Stability Analysis for Major Yield Traits in Newly Developed Breeding Lines of Soybean [*Glycine max* (L.) Merrill]

THESIS

Submitted to the
Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya,
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In

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(Genetics and Plant breeding)

By
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CERTIFICATE – I

This is to certify that the thesis entitled **"Stability Analysis for Major Yield Traits in Newly Developed Breeding Lines of Soybean [*Glycine max* (L.) Merrill]"** submitted in partial fulfillment of the requirement for the **DEGREE OF MASTER OF SCIENCE (Genetics and Plant breeding)** of the Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior is a record of the bonafied research work carried out by **Mr. JEEVAN RATHORE ID. No 20131602** under my guidance and supervision. The subject of the thesis has been approved by the Student's Advisory Committee and the Director of Instruction.

No part of the thesis has been submitted for any degree or diploma (Certificate awarded etc.) or has been published. All the assistance and help received during the course of the investigation has been acknowledged.

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Member (Dr. S.R.J. Singh) ………………………………………….

CERTIFICATE –II

Aadhar No………………………

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This is to certify the thesis entitled **"Stability Analysis for Major Yield Traits in Newly Developed Breeding Lines of Soybean [*Glycine max* (L.) Merrill]"** submitted by **Mr. JEEVAN RATHORE ID. No. 20131602** to the Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior in partial fulfillment of the requirements for the degree of Master of Science in **Agriculture (Genetics and Plant breeding) in Department of Genetics and Plant breeding, R.A.K. College of Agriculture, Sehore** has been accepted after evaluation by the External Examiner and approved by the Student's Advisory Committee after an oral examination on the same.

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Place: Sehore **(JEEVAN RATHORE)**

Date:

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&	And
@	At the rate of
^{o}C	Degree Celsius
Cm	Centimeter
C.V.	Coefficient of Variation
d.f.	Degree of Freedom
et al.	And others
Etc	and the rest
g	Gram
GEI	Genotype x environmental interactions
Ha	Hectare
HI	Harvest Index
i.e.	That is
Kg	Kilogram (s)
kg/ha	Kilogram per hectare
MSS	Mean sum of squares
Mg	Milligram
no.	Number (s)
NS	Non significant
R.V.S.K.V.V.	Rajmata Vijayaraje ScindiaKrishiVishwaVidyalaya
R.A.K.	Rafi Ahmed Kidwai
₹	Rupees
S.Em.±	Standard error of mean
S.S.	Sum of Squares
viz.	Namely
√	Square root
%	Percent
±	Plus , Minus
Nod/Plant	Nodules per plant
Vig.	Vigour
Wt.	Weight
YLD.	Yield
IDX.	Index
%age	Percentage
r	Correlation
Env.	Environment
+ve	Positive
-ve	Negative

CHAPTER I

INTRODUCTION

Soybean belongs to legume family widely grown for oilseed purpose. It is a native from East Asia and also known as wonder crop. Soybean is an important leguminous crop used for oilseed, protein purpose and various dairy products. Soybean is known as the “Golden Bean” Of the 20th century. Soybean (*Glycine max L. Merrill*) is an annual plant with self pollination belongs to family fabaceae, sub family Papilonaceae. It is autogamous crop having diploid chromosome number 2n =40, with trifoliate leaves having 3-4 leaflets per leaf. Soybean develop a main taproot, but soon after emergence numerous lateral roots to produce a fibrous root system. Young soybean roots develop root nodules within a week after emergence. Rhizobium, a nitrogen-fixing bacterium enters the nodules and after ten to fourteen days are able to supply most of the plant’s nitrogen needs.

Regarding flower development, there is two main types soybeans determinate and indeterminate. Indeterminate soybeans continue growing upward at the tip of the stem for several weeks after flowering begins lower on the stem. Upper nodes will not flower until later. Most commercial varieties are indeterminate. Indeterminate soybeans usually grow taller and do well in short growing seasons. Determinate soybean plants complete their growth in height and then produce all the flowers at about the same time and usually one-half to two-thirds as tall as indeterminate varieties.

Plant height in general between 51-127cm and having rooting depth between 76-152 cm. Soybean contain 20-22% of oil and 40-42% of protein. Soybeans also have some essential amino acids (5%), carbohydrates, vitamins (thiamine and riboflavin) and minerals. Soybean as a legumes play an important role in agriculture as they are widely distributed in natural ecosystem. Soybean is popularly known as “Miracle. Soybean is a short day kharif crop, requiring hot climatic conditions, sensitive to water logging but tolerant to drought conditions during commercial cultivation.

