A)	51.65	100.30	55.24	4.03	20.50	25.00	53.05	2.14	10.05	30.53	33.89	0.54	18.15	40.34	11.60
7	TGX 855-39E	45.65	96.30	62.54	4.03	16.70	22.40	59.05	2.17	10.75	25.20	43.29	0.44	15.90	41.72	12.14
8	AMS 77-3-6	48.65	95.30	70.44	4.03	18.10	20.00	51.05	2.39	12.92	33.94	37.29	0.61	17.25	40.52	13.94
9	AMS 2005-19	48.65	98.30	54.04	3.03	17.70	19.00	52.05	2.14	7.57	34.92	23.29	0.64	17.80	41.36	9.40
10	EC 16738	56.65	97.30	82.54	5.03	16.30	38.40	76.05	2.16	7.29	36.46	33.29	0.67	18.50	40.37	13.43
11	EC 37937	46.65	95.30	69.04	6.03	17.50	20.40	53.05	2.01	11.12	34.44	34.09	0.63	14.50	43.44	13.02
12	EC 39362	46.65	94.30	61.64	6.03	19.70	32.20	61.05	2.26	9.56	32.05	37.29	0.57	14.35	41.75	13.22
13	EC 39491	46.65	91.30	55.44	2.03	16.50	24.20	56.65	2.06	10.26	38.37	29.29	0.72	17.25	39.05	12.54
14	EC 65772	46.65	93.30	69.54	4.03	19.90	28.00	59.05	2.06	10.36	31.06	41.69	0.55	14.20	43.00	14.22
15	RVS 2006-27	51.65	98.30	67.64	2.83	20.10	21.00	55.05	2.29	7.10	28.91	31.29	0.51	19.60	39.54	10.28
16	EC 95291	45.65	97.30	41.24	2.03	9.50	17.00	27.85	1.87	10.60	22.74	15.29	0.39	19.25	37.26	4.65
17	EC 100027	48.65	93.30	50.34	3.03	14.70	26.20	59.05	1.97	8.52	27.27	37.29	0.47	15.30	41.12	11.41
18	IC 13051	47.65	95.30	91.94	6.03	21.50	40.20	75.05	2.06	7.30	45.65	31.49	0.94	19.80	40.78	15.73
19	EC 14626	52.65	97.30	72.14	4.03	17.70	30.00	63.05	1.85	6.86	22.96	33.29	0.40	13.70	39.24	8.84
20	JS 82	46.65	96.30	55.24	4.03	14.90	29.00	52.05	2.23	8.81	34.13	26.29	0.62	14.75	37.09	10.24
21	PI 283327	46.65	93.30	43.54	5.03	12.10	28.00	60.05	2.25	8.91	45.20	24.29	0.93	17.30	40.99	12.32
22	PK 765	48.65	97.30	51.34	4.03	17.50	31.60	68.45	2.21	6.50	32.65	24.89	0.59	18.00	40.50	9.38
23	MACS 1394	59.65	99.30	69.14	4.03	17.70	38.80	76.05	2.14	8.64	40.34	27.29	0.78	17.55	39.62	12.32
24	GP 305	50.65	105.30	72.04	2.03	18.30	27.00	55.85	2.12	5.11	34.05	22.09	0.62	13.85	43.84	8.78
25	RPSP 935-E	50.65	115.30	57.94	4.03	20.50	24.60	54.05	2.11	8.52	25.84	33.29	0.45	17.65	40.26	9.82
26	GP 465	49.65	106.30	62.04	4.03	17.10	32.20	60.05	1.85	7.65	23.12	34.29	0.40	19.15	40.81	9.13
27	Himso 175	51.65	108.30	50.94	3.03	18.70	23.00	52.05	1.97	7.96	26.93	31.29	0.47	19.10	39.30	9.65
28	GP 448	48.65	101.30	58.44	3.03	16.50	34.20	74.05	2.12	8.08	32.27	34.29	0.58	17.50	42.03	12.33
29	WT 150	50.65	109.30	51.54	3.03	13.20	28.20	55.65	2.15	9.31	35.29	27.23	0.47	19.35	40.55	10.84
30	MAUS 76	48.65	109.30	50.04	3.03	15.50	18.00	39.05	2.23	9.80	29.29	26.04	0.45	20.20	40.00	8.84
31	MAUS 102	48.65	99.30	48.64	4.03	17.90	18.40	48.05	2.69	8.12	25.29	46.51	0.97	17.50	41.25	13.12
32	MAUS 489	50.65	95.30	39.44	3.03	9.90	23.20	52.05	2.52	7.44	29.29	32.00	0.57	18.75	40.16	10.63