Soybean production in India during 2020-21 is estimated to be 13.58 million tons from an area of 12.12 million hectares and a productivity of 1125 kg/ha as per 1st advance estimates of DAC&FW. Madhya Pradesh (5.85 m ha), Maharashtra (4.32 m ha) and Rajasthan (1.1 m ha) are the major states for soybean cultivation. Karnataka, Telangana, Gujarat, and Chhattisgarh with an area of 0.332, 0.16, 0.15 and 0.08 m ha, respectively are rest of others soybean growing states in the country. Due to its high production and acreage, Madhya Pradesh is known as soya state.

Soybean oil and its By-products requirement increasing day to day and thus creating its high demand. Various beneficiary products are available which play a vital role in human diet. Products like soya milk, Soya paneer, yogurt and too many other products contain high level of protein. Around 135 varieties have been developed in India for various agro-climatic conditions.

High yield is main object of all breeding programmes. Direct and indirect selections are significant to get better yield. There are some biometrical techniques such as correlation, discriminate function analysis and stability analysis provide details about the relative contribution of various component traits towards economic yield. Correlation coefficients, although useful in quantifying the extent and direction of trait associations, can be misleading if the high correlation between two traits is a consequence of the indirect effect of the traits (Dewey & Lu, 1959). Thus, knowledge of the relationship between those characteristics that make up the final yield of soybean genotype is important in enabling a more precise identification of the components that can determine a more productive plant. Discriminant function helps to identify combining characters having high selection efficiency of yield then direct selection. Stability parameters determines the performance of genotypes with respective changes over environment's is primary breeding objective to obtain sustainable yield in Soybean.

Improvement through selection depends upon the variability existing in the available genotypes, which may be either due to different genetic constitution of cultivars or variations in the growing environments. Selection is effective only when the observed variability in the population is heritable in nature. Genetic variability in a group of germplasm is a pre-requisite for a successful breeding programme. Since, most of the characters influencing yield are polygenic, it is essential for plant breeders to estimate the type of variation available in the germplasm. The type of breeding programme for developing suitable varieties depends largely on the availability of genetic variability in a given population. Heritability estimates give a measure of transmission of characters from one generation to the other, as consistency in the performance of the selection depends on the heritable portion of the variability. Thus, enabling the plant breeder for the variation and the estimates of the heritability and genetic advance are the important parameters on which the success of selection lines.

The impact of GEI on genotypes can be described by particular trait stability. Typically, phenotypic stability of distinct traits, either yield or quality traits, is the ability of a genotype to perform consistently in various environments. It is worth noting that determining the stability pattern of genotypes is a prerequisite for understanding their response to different environments, Identification of stable and widely adapted genotypes are thus pre-requisite for breeding new cultivars that could adapt to the different environments. Hence, plant breeders' always aim to select varieties with high performance across different environments. The differences observed in the stability of genotypes are usually a result of GEI (Genotype – environment interaction). However, the selection of highly stable varieties can be difficult when a breeder has to consider individual GEI of multiple traits under multiple environments. Notably, the GEI of quality characters of soybean has been studied previously by several investigators. In the selection process, besides choosing the best statistical model to predict genetic values, plant breeders usually handle multiple traits simultaneously to put in our variety.

Madhya Pradesh is mini-India comprised maximum production gap due to soil types, topography, soil slope, fertility status and finally economic status of farmers which leads to maximum genotypes x environmental interaction on seed yield of soybean. Therefore, stable soybean variety may be to some extent suitable for sustainable yield advantages.

Stability explained that the average performance of genotypes over wide range of environments as the model given by Ebert hard & Russell (1966) is useful for judging the stability behavior in present breeding lines.

Considering the above aspects in view the present investigation has been undertaken on 15 advance breeding lines developed in All India Coordinated Research Project, RAK College of Agriculture, Sehore (Madhya Pradesh) with following objectives:

1. To find out heritable variations for different major seed yield traits.
2. To compute the correlation coefficients among seed yield traits.
3. To find out better stable breeding lines.

CHAPTER II

REVIEW OF LITERATURE

The literature consulted on different aspects of the present study has been described in this chapter under the following heads :-

2.1 Genetic variation

2.2 Genetic advance

2.3 Heritability

2.4. Correlation

2.5 Stability

2.1 Genetic variation:

The development of an efficient plant breeding programme depends upon the existence of genetic variation. The efficiency of selection largely depends upon the nature and magnitude of genetic variability present in the genetic stock. Thus, the success of genetic improvement in any character depends on the magnitude and nature of variability present in the genetic pool.

Das *et al.* (2001) reported significant variation among genotypes for all 11 traits studied i.e. days to 50% flowering, days to maturity, plant height, number of branches per plant, inter node length, number of pods per plant, pod length, number of seed per pod, 100 seed weight, oil content and seed yield per plant while studying 65 soybeans genotype.

Dixit *et al.* (2002) studied biometrical parameters in 38 newly developed genotypes of soybean. Harvest index, seed yield per plant and biological yield per plant showed comparatively high estimates of genetic variation, hence direct selection for these traits was suggested for yield improvement in soybean.