S.No.	Genotype	Character evaluated														
		DTF	DTM	PH (cm)	NBP	NNP	NPB	NPP	NSP	HSW (g)	DWP (g)	HI (%)	SYE	OC (%)	PC (%)	SYP (g)
33	MAUS 38	51.65	97.30	68.94	5.03	22.30	32.00	68.05	2.16	7.55	24.29	38.24	0.72	17.85	35.83	10.58
34	MAUS 85	50.65	102.30	45.24	3.03	16.50	18.00	34.05	2.28	8.94	21.29	29.07	0.51	17.55	40.98	7.41
35	MAUS 149	46.65	97.30	44.44	4.03	16.70	19.80	50.05	2.19	9.58	28.29	35.15	0.64	16.75	41.68	11.22
36	AMS 2005-24	51.65	96.30	64.04	5.03	21.70	24.40	59.05	2.29	7.90	35.29	26.70	0.46	20.45	41.28	10.65
37	MAUS 164	48.65	111.30	38.54	4.03	15.90	21.00	48.05	2.41	10.10	30.29	36.35	0.67	16.40	41.24	12.30
38	EC 963805	62.65	111.30	61.04	3.03	17.10	22.20	51.05	2.16	8.13	27.29	30.87	0.55	20.40	36.96	9.67
39	EC 281462	51.65	98.30	68.14	6.03	20.70	27.20	58.05	2.33	6.66	34.29	25.89	0.45	17.50	41.33	10.10
40	EC 116343	48.65	95.30	57.24	4.03	17.10	17.00	41.05	2.41	8.89	21.29	36.02	0.66	19.90	37.60	8.94
41	EC 172607	47.85	92.30	72.30	4.83	13.50	27.80	54.45	2.31	7.95	25.39	42.69	0.59	18.81	40.03	9.02
42	EC 33940	50.85	96.30	62.90	3.83	21.90	25.00	50.45	2.33	7.53	26.39	37.96	0.47	19.56	40.69	8.23
43	EC 2581	47.85	96.30	58.80	4.83	19.10	23.40	56.45	2.43	9.63	41.39	34.59	0.40	18.71	37.33	12.06
44	EC 118443	47.85	94.30	62.90	4.83	16.10	21.40	52.45	2.67	8.73	31.39	44.07	0.63	16.76	40.02	11.79
45	RKS 30	55.85	112.30	76.30	3.83	22.30	22.40	52.45	2.24	6.39	35.39	24.37	0.21	15.81	36.84	6.71
46	RKS 27	47.85	104.30	55.50	3.83	15.70	13.60	43.45	1.98	11.58	30.39	37.51	0.46	16.91	39.10	9.48
47	AMS 243-7-3	47.85	96.30	71.30	3.83	19.10	21.00	48.45	2.41	7.85	35.39	29.41	0.30	16.26	39.06	8.43
48	AMS 42	47.85	100.30	69.80	6.83	18.10	27.40	75.45	2.98	9.93	53.39	44.92	0.65	16.16	40.12	21.17
49	AMS 50B	52.85	112.30	92.90	4.83	23.30	37.40	76.45	2.46	8.89	55.39	31.49	0.33	14.01	42.97	14.74
50	AMS 100-16-4-1-3	47.85	94.30	61.70	7.83	16.70	28.80	89.45	2.71	9.00	59.39	40.13	0.52	17.01	41.41	20.88
51	AMS -25-5-1	50.85	101.30	69.50	2.83	13.50	21.00	56.25	2.23	6.82	20.39	41.65	0.56	16.76	41.63	6.86
52	AMS 100-25-5	50.85	110.30	110.30	5.83	14.10	40.20	63.45	2.50	8.84	51.39	29.66	0.30	17.36	40.75	12.71
53	AMS 100	45.85	93.30	57.80	2.83	11.70	21.80	47.45	2.53	9.06	29.39	43.48	0.61	17.26	40.41	10.81
54	AMS 115	44.85	104.30	67.90	4.83	13.70	20.00	44.45	2.82	9.70	31.39	43.47	0.61	18.46	38.88	11.61
55	AMS 2005-13	44.85	96.30	50.40	2.43	15.10	28.80	48.45	2.24	7.59	39.39	26.96	0.25	20.61	40.84	8.54
56	AMS MB 5-19	47.85	98.30	72.40	3.83	13.10	18.80	41.45	2.25	7.48	21.39	35.19	0.41	19.46	39.48	5.95
57	AMS MB 5-18	44.85	94.30	65.40	2.83	12.10	21.00	59.65	2.32	6.69	27.39	37.71	0.47	16.51	42.18	8.51
58	AMS 56	50.85	96.30	64.20	3.83	12.50	28.40	54.45	2.37	7.49	28.39	39.11	0.50	19.41	42.26	9.23
59	AMS 59	50.85	96.30	64.70	3.83	13.70	22.00	53.45	2.24	7.21	22.39	46.11	0.69	19.56	39.45	8.56
60	AMS 38-24	37.85	99.30	56.90	3.83	10.70	23.00	51.45	2.32	12.56	39.39	41.89	0.56	21.81	38.95	14.21
61	EC 685243	36.85	92.30	39.00	4.83	12.70	20.20	48.45	2.20	15.43	40.39	44.11	0.63	19.71	38.98	15.46
62	RVS 2006-19	45.85	96.30	46.20	2.63	16.70	20.60	47.45	2.34	8.64	32.39	32.67	0.36	18.11	42.21	8.66
63	EC 457174	41.85	100.30	51.80	2.83	11.70	20.40	55.65	2.38	12.90	31.39	33.14	0.37	17.56	41.23	8.51
64	IC 437079	43.85	101.30	59.00	1.83	11.10	10.80	38.45	2.22	9.03	24.39	36.61	0.44	17.91	39.01	7.23
65	SL 983	47.85	105.30	66.30	2.83	14.10	14.80	39.85	2.19	8.24	20.39	43.23	0.61	18.31	37.38	7.16
66	K 88-262A	49.85	106.30	71.40	3.83	13.70	19.40	45.45	2.44	10.67	31.39	41.02	0.55	20.91	40.16	10.87
67	GP 393	49.85	109.30	61.50	1.83	11.30	17.60	36.45	2.36	10.82	29.39	35.05	0.41	21.81	38.79	8.45
68	GP 67	50.85	106.30	71.80	3.83	12.50	29.20	62.45	2.37	8.13	46.39	27.67	0.26	20.11	35.21	10.50