Chamundeswari and Aher (2003) observed significant genetic variation for number of days to maturity, plant height at maturity, number of branches per plant, number of clusters per plant, number of pods per cluster and per plant, number of seed per pod, harvest index, mechanical damage, 100-seed weight, grain yield per plant, protein content, oil content and biological yield per plant. Genotypic coefficient of variation was highest for biological yield per plant.

Dhillon *et al*. (2005) Genetic variation and heritability for different characters (days to 50% flowering, plant height, number of pods per plant, days to maturity, 100- seed weight, seed yield per plant, harvest index, and protein, oil and fatty acid content were estimated in 30 soybean strains grown kharif 1999 in Ludhiana, Punjab, India. Most of the characters possessed sufficient genetic variability.

Gohil *et al*. (2006) studied the genetic variation, for seed yield and its component traits in 55 diverse soybean *(Glycine max)* genotypes collected from different soybean growing states of India. Largest genotypic coefficient of variation was observed for number of pods per plant followed by seed yield per plant.

Malik *et al.* (2007) studied 27 genotypes of soybean to determine the correlation and path analyses of yield and its components. Significant differences among genotypes for characters viz., leaf area, chlorophyll content, first pod height, days to 50% flowering, days to flowering completion, days to pod initiation, days to 50% maturity, plant height, number of pods per plant, number of branches per plant, number of unfilled pods, number of shattered pods, 100-seed weight, grain yield and oil content were observed while protein content was statistically non-significant. Genotypic correlations were higher than the phenotypic and environmental ones for most of the characters exhibiting high degrees of genetic association among traits under consideration. Correlation coefficient for bean yield was positive with leaf area, first pod height, days to flowering, days to maturity, plant height and number of branches per plant. Therefore, increase in these traits will ultimately increase the grain yield. Path coefficient analysis revealed that days to flowering completion had maximum direct contribution to yield followed by days to pod initiation, chlorophyll content, number of pods per plant and plant height.

Iqbal *et al*. (2010) observed that the analysis of variation showed significant differences among genotypes in term quantitative traits under study, which indicates the existence of high genetic variation for major yield traits.

Sharma *et al.* (2011) showed that both phenotypic coefficient of variation and genotypic coefficient of variation were higher for most of the traits and was a close relationship between PCV and GCV. High genetic coefficient of variation accompanied with high heritability and genetic gain were recorded for days to flowering and maturity, plant height, number of pods per plant and 100-seed weight indicating the additive type of gene action.

Hamawaki *et al.* (2012) there are many multivariate approaches to study the variation among soybean groups, such as dissimilarity measures, cluster analysis, principal components and canonical variables. The heritability estimation, genetic gain and genetic correlation are important parameters which permit the breeder to choose the best improvement strategy.

Reni *et al.* (2013) reported forty five genotypes of soybean of diverse origin were evaluated for variation and genetic advance. Observations on thirteen characters were recorded. Analysis of variance revealed highly significant differences among the genotypes for the all the characters. High PCV coupled with high GCV, observed for branches per plant, pods per plant, biological yield, harvest index and yield per plant indicate the presence of wider adaptability for these traits in the genotypes studied, suggested the less influence of environment in the expression of characters.

Baraskar *et al*. (2014) evaluated sixty one genotypes of soybean to determine genetic variation, heritability and genetic advance for 15 contributing characters. The analysis of variance revealed significant variations for all characters. The estimates of phenotypic (PCV) and genotypic (GCV) coefficients of variation indicated that the values of PCV were higher than that of GCV, but the differences were closer between these two estimates for all the traits. This indicated that expression of characters under study was less influenced due to environmental factors. The high values of GCV and PCV were observed for number of clusters per plant, seed yield per plant, biological yield per plant, number of pods per plant and plant height indicating presence of sufficient genetic variability for selection in these traits. High heritability accompanied by high genetic advance for plant height, number of clusters per plant, number of primary branches per plant, seed yield per plant, biological yield per plant and number of pods per plant suggested selection could be effective for these traits.

Jarman *et al.* (2014) studied line X tester analysis on existing soybean varieties viz. JS 335, JS 93-05, JS 93-37, and reported that additive gene action for pods per plant, hundred seed weight and seed yield per plant were found better general combiners for yield, pods per plant and hundred seed weight they further reported good cross combination of JS 20-10 X JS 93-05 out of 4 crosses.

Mahbub *et al.* (2015) studied twenty eight soybean genotypes for eleven morphological characters. Analysis of variance revealed significant differences among the genotypes for all the traits. The phenotypic variance was higher than the corresponding genotypic variance for all the characters. All the characters showed moderate to low phenotypic and genotypic coefficient of variation. Genotypic coefficient of variation was the highest for seed yield per plant (31.45%) followed by number of branches per plant (29.9%) and plant height (27.42%). Days to maturity (99.93%) had the highest heritability. Plant height, pod length, number of seeds per pod, number of pods per plant, hundred seed weight, branches per plant and number of seeds per pod showed significant positive genotypic and phenotypic correlation with seed yield.

Ramgiry *et al*. (2016) revealed significant differences among the genotypes for all the traits. The phenotypic variance was higher than the corresponding genotypic variance for all the characters. Moderate phenotypic and genotypic coefficient of variation was observed for plant height followed by harvest index, number of seeds per pod and seed yield per plant.

Chandrawat *et al.* (2017) conducted an experiment to evaluation of genetic variability present in the 41 genotypes and five checks (two local + three national checks) and observations were recorded on various yield and yield contributing characters viz., days to 50% flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, 100 seed weight, harvest index and grain yield per plant at field level and oil content, protein content and trypsin inhibitor content in the laboratory.

Kuswantoro *et al*.(2018) studied 16 soybean varieties that arranged in a randomized block design with three replications. The results showed that days to flowering, number of branches per plant, number of reproductive nodes, number of unfilled pods per plant, weight of 100 seeds, and grain yield revealed broad GCV (Genetic Coefficient of Variance), whereas the days to maturity, plant height, number of pods per plant had a narrow GCV. PCV (Phenotypic Coefficient of Variance) value higher than the value of GCV on all the observed characters with a slight difference, except for grain yield. The broad sense heritability varied from low (seed yield), medium (the number of branches, number of reproductive nodes, number of pods and the number of unfilled pods), and high (days to flowering, days to maturity, plant height, and weight of 100 seeds). Characters of days to flowering and weight of 100 seeds are effectively used as selection criteria because they had a broad CVG and high heritability.

Kitabatake *et al.* (2020) estimates that analysis of variance revealed a significant interaction between cultivar and planting density for seed yield, number of pods and number of pods per node. The lower branching cultivar T22 with long terminal racemes produced a higher yield under non-lodging conditions than the conventional low branching cultivar.

Dhaka (2021), worked on eleven qualitative and twelve quantitative characters of soybean to assess genetic divergence, genetic variability and their effect and Result showed that qualitative characters play an important role in crop diversity and the character flower color and hilum color contributed maximum towards genetic diversity.

Lekota *et al.* (2021) estimate that results of analysis of variance revealed highly significant difference ($p<0.001$) among soybean cultivars for plant height, weight per plot and weight of 100 grains while no significant differences were observed among leaf shape, number of pods per plant and leaf size.

2.2 Genetic advance

Genetic advance explains the degree of gain obtained in a character under a particular selection pressure. High genetic advance coupled with high heritability estimates offers the most suitable condition for selection.

Shrivastava *et al*. (2005) found high genetic advance for seed yield and days to maturity. Seed yield and days to maturity were observed to be controlled by additive gene action as these showed high per moderate heritability and high genetic advance.

Karthika and Lakshmi (2006) observed high genetic advance for seed number per plant, seed yield per plant and 100-sed weight for both mutagens and cultivars. Results showed that these characters are governed by additive gene effects, which may favourably be exploited in the M2 generation.

Yadav (2007) reported that the high genetic advance as percentage of mean for plant height, pod bearing length, pods per plant, seeds per plant and seed yield per plant.

Reni *et al.(2013)* Forty five genotypes of soybean (Glycine max (L.) Merrill.) of diverse orgin were evaluated in randomized block design with three replications for genetic advance during kharif 2007. Observations on thirteen characters were recorded. High heritability coupled with high genetic advance as percent of mean was observed for days to 50% flowering, plant height, branches per plant, pods per plant, pod length, seeds per pod, 100 seed weight, biological yield, harvest index and seed yield per plant indicating operation of additive gene action and the ample scope for improvement in these traits through simple selection.

Amrita *et al*. (2014) studied twenty six advanced generation genotypes of soybean. Different genetic parameters namely, genetic variability, heritability, genetic advance, correlation were studied. Number of branches per plant, number of pods per plant, number of seeds per plant, biological yield per plant and yield per plant showed high heritability and high genetic advance whereas, high heritability with moderate genetic advance was found for plant height and 100-seed weight indicating the preponderance of additive gene action. Seed yield per plant exhibited positive and highly significant correlation with biological yield, number of pods per plant, number of seeds per plant, plant height, harvest index, vegetative phase and number of seeds per pod.

Mehbub *et al*. (2016) High heritability coupled with high genetic advance was recorded for number of branches per plant, plant height, number of seeds per plant, number of pods per plant and 100-seed weight. This indicates the effectiveness of selection to improve these five characters. Plant height, pod length, number of seeds per pod, number of pods per plant, hundred seed weight, branches per plant, and number of seeds per pod showed significant positive correlation with seed yield.