S.No.	Genotype	Character evaluated														
		DTF	DTM	PH (cm)	NBP	NNP	NPB	NPP	NSP	HSW (g)	DWP (g)	HI (%)	SYE	OC (%)	PC (%)	SYP (g)
69	SL(E) 1	39.85	100.30	71.20	3.83	13.70	33.40	58.45	2.15	8.40	25.39	44.92	0.65	22.36	37.00	9.55
70	AGS 751	44.85	106.30	52.40	3.83	11.10	13.60	35.45	2.28	14.10	25.39	46.07	0.69	20.31	41.23	9.83
71	DT 21	45.85	102.30	49.80	2.83	10.10	13.80	42.45	2.36	10.25	25.39	45.19	0.66	19.86	40.30	9.62
72	Cat. 118	43.85	96.30	58.90	3.83	11.70	18.60	36.45	2.31	11.49	23.39	45.94	0.68	19.01	39.85	8.95
73	Cat. 50 (A)	43.85	95.30	76.00	2.83	12.50	27.00	49.45	2.40	9.15	24.39	46.31	0.70	15.91	41.44	9.46
74	Cat. 209	37.85	89.30	37.80	2.83	11.50	12.60	28.45	2.17	8.36	15.39	40.87	0.54	18.16	42.56	4.84
75	Cat. 142	47.85	95.30	43.40	4.83	12.70	23.80	43.45	2.39	9.19	26.39	40.68	0.54	16.06	41.67	8.91
76	Cat. 133	51.85	102.30	64.40	4.83	11.70	26.00	72.45	2.39	8.09	38.39	43.10	0.60	18.86	40.96	14.27
77	Cat. 886	52.85	103.30	52.20	3.83	11.10	18.20	41.45	2.34	7.01	19.39	38.99	0.50	17.01	42.96	6.00
78	Cat. 305	50.85	96.30	63.80	4.83	12.50	23.60	49.45	2.28	7.72	27.39	34.83	0.40	19.06	40.49	7.76
79	Cat. 2503	38.85	92.30	62.00	3.83	12.70	19.40	43.45	2.19	6.60	23.39	31.35	0.33	15.16	42.85	5.74
80	Cat. 780	45.85	94.30	48.80	2.83	10.90	15.40	36.25	2.43	7.03	24.39	32.14	0.35	18.66	41.88	6.20
81	Cat. 148	47.65	92.90	61.98	5.23	12.30	25.20	57.05	2.23	5.52	26.39	23.11	0.33	13.39	42.71	6.72
82	Cat. 3284	50.65	97.90	50.38	3.23	13.10	11.80	35.05	2.44	9.31	16.39	31.20	0.49	15.49	42.11	5.57
83	Cat. 2430	45.65	96.90	55.58	2.23	14.30	13.40	38.05	2.54	8.41	20.39	30.37	0.47	15.49	41.24	6.73
84	Cat.103	46.65	95.90	55.98	3.23	14.70	21.00	52.85	2.19	6.61	15.39	39.91	0.71	14.49	41.75	6.63
85	Cat. 537	51.65	99.90	63.78	4.23	14.50	18.20	53.45	2.34	7.00	26.39	26.94	0.40	14.14	42.17	7.75
86	Cat. 366	51.65	102.90	70.98	5.23	15.10	20.60	48.25	2.23	7.85	25.39	27.16	0.40	16.34	41.55	7.52
87	Cat. 3327	51.65	103.90	73.88	5.23	14.70	23.00	57.05	2.12	7.83	29.39	26.78	0.39	15.14	39.29	8.58
88	Cat. 783	51.65	101.90	71.38	4.23	13.30	16.60	48.05	2.29	6.62	19.39	31.95	0.50	18.09	37.48	6.72
89	Cat. 181	55.65	104.90	66.28	4.23	15.10	17.00	46.05	2.32	8.77	25.39	22.77	0.32	17.19	40.46	6.37
90	Cat. 307	45.65	94.90	87.48	5.23	15.30	22.80	52.05	2.61	9.68	37.39	27.48	0.41	17.39	39.86	11.16
91	Cat. 195	45.65	95.90	45.38	3.23	14.30	25.40	55.05	2.36	8.64	26.39	33.85	0.55	17.44	40.25	9.62
92	Cat. 2388	45.65	95.90	57.58	3.23	18.10	18.00	46.05	2.26	7.42	20.39	31.18	0.49	17.59	40.04	6.90
93	EC 2581	47.65	94.90	50.68	6.23	16.50	32.00	64.05	2.59	10.70	44.39	31.98	0.51	18.64	39.88	15.26
94	RVS 2002-6	49.65	96.90	44.18	3.43	15.90	23.00	54.05	2.38	7.52	29.39	25.92	0.38	21.04	38.25	8.32
95	RVS 2002-7	49.65	93.90	59.58	4.83	16.30	25.80	59.05	2.53	11.09	39.39	33.55	0.54	22.34	36.70	14.18
96	MACS 993	51.65	113.90	63.78	6.23	17.90	36.20	84.05	2.33	8.37	54.39	24.00	0.34	18.74	39.50	14.28
97	RVS 2006-1	36.65	96.90	48.78	3.63	14.90	21.80	44.05	2.23	10.55	24.39	32.29	0.51	21.34	38.48	8.51
98	EC 457161	44.65	104.90	52.58	4.23	14.50	18.80	61.05	2.34	9.16	40.39	27.19	0.40	16.74	40.79	11.93
99	Chocalete Bold	44.65	102.90	43.98	4.03	14.90	18.20	48.65	2.08	8.09	31.39	20.10	0.27	15.09	41.29	7.02
100	Cat. 2755	45.65	98.90	66.88	4.23	16.50	21.80	37.05	2.32	14.04	22.39	33.68	0.55	15.24	41.04	8.14
101	IC 49685	45.65	95.90	63.38	3.23	17.50	17.00	38.05	2.46	8.26	26.39	21.59	0.30	15.99	38.58	6.31
102	Cat 2511	48.65	107.90	60.98	4.23	16.30	18.20	46.05	2.41	8.76	26.39	27.93	0.42	15.49	39.28	8.02
103	Cat. 779	51.65	103.90	57.48	3.23	18.50	24.40	47.05	2.48	7.18	31.39	19.97	0.27	14.29	40.02	6.97
104	Cat. 710	47.65	97.90	48.28	3.23	14.90	19.00	39.05	2.38	10.27	29.59	23.05	0.32	15.64	39.78	7.51

S.No.	Genotype	Character evaluated														
		DTF	DTM	PH (cm)	NBP	NNP	NPB	NPP	NSP	HSW (g)	DWP (g)	HI (%)	SYE	OC (%)	PC (%)	SYP (g)
105	Cat. 891	50.65	105.90	39.38	4.23	11.30	27.00	55.05	2.23	6.29	23.39	27.02	0.40	13.14	42.50	6.90
106	Cat. 340	47.65	92.90	44.78	3.23	16.50	17.60	38.05	2.45	9.81	26.39	28.00	0.42	15.04	42.25	8.04
107	Cat. 805	44.65	95.90	53.98	5.23	17.70	25.20	44.05	2.40	11.67	34.39	28.37	0.43	17.29	41.11	10.58
108	F4P21	49.65	97.90	64.38	3.23	13.10	20.40	55.05	2.39	7.01	32.39	23.00	0.32	18.89	39.08	8.20
109	MACS 303	50.65	98.90	43.38	4.23	14.90	23.20	57.05	2.30	6.50	30.39	21.54	0.30	18.04	41.96	7.24
110	G 620	50.65	103.90	40.58	3.23	16.30	22.40	49.05	2.40	8.31	20.39	39.57	0.70	15.54	39.92	8.66
111	G5P22 (PI)	45.65	91.90	29.38	2.23	8.70	13.80	37.05	2.19	8.99	21.39	26.21	0.38	16.74	41.54	6.14
112	EC 457198	47.65	93.90	42.48	6.23	13.30	20.40	56.05	2.44	11.61	39.39	33.57	0.54	16.24	41.19	14.18
113	Cat. 135A	44.65	97.90	51.38	2.23	15.50	17.00	46.05	2.37	12.05	34.39	31.48	0.49	14.54	42.53	11.67
114	Cat. 902	51.65	105.90	58.78	6.23	19.50	47.40	64.05	2.35	5.32	35.39	18.38	0.25	15.19	40.01	7.29
115	G 11	50.65	101.90	55.48	4.23	18.30	22.80	50.05	2.29	7.07	34.39	18.88	0.25	15.64	41.96	7.26
116	Cat. 746	47.65	101.90	39.08	3.23	15.70	13.40	36.05	2.09	8.55	14.39	30.54	0.47	17.44	40.66	4.80
117	Cat. 938	43.65	103.90	42.48	3.23	13.70	18.40	45.05	2.29	7.69	23.39	26.52	0.39	18.34	40.00	6.78
118	PP 6 (PI)	43.65	100.90	41.28	4.23	12.30	29.20	50.05	2.63	8.25	25.39	34.00	0.55	18.19	39.93	9.30
119	PS 1024	47.65	107.90	26.38	3.23	11.30	15.00	35.05	2.51	8.32	19.39	26.85	0.40	21.04	39.25	5.70
120	Typical Bhatt (B)	55.65	105.90	84.38	4.63	19.40	26.80	61.85	2.43	4.35	31.39	22.29	0.31	13.55	43.55	7.72
121	PK 327	47.85	102.50	50.98	3.11	16.90	16.60	38.45	2.39	9.08	24.93	35.45	0.55	17.41	41.59	8.67
122	PS 564	47.85	102.50	34.78	3.31	13.90	17.80	32.45	2.39	10.03	22.93	35.52	0.55	20.56	38.28	7.95
123	PS 1225	52.85	106.50	50.78	7.91	12.90	31.60	81.45	2.44	10.00	49.93	41.95	0.73	18.21	40.90	21.06
124	PS 1551	45.85	102.50	53.58	4.91	15.30	21.20	52.85	2.39	12.34	45.93	31.60	0.46	20.46	39.96	14.58
125	PS 1480	50.85	106.50	73.18	5.11	17.30	26.60	50.45	2.69	10.23	44.93	31.14	0.45	21.11	37.19	14.04
126	Shilajeet	50.85	94.50	23.98	4.71	13.90	18.80	58.45	2.29	8.55	33.93	34.23	0.52	18.76	40.03	11.55
127	Ankur	50.85	96.50	52.18	4.11	14.50	25.00	47.45	2.29	9.70	41.93	25.39	0.33	18.46	38.28	10.66
128	PS 1029	47.85	101.50	52.58	3.11	15.50	25.80	42.45	2.29	8.01	33.93	24.90	0.32	19.61	39.65	8.37
129	Alankar	50.85	100.50	54.38	4.91	15.90	21.00	49.45	2.24	10.37	35.93	33.81	0.51	19.61	40.90	12.10
130	PK 416	47.85	110.50	62.98	3.51	14.30	20.00	31.45	2.49	11.81	27.93	33.44	0.50	21.61	39.19	9.20
131	PK 262	50.85	110.50	59.98	5.91	15.90	28.80	58.45	2.44	11.35	49.93	32.44	0.48	18.26	39.84	16.31
132	PS 19	47.85	109.50	40.58	4.71	16.90	10.20	56.45	2.29	9.80	44.93	28.52	0.39	20.16	39.30	12.87
133	Kalitur	50.85	112.50	107.78	5.31	26.10	25.00	35.45	2.34	7.51	20.93	29.08	0.40	17.31	38.84	5.87
134	EC 250608	39.85	93.50	67.18	3.91	19.10	22.80	53.45	2.09	5.18	17.93	36.65	0.58	14.51	42.11	6.32
135	JS 20-41	44.85	92.50	55.18	2.91	15.70	20.80	40.45	2.19	9.54	29.93	28.50	0.39	17.86	40.66	8.41
136	EC 251358	44.85	94.50	55.38	2.91	20.30	22.80	37.45	2.39	9.45	21.93	40.58	0.69	17.61	40.08	8.70
137	JS 20-27	43.85	94.50	44.58	2.11	14.30	16.00	35.45	2.19	8.32	17.93	39.15	0.65	17.11	41.19	6.77
138	JS 20-61	43.85	96.50	51.98	2.91	15.50	24.40	48.45	2.64	9.97	44.93	25.67	0.34	18.41	37.17	11.58
139	JS 20-34	36.85	93.50	33.98	2.91	10.90	10.20	30.65	2.34	10.29	31.93	25.18	0.33	17.31	41.39	7.94
140	JS 20-38	37.85	94.50	33.58	2.71	13.10	13.80	39.45	2.29	7.17	24.93	26.79	0.36	14.16	42.48	6.50