Mofokeng *et al.* (2018) The results showed highly significant differences among the genotypes based on days to flowering, branch number per plant, hundred seed weight, pod weight per plant, pod length, seed number per plant, seed number per pod and grain yield. The expected genetic advance was high for most of the traits, medium for seed number per pod and hundred seed weight and low for pod number per plant. The expected genetic advance as percent of mean was variable and high for all traits. There was vast variation observed among the soybean genotypes evaluated based on the yield and yield related traits.

Baria (2019) observed high heritability coupled with high genetic advance as percent of mean for days to 50% flowering, plant height, number of branches per plant, number of pods per plant, 100-seed weight, seed yield per plant and fodder yield per plant.

Kumar *et al.* (2020) The analysis of variance revealed the presence of sufficient genetic variability in the breeding material. High PCV and moderate GCV were recorded for harvest index and biological yield/plant. High heritability coupled with high genetic advance were observed for harvest index followed by biological yield /plant, seed yield /plant, number of pods/plant and 100-seed weight indicating the predominance of additive gene action in controlling the trait. Number of branches /plant, number of seeds /pod, biological yield/plant and harvest index exhibited significantly positive correlation with seed yield /plant both at phenotypic and genotypic levels. Two traits viz., harvest index and biological yield /plant could be considered as direct selection indices for yield improvement in soybean.

Shruthi *et al.* (2021) estimates 18 quantitative traits and observed high heritability coupled with high genetic advance in all quantitative traits except for days to maturity. The traits with higher heritability and GA value may indicate their variability and high selective value.

Mejaya *et al.*(2022) Results of the study showed that based on the genetic advance value, the number of branches per plant and the number of fertile pods per plant could be used as soybean selection criteria in normal irrigation and drought condition, respectively. In general, the mean of all traits in drought condition were lower than those in normal irrigation condition. Seed yield (t/ha) showed the lowest drought stress tolerant index (STI) (0.72). Based on the drought STI, four soybean lines (TGm-161-25-10, AB-142-40-21, AB-157-41-22, and ARG/GCP) had STI values of 1.0 and above 1.0 which are equivalent to the check drought tolerance variety Dering 1. These soybean lines could be grown in drought-stressed conditions.

2.3 Heritability:

Selection is the most important activity in all plant breeding programmes. The success of selection program largely depends on the extent of genetic variability present in the population and the heritability of the concerned character. Selection is generally more effective for characters which have high heritability than those having low heritability.

Sharma *et al.* (2005) conducted an experiment was in kharif 2002 to estimates heritability, coefficient of variation and genetic advance as percent of mean of 62 Indian cultivars of soybean and found higher estimates of heritable for biological yield and harvest index.

Bhushan *et al*. (2006) reported that generally, the estimates of phenotypic coefficients of variation (PCV) for all the characters were largest than the genotypic coefficients of variation (GCV). Largest estimates of GCV were observed for branches per plant, pods per plant and biological yield per plant. Moderate estimates of GCV were observed for seed yield per plant, plant height and 100-seed weight. Low estimates of variability were reported for harvest index, seed protein, oil content and days to 50% flowering. High heritability was observed for pods per plant, plant height and biological yield per plant in the 198 soybean germplasms.

Costa *et al.* (2008) observed highly significant difference, the experimental coefficient of variation (CVe), the CVg/CVe ratio and the heritability showed wide variation among traits, being the highest values found for number of pods, number of seeds and grain yield, making evident the existence of variance to be exploited by breeding.

Karnwal and Singh (2009) found that total dry matter weight/plant, primary branches per plant, pods per plant, seed yield efficiency, 100-seed weight and harvest index were significantly and positively correlated with seed yield. Protein and oil contents showed significant and negative association with each other.

Singh *et al.* (2010) observed high estimates of heritability, plant height, 50% flowering and days to maturity in inter-specific cross of soybean.

Rajkumar *et al.* (2010), reported larger magnitude of variation for the plant height, nodes per plant, number of branches per plant, 100-seed weight, days to 50% flowering, days to maturity, grain yield. Similarly larger heritability were recorded for days to maturity, days to 50% flowering and plant height.

Bhat *et al.* (2012) observed high heritability values for traits viz., number of pods per plant and harvest index.

Patel (2012) estimated significant difference among genotype for all the character except, pod bearing length, secondary branches per plant and seeds per pod. He reported high genotypic and phenotypic coefficient of variation for primary branches per plant, seeds per pod, 100-seed weight and seed yield per plant.

Osekita and Olorunfemi (2014) reported high heritability with high genetic advance for days to maturity, days to germination, seed yield, seed dry weight and hundred seed weight in advance generation (F_3) of soybean.

Singh *et al.* (2015) observed high estimates of heritability, plant height, 50% flowering and days to maturity in interspecific cross of soybean.