S.No.	Genotype	Character evaluated														
		DTF	DTM	PH (cm)	NBP	NNP	NPB	NPP	NSP	HSW (g)	DWP (g)	HI (%)	SYE	OC (%)	PC (%)	SYP (g)
141	JS 20-30	45.85	101.50	36.78	4.91	14.10	21.20	59.45	2.39	6.85	26.93	36.50	0.57	21.36	39.66	9.68
142	AMS 62	48.85	97.50	56.98	4.11	20.10	19.20	24.45	2.09	8.28	20.93	23.20	0.29	19.21	40.38	4.63
143	EC 250619	43.85	92.50	50.78	3.31	15.50	27.20	47.45	2.79	6.06	31.93	24.31	0.31	17.81	39.73	7.66
144	JS 20-75	49.85	99.50	53.98	2.91	18.50	15.60	30.45	2.54	7.46	18.93	33.45	0.50	17.51	41.98	6.09
145	JS 20-60	44.85	101.50	48.58	2.31	15.50	14.00	31.45	2.39	6.87	25.93	19.72	0.23	15.86	42.41	4.94
146	JS 20-21	44.85	98.50	47.48	3.91	14.70	15.80	44.45	2.54	7.26	30.93	26.03	0.34	17.96	42.26	7.94
147	JS 20-31	49.85	96.50	56.98	1.91	17.70	19.60	55.45	2.39	6.63	31.93	27.13	0.36	18.01	38.28	8.57
148	JS 20-23	51.85	99.50	60.58	2.91	19.50	17.60	37.45	2.74	7.71	24.93	32.28	0.47	22.86	37.69	7.88
149	EC 396053	43.85	102.50	61.18	4.31	19.70	25.20	40.45	2.59	7.49	23.93	34.10	0.51	15.51	40.04	7.98
150	EC 250607	38.85	91.50	44.98	3.91	13.90	10.20	52.45	1.89	9.27	28.93	31.83	0.46	15.86	42.74	9.08
150	EC 325099	52.85	104.50	59.18	5.31	20.90	31.60	43.45	2.39	9.54	34.93	28.10	0.38	17.26	38.66	9.75
152	JS 20-29	44.85	95.50	54.78	4.31	18.50	26.40	44.45	2.49	13.00	37.93	37.24	0.59	19.11	40.77	14.10
153	JS 20-25	35.85	107.50	47.58	3.31	16.10	25.20	39.45	2.59	6.48	25.93	27.98	0.38	16.71	41.46	7.09
154	JS 20-51	50.85	90.50	67.18	4.11	19.50	26.80	57.45	2.39	7.58	49.93	19.85	0.24	19.91	40.98	10.01
155	JS 20-54	50.85	108.50	59.38	1.51	17.70	12.60	32.45	2.34	7.02	15.93	32.74	0.48	18.46	40.03	4.94
156	JS 20-79	50.85	98.50	76.18	4.91	21.30	33.00	82.45	2.79	7.54	61.93	31.32	0.45	19.91	38.26	19.64
157	JS 20-53	50.85	100.50	63.98	4.31	15.10	22.00	29.45	2.39	11.03	24.93	23.87	0.30	18.61	39.28	5.77
158	JS 20-52	50.85	102.50	70.58	4.91	17.10	21.00	58.45	2.34	7.77	42.93	21.75	0.27	16.11	40.66	9.36
159	AMS 77-3	50.85	90.50	59.78	2.91	19.70	19.80	43.45	2.19	12.17	35.93	33.37	0.50	18.41	40.78	11.95
160	AMS 210-6	46.85	98.50	51.18	4.31	17.30	21.40	43.85	1.99	8.37	24.93	31.11	0.45	18.71	40.56	7.58
161	SL 688 (C)	49.00	116.25	61.50	7.50	22.50	46.50	67.50	2.42	9.91	48.50	32.16	0.46	20.07	38.48	15.25
162	PS 1347 (C)	49.75	117.50	56.35	7.00	21.25	30.00	66.25	2.61	9.31	36.00	43.65	0.78	20.56	40.39	15.64
163	PS 1092 (C)	41.00	112.00	51.85	7.25	20.50	28.50	64.25	2.57	9.69	41.00	38.30	0.63	21.02	40.78	15.67
164	Bragg (C)	49.00	113.75	54.98	6.50	23.50	30.25	58.75	2.73	10.09	33.00	42.81	0.80	20.35	40.78	14.54
165	PS 1042 (C)	46.50	114.00	53.93	5.40	20.50	50.75	79.50	2.45	9.76	55.45	33.06	0.48	20.94	40.88	17.98