Hunde (2017) evaluated sixteen soybean genotypes and found high heritability with high genetic advance as percent of mean were found for plant height, pod length, and biomass yield, respectively. Whereas high heritability was associated with moderate genetic advance were found for number of pod/plant and days to 95% maturity respectively.

Garg *et al.* (2017) studied that the higher genotypic and phenotypic coefficient of variation was observed for electrical conductivity test, germination after accelerating ageing (96hr), seedling vigour index II and seedling dry weight. High heritability coupled with high genetic advance was recorded for seedling dry weight, seedling vigour index I, seedling vigour index II, electrical conductivity, germination after accelerating ageing (48hr), germination after accelerating ageing (72hr), germination after accelerating ageing (96hr). Association analysis indicated that standard germination showed a significant and positive correlation with shoot length, root length, seedling length, seedling dry weight, seedling vigour index I, seedling vigour index II and germination after accelerating ageing (48, 72 and 96hr).

Mofokeng *et al.* (2018) The results showed highly significant differences among the genotypes based on days to flowering, branch number per plant, hundred seed weight, pod weight per plant, pod length, seed number per plant, seed number per pod and grain yield. Heritability of yield and yield components were ranged from 5.9% to 100%. The most heritable traits were hundred seed weight (100 %), days to flowering (64.13 %) and seed number per pod (67.37%). The genotypic variance ranged from 0.3% to 33% while the phenotypic variation ranged from 1.5% to 44%. The phenotypic and genotypic coefficient of variations was high for grain yield, medium for days to flowering and lowest for hundred seed weight. The phenotypic coefficient of variations (PCV) was higher than genotypic coefficient of variation (GCV) for all characters indicating the influence of environmental factors.

Neelima *et al. (*2018) conducted experiment to heritability in broad sense, genetic advance and genetic advance as percentage of mean were estimated for 13 different characters. The values of phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all the characters indicating the influence of environmental factors. The magnitude of heritability was observed to be high for all the characters under study indicated that the larger portion for total variation would be under genetic control and selection based on phenotypic levels would be useful for the improvement of these traits. High estimates of heritability coupled with high genetic advance expressed as percentage of mean were observed for plant height, number of branches per plant, number of pods per plant and seed yield per row which may be attributed to the preponderance of additive gene action and possess high selective value and thus, selection pressure could profitably be applied on this character for their improvement.

Bianchi *et al.* (2020) The objectives of this study were to examine the implication of the genotype × environment interaction (G × E) .The traits of days to flowering, days to full maturity, plant height, bottom pod height, lodging, and grain yield were evaluated. The genetic and phenotypic parameters, expected gain from selection, genetic correlation, correlated response, achieved heritability, and frequency distribution of the adjusted means were estimated. The estimates of the components of variance showed the existence of variability among the progenies, enabling the selection of superior genotypes. There was an effect of the G × E interaction for all traits, and most of the interaction was due to complex interaction. From the analysis of genotypic correlation, significant estimates were observed between the traits. The G × E interaction affected the estimates of genetic and phenotypic parameters in the soybean, and the achieved heritability is a tool to study this interaction.

Goonde *et al.* (2021) estimates high genotypic and phenotypic coefficients of variations for number of primary branches per plant, number of pods per plant, biological yield and seed yield. Higher values of broad sense heritability estimates coupled with higher values of GAM observed for days to 50% emergence, grain filling period, biological yield and seed yield.

Fufa (2021) evaluated 49 genotypes and found traits such as number of nodules per plant, number of pods per plant, number of primary branches per plant, plant height, dry weight and total number of seed per plant showed high broad sense heritability coupled with high genetic advance as percent of the mean showing possibility of improving these genotypes through simple selection.

2.4 Correlation coefficient:

High yield is the prime objective in all breeding programmes, but generally yield has low heritability and direct selection is not effective. Correlation measures the mutual relationship among various plant characters and helps in determining the yield components on which indirect selection can be based for improvement in yield.

Saharan *et al.* (2006), observed that seed yield per plant was positively correlated with number of pods per plant, biological yield per plant, number of branches per plant, harvest index, 100 seed weight, protein content and soluble protein content.

Gaikwad *et al.* (2007), the correlation analysis revealed that seed yield per plant showed highly significant positive association with 100-seed weight, followed by number of pods per plant and protein content. The characters branches per plant and seeds per pod showed negative and non- significant association with seed yield per plant.

Yadav *et al.* (2007), reported that seed yield was significantly correlated with plant height, pod bearing length, pod number per plant and seed number per plant.

Karnwal *et al.* (2009), found that total dry matter weight per plant, primary branches per plant, pods per plant, seed yield efficiency, 100-seed weight and harvest index significantly and positively correlated with seed yield. Protein and oil contents showed significant and negative association with each other.

Suneeta *et al.* (2010), evaluated fifty nine individual plants derived from a cross i.e. Birsa soy-1/JS-71-05 for eight quantitative characters. They found the genotypic correlation coefficients were generally higher than phenotypic correlation coefficients. Seed yield per plant was significantly and positively correlated with number of pods per plant.

Aditya *et al.* (2011), work out association analysis for eight quantitative traits including grain yield were studied in thirty one soybean genotypes. Grain yield per plant exhibited highly significant and positive genetic correlation number of primary branches per plant, number of pods per plant and harvest index.

Sarutayophat (2012), reported positive and significant correlation between the plant height and number of marketable pods per plant (0.821), plant height and marketable pod yield (0.520), and number of marketable pods per plant and marketable pod yield. Indirect effect of the plant height on marketable pod yield through its association with number of marketable pods per plant was positive and significant (1.075). The results of this study suggested that the number of marketable pods per plant, green pod weight and plant height were important characters that should be taken into account as selection criteria in improving marketable pod yield of the vegetable soybean.

Oluwatoyin *et al.* (2014), reported significant and positive correlation of seed yield with number of seeds per plant (0.43) and seed dry weight (0.936) while negative association with days to 50% flowering (-0.786) and days to maturity (-0.396).

Parmar e*t al.* (2014), reported significant positive correlation of seed yield with seeds per plant, pod per plant, 100-seed weight and biological yield per plant (0.858, 0.855, 0.638 and 0.555) respectively.

Jain and Ramgiry (2015), found branches per plant, nodules per plant, pods per plant (0.54), seeds per plant and seed index were positively and significantly correlated with seed yield.

Akram *et al.* (2016), conducted an experiment using a randomized complete block design to estimate genetic variability, and to analyse correlation and path coefficient between yield and its components of eleven soybean genotypes. Path coefficient analysis showed that the seeds per plant had the highest (2.848) positive direct effect on yield per plant, followed by pods per plant, days to first flowering, number of branches per plant, 100-seed weight, plant height, and pod length. So, the number of pods per plant and seeds per plant could be considered as important selection criteria for yield improvement in soybean.

Balla *et al.* (2017), showed positive genotypic correlations for grain yield with days to 50% flowering, days to maturity, plant height, number of pods per plant and fodder yield. Path analysis revealed that fodder yield, plant height and days to maturity had the highest positive direct effect on grain yield. Number of pods per plant via plant height gave the highest positive indirect effect on grain yield. These results indicate that fodder yield, plant height and days to maturity can be used as selection criteria for the improvement of soybean grain yield.

Shree *et al.* (2018), evaluated ninety genotypes of soybean including five checks to know the correlation between yield and yield attributing traits in soybean during *kharif*. Grain yield was found to be positively and highly significantly associated with number of pods per plant, seeds per pod, 100 seed weight, both at genotypic and phenotypic levels. Protein % showed positive and significant association with number of pods per plant while oil content showed negative and significant association with plant height at both genotypic and phenotypic level.

Thi *et al.* (2019), reported that there were consistencies of correlations across generations and higher direct and indirect effects in F_6 than in F_7. Most direct effects were in agreement with correlations, indicating true associations. Significant positive correlations (r) and highly positive direct effects on grain yield were observed for total number of pods (r=0.406-0.928), total number of seeds (r=0.434-0.939) and 100-seed weight (r=0.361-0.626) across generations and crosses. Ratio of first pod insertion height to plant height had significant indirect effects on yield via component traits.

Ghanbari *et al. (*2019), examined 18 genotypes of soybean to investigate the relationships between some principal attributions of morphology with seed yield per soybean, by Random Complete Block Design (RCBD) study. The results of variance analysis indicated that, there were significance differences among all soybean genotypes. The results of correlated analysis revealed that biological yield (0.96), harvest index (0.92), and number of branches (0.92) had the uttermost correlation with seed yield.

Pawar *et al*. (2020), The genotypic correlation coefficients were high in magnitude than their corresponding phenotypic correlation coefficients for all the characters. The seed yield per plant showed a highly significant positive association with number of pods per plant, number of seeds per pod, 100 seed weight, SPAD value, plant height, days to 50 percent flowering, oil content, number of primary branches per plant and 50 percent flowering at genotypic level.

Phetole Mangena (2021), reported a positive relationship between seed vigour, germination and multiple shoot initiation as indicated by the pearson's correlation coefficient reported. According to the findings seed vigour could serve as a major obstacle to efficient germination and shoot proliferation.

Mustofa *et al.* (2021), observed that the number of branches, productive nodes and filled pods, 100-seed weight, pod weight and the number of seeds per pod correlated to seed yield per plant. Characters of productive nodes, number of filled pods, 100-seed weight, and pod weight directly affected the plant's seed yield. The indirect effect of the number of productive nodes on seed yields was significant through the number of filled pods and pod weight. The character of the number of filled pods had an indirect effect through productive nodes, the 100-seed weight, and the weight of pods. The 100-seed weight showed a significant indirect effect on seed yield through the number of productive nodes, filled pods, and pod weight. The significant indirect effect was also shown by pod weight through the number of productive nodes, number of filled pods, and 100-seed weight.