Note: DTF= Days to 50% flowering; DTM= Days to maturity; PH= Plant Height (cm); NBP= Number of primary branches per plant; NNP= Number of nodes per plant; NPB= Number of pod bearing nodes per plant; NPP= Number of pods per plant; NSP= Number of seeds per pod; HSW= Hundred seed weight (g); DWP= Dry matter weight per plant (g); HI= Harvest Index (%); SYE= Seed yield efficiency; OC= Oil content (%); PC= Protein content (%) and SYP= Seed yield per plant (g).

VITAE

The author of this manuscript was born on 27th July, 1991 at Guntur, India. He passed his High School Examination from Government Boys High School, Guntur, (Andhra Pradesh) and Intermediate examination from Sagarmatha Junior College, Rentachintala, Andhra Pradesh. He completed his graduation (B. Sc. Agriculture) from University of Agricultural Sciences, Bangalore, Karnataka in 2014. He took admission through ICAR-JRF (PGS) in the same year and completed M.Sc. (Ag.) degree in Genetics and Plant Breeding from G. B. Pant University of Agriculture and Technology, Pantnagar (U. S. Nagar), Uttarakhand, in 2016.

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ABSTRACT

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Major : Genetics and Plant Breeding **Department** : Genetics and Plant Breeding
Thesis Title : "Studies on genetic parameters for quantitative and qualitative traits in soybean [*Glycine max* (L.) Merrill]"
Advisor : Dr. Kamendra Singh

The present investigation was carried out at N. E. Borlaug Crop Research Centre of G.B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand, India, during *khari*, 2014 with 165 genotypes (160 entries and 5 checks) of soybean for eight qualitative and fifteen quantitative characters to assess genetic divergence, genetic variability, inter-character correlation and their direct and indirect effects, screening of genotypes against YMV, BP and RAB and protein profiling of selected genotypes using SDS-PAGE to evaluate the diversity in protein content.

Results showed that qualitative characters played an important role in crop diversity and the characters flower colour and hilum colour contributed maximum towards genetic diversity. Analysis of variance showed significant differences among the genotypes for all the characters under study, which indicated adequate genetic variability among the experimental material. Based on Hierarchical cluster analysis, the 165 genotypes were grouped into 10 clusters. The maximum numbers of genotypes (124) were grouped in Cluster VII and minimum (1) in Clusters I and VI. The maximum divergence was observed between Clusters II and III (91.59) followed by I and IX (79.32) and III and X (78.13), while the least divergence was observed between Clusters IV and V (33.06). Cluster IX was found to include the most desirable genotypes as it exhibited highest cluster mean values for majority of the characters under study. Based on inter-cluster distance, cluster mean values and *per se* performance, the potential parental combinations that could be considered for enhancing the overall yield levels in soybean were, PS 1225 x Jupiter, PS 1225 x JS 20-79, PS 1225 x Cat 209, PS 1225 x SL (E) 1, PS 1225 x AMS 100-16-4-1-3, Jupiter x JS 20-79, Jupiter x Cat 209, Jupiter x AMS 100-16-4-1-3, JS 20-79 x Cat 209, JS 20-79 x SL (E) 1, JS 20-79 x AMS 100-16-4-1-3, Cat 209 x SL (E) 1, Cat 209 x AMS 100-16-4-1-3, SL (E) 1 x AMS 100-16-4-1-3, while the crosses Jupiter x SL (E) 1 and Cat 209 x AMS 50B would be promising to recover superior segregants for oil and protein contents, respectively.

In general, the magnitudes of PCV were higher than those of GCV and ECV for all the characters with a close correspondence between the values of PCV and GCV for majority of the characters under study. This indicated a minimum role of environment in their expression and hence, selection based on phenotype could be rewarding for such characters. Highest and lowest values of PCV, GCV and Genetic advance as % of mean was observed for seed yield per plant and protein content, respectively. High estimates of heritability and genetic advance were reported for plant height, number of nodes per plant, number of pod bearing nodes per plant, number of pods per plant, 100-seed weight, dry matter weight per plant, harvest index, seed yield efficiency, oil content and seed yield per plant which indicated a role of additive gene effects in their expression.

Correlation studies showed that seed yield exhibited significant positive correlations with majority of the characters like plant height, number of primary branches per plant, number of nodes per plant, number of pod bearing nodes per plant, number of pods per plant, number of seeds per pod, 100-seed weight, dry matter weight per plant, harvest index, seed yield efficiency and oil content. However, a significant but negative correlation was recorded between oil and protein contents. Path analysis indicated that, dry matter weight per plant, seed yield efficiency, number of pods per plant, 100-seed weight, number of seed per pod and number of primary branches per plant exhibited positive direct effect in influencing seed yield.

Screening of genotypes against YMV, BP and RAB showed that only two genotypes i.e., PS 1225 and PS 1480 were highly resistant against these three diseases. Also, 31 genotypes showed high resistance to YMV and BP, however, the rest all were found to be susceptible to one or the other of these three concerned diseases. Based on the estimates of protein content, 11 significantly divergent genotypes were selected from three arbitrary groups containing high, medium and low protein contents to study the diversity in total seed protein using SDS-PAGE. Although, significant differences in protein content were observed among the 11 selected genotypes, results obtained from their protein profiling through SDS-PAGE revealed only qualitative differences with a few bands absent in certain genotypes, but no quantitative differences in terms of protein content were observed.

On the basis of genetic diversity analysis, the genotypes PS 1225, AMS 100-16-4-1-3, JS 20-79, Jupiter, Cat 209, SL (E) 1 and AMS 50B were identified as superior donors for yield contributing traits, whereas the studies on genetic variability, correlation and path coefficient analysis showed that the number of primary branches per plant, number of nodes per plant, number of pods per plant, number of seeds per pod, 100-seed weight, dry matter weight per plant, seed yield efficiency and oil content were the most important yield attributes to be emphasized during selection programs for increasing the overall yield levels in soybean.


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सारांश

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सत्र एवं प्रवेश वर्ष	: प्रथम, 2014-15	उपाधि	: स्नातकोत्तर (कृषि)
मुख्य विषय	: आनुवंशिकी एवं पादप प्रजनन	विभाग	: आनुवंशिकी एवं पादप प्रजनन
शोध शीर्षक	: "सोयाबीन (ग्लाइसीन मैक्स (एल.) मेरिल) में आनुवंशिक मापदंडों पर विभिन्न मात्रात्मक एवं गुणात्मक लक्षणों का अध्ययन"		
सलाहकार	: डॉ. कामेन्द्र सिंह		

वर्तमान शोध गोविन्द बल्लभ पन्त कृषि एवं प्रौद्योगिक विश्वविद्यालय, पन्तनगर, उत्तराखण्ड, भारत के नार्मन ई. बोरलॉग फसल अनुसंधान केन्द्र में खरीफ 2014 में 165 जीनप्रारूप (160 प्रविष्टियाँ + 5 चैक) के साथ किया गया। इस शोध के अर्न्तगत 8 गुणात्मक एवं 15 मात्रात्मक लक्षणों का आनुवंशिक विविधता, आनुवंशिक विचलन, लक्षणों में सहसम्बन्ध और उनके प्रत्यक्ष और अप्रत्यक्ष प्रभाव, पीला विषाणु, जीवाणु स्फोट एवं राइजोक्टोनिया वायव अंगमारी बीमारियों के प्रति छटनी और चयनित जीनप्रारूपों में एस.डी.एस.-पी.ए.जी.इ. द्वारा प्रोटीन में विविधता का अध्ययन किया गया।

गुणात्मक लक्षणों ने फसल विविधता में एक महत्वपूर्ण भूमिका निभाई है। पुष्प एवं नाभिका के रंग ने आनुवंशिक विविधता के प्रति अधिकतम योगदान दर्शाया। विचरण (एनोवा) विषलेक्षण के तहत सभी लक्षणों के लिए जीनप्रारूप के बीच महत्वपूर्ण अन्तर पाया गया, जिससे प्रयोगात्मक सामग्री के बीच आनुवंशिक परिवर्तनशीलता की पर्याप्त मात्रा साबित हुई। श्रेणीबद्ध समूह विषलेक्षण के आधार पर 165 जीनप्रारूपों को 10 समूहों में बांटा गया। सर्वाधिक जीनप्रारूप समूह 7 में (124) और न्यूनतम जीनप्रारूप समूह 1 तथा 6 में (1) पाया गया। अधिकतम विचलन समूह 2 और 3 (91.59) इसके बाद समूह 1 और 9 (79.32) और समूह 3 और 10 (78.13) में पाया गया जबकि न्यूनतम विचलन समूह 4 और 5 (33.36) के बीच में पया गया। समूह 9 अधिकतम लक्षणों के लिए सर्वाधिक समूह औसतमान के आधार पर वांछित जीनप्रारूप के लिए उचित पाया गया। अंतः समूह विचलन, समूह औसत मान और प्रति प्रदर्शन के आधार पर सम्भावित पैतृक संयोजक जैसे पी.एस. 1225 X जुपिटर, पी.एस 1225 X जे.एस. 20-79, पी.एस. 1225 X कैट 209, पी.एस. 1225 X एस.एल (ई) 1, पी. एस. 1225 X ए.एम.एस. 100-16-4-1-3, जुपिटर X जे.एस. 20-79, जुपिटर X कैट 209, जुपिटर X ए.एम.एस. 100-16-4-1-3, जे. एस. 20-79 X कैट 209, जे.एस. 20-79 X एस.एल. (ई) 1, जे.एस. 20-79 X ए.एम.एस. 100-16-4-1-3, कैट 209 X एस.एल. (ई) 1, कैट 209 X ए.एम.एस. 100-16-4-1-3 और एस.एल. (ई) 1 X ए.एम.एस. 100-16-4-1-3 सोयाबीन में उपज बढ़ाने हेतु उचित पाये गये एवं जुपिटर X एस.एल. (ई) 1 और कैट 209 X ए.एम.एस. 50बी तेल तथा प्रोटीन बढ़ाने के लिए बेहतर संयोजक पाये गये।

सामान्यतौर पर पी.सी.वी. के परिमाण जी.सी.वी. और इ.सी.वी. के परिमाण से सभी लक्षणों के लिए अध्ययन के तहत अधिक पाये गये जबकि पी.सी.वी. और जी.सी.वी. के परिमाण समान्य तौर पर एक दूसरे के प्रति समकक्ष पाये गये, इ.सी.वी. की न्यूनतम भूमिका का संकेत पाया गया जिससे दृश्यप्रारूप के आधार पर चयन फायदेमन्द हो सकता है। अधिकतम एवं न्यूनतम पी.सी.वी., जी.सी.वी. और आनुवंशिक अग्रिम औसत मान प्रतिशत क्रमशः प्रति पौध बीज उपज एवं प्रोटीन सामग्री में पाया गया। आनुवंशिकता और आनुवंशिक अग्रिम का उच्च अनुमान पौधों की उँचाई, प्रति पौध गाठों की संख्या, प्रति पौध फली धारण वाली गाठों की संख्या, प्रति पौध फलियों की संख्या, 100-बीज भार, प्रति पौध शुष्क पदार्थ का भार, उपज सूचकांक, बीज उपज दक्षता, तेल सामग्री और प्रति पौध उपज में पाया गया जिससे इन लक्षणों में एडिटिव जीन प्रभाव के भूमिका का संकेत मिला।

सह-संबंध अध्ययन से पता चला कि बीज उपज प्रति पौध का पौधों की उँचाई, प्रति पौध प्राथमिक शाखाओं की संख्या, प्रति पौध गाठों की संख्या, प्रति पौध फली धारण वाली गाठों की संख्या, प्रति पौध फलियों की संख्या, प्रति फली दानों की संख्या, 100-बीज भार, प्रति पौध शुष्क पदार्थ का भार, उपज सूचकांक, बीज उपज दक्षता और तेल सामग्री के साथ महत्वपूर्ण सकारात्मक सह-संबंध है। जबकि तेल सामग्री और प्रोटीन सामग्री के बीच में महत्वपूर्ण नकारात्मक सह-संबंध पाया गया। पथ गुणांक विषलेक्षण दर्शाता है कि प्रति पौध शुष्क पदार्थ का भार, बीज उपज दक्षता, प्रति पौध फलियों की संख्या, 100-बीज भार, प्रति फली दानों की संख्या और प्रति पौध प्राथमिक शाखाओं की संख्या का सकारात्मक प्रभाव बीज उपज पर पाया गया।

पीला विषाणु, जीवाणु स्फोट एवं राइजोक्टोनिया वायव अंगमारी बीमारियों के प्रतिरोध विषलेक्षण के उपरान्त केवल दो जीनप्रारूप पी.एस. 1225 एवं पी.एस. 1480 इन रोगों के प्रति उच्च प्रतिरोधी क्षमता दर्शाया। 31 जीनप्रारूप में पीला विषाणु, जीवाणु स्फोट के प्रति उच्च प्रतिरोध क्षमता दर्शायी जबकि अन्य जीनप्रारूपों में तीनों बीमारियों में से किसी न किसी के प्रति अति संवेदनशीलता दर्शाया। प्रोटीन सामग्री विषलेक्षण के आधार पर चयनित 11 जीनप्रारूपों का एस.डी.एस.-पी.ए.जी.इ. द्वारा प्रोटीन सामग्री में विविधता का अध्ययन किया गया। अध्ययन परिणामों से ज्ञात हुआ कि इनमें गुणात्मक विविधता कुछ जीनप्रारूपों में पोलीपेप्टाइड बैंड की अनुपस्थिति के आधार पर पाया गया। लेकिन मात्रात्मक अन्तर प्रोटीन सामग्री के आधार पर नहीं पाया गया।

आनुवंशिक विविधता विषलेक्षण के अध्ययन के आधार पर उपज में योगदान देने वाले कुछ दाता जीनप्रारूप पी.एस. 1225, ए. एम.एस. 100-16-4-1-3, जे.एस. 20-79, जुपिटर, कैट 209, एस.एल. (ई) 1 और ए.एम.एस. 50 बी की पहचान की गई। जबकि आनुवंशिक विचलन, सह-संबंध और पथ गुणांक के विषलेक्षण के आधार पर उक्त अध्ययन में प्रति पौध प्राथमिक शाखाओं की संख्या, प्रति पौध गाँठों की संख्या, प्रति पौध फलियों की संख्या, प्रति फली दानों की संख्या, 100-बीज भार, प्रति पौध शुष्क पदार्थ का भार, बीज उपज दक्षता और तेल सामग्री लक्षण, सोयाबीन गुणवत्ता एवं उपज सुधार के लिए उपयोगी पाये गये।



(कामेन्द्र सिंह)
सलाहकार



(कुंदुरु भरत)
लेखक