Karyawati *et al*. (2021), analysis correlation and showed that the number of branches, number of field pods, number of seed per plant, weight of 100 seeds and weight of seeds per plant had a positive correlation value to the yield.

2.5 Stability:

Joshi *et al.* (2005) observed wide variation among genotypes, environments (location) and genotype × environment interactions for all traits. Both linear and non linear components of G×E interactions were significant for plant height, 100 seed weight and seed yield, whereas the non linear component alone was significant for days to 50% flowering and days to maturity. Three genotypes, ie. J-793,SL-87 and JS-335, were identified as stable for seed yield.

Mahajan *et al.* (2006) evaluated the advance lines of Soybean over years at mid-altitudes of north-west Himalayas. Genotypes, years and their interaction were found significant for yield, plant height, days to flowering and maturity. VLS 2157 and VS 495 were superior for yield over VLS 47 and responsive to the better environments; and at par for other characters VS 2173 and VS 2174 was stable and dwarf and at par with VLS 47 for yield and other character.

Pan *et al.* (2007) indicated the presence of linear and non linear components of genotype × environment interaction by the significant linear interaction for graded green pod yield per plant, number of pods per plant, 100 seed weight and pooled deviation for number of days to 50%flowering, plant height, harvest index. The line EC 384907-EC and EC 344906 were found stable performance for above traits.

Holkar *et al.* (2008) tested nine promising soybean genotypes belonging to different maturity groups for seed yield, water use efficiency and other attributes. Impact of environment was significant on most of the characters except for the leaf area per plant and harvest index. Genotype × environment(linear) interaction was also significant for days to flower initiation, physiological maturity. Genotype JS 9305 was the only stable genotype for the characters namely days to flowering, days to maturity and reproductive phase.

Verma *et al.* (2011) stability analysis carried out in 8 genotype over 4 environments. Pooled analysis of variance shows significance for number of branches per plant, number of pods per plant, 100 seed weight, days to maturity and seed yield (kg/plot) indicates significant variation in selected material. Significant mean squares due to environment are indicative of confirming that the nature of environments which influenced the expression of most of the traits selected for stability studies.

Khan *et al.*(2012)Seventeen genotypes of soybean were evaluated in randomized block design over six environments (three years and two locations) and observations were recorded for eight quantitative traits namely, plant height, primary branches/plant, secondary branches/plant, days to 50% flowering, days to maturity, pods/plant, pod length, seeds/pod and seed yield. ‘MAUS 47’ and ‘VL Soya 2’ were found stable across the environments. Moreover, ‘Himso 1580’, Shivalik and ‘Punjab 1’ could be considered stable on the basis of higher average response for many characters.

Nagalamu *et al*. (2013) evaluate genetic variability of five soybean genotypes, and assess genotype × environment effect on seed yield and yield related traits. The effect of genotype (G), environment (E) and G × E interactions on pod number per plant; plant height, first pod height, number of branches per plant, leaf area, number of days to 50% flowering and seed yield were found significant at P=0.05. The highest mean seed yield was obtained from TG x 1937-1F (0.98 t/ha). Beside TG x 1740-2F, TG x 1904-6F and Soja were significantly higher than NA 5009 RG in all environments for seed yield. TG x 1937-1F was an intermediate maturing and best in terms of number of pods per plant, number of branches per plant, and leaf area. Correlation coefficient for seed yield showed significant association with days to 50% flowering and leaf area.

Solanki *et al.*(2014) Thirty newly developed genotypes of soybean were grown at three sowing dates in randomized block design with three replications during kharif 2010-11. Analysis of variance for all the ten characters for each environment and on pooled basis indicated substantial amount of variability for most of the yield and yield contributing traits except for days to maturity in environment II and pooled environments. Genotype X environment extractions was found significant for number of primary branches plant-1, plant height, number of pods plant-1, biological yield plant-1, number of seeds plant-1, seed yield plant-1 and 100 seed weight. The genotypes × environments (Linear) mean sum of squares were significant for all the characters except for number of pods plant-1. Genotypes namely RVS 2006-14, RVS 2006-25, RVS 2006-27 and RVS 9560 showed stable performance for all the yield and yield components. Therefore, these genotypes could be recommended for commercial cultivation as well as for inclusion in further breeding programme as donor parents

Hamawaki *et al.* (2015) to evaluate the performance of 14 soybean genotypes, from the Soybean Breeding Program of the Federal University of Uberlandia, in their adaptive capacity and seed yield stability at 3 locations and 2 growing seasons. For the adaptability and stability analysis the Toler and Centroid methods were used; 5 genotypic groups were identified in the first whereas 4 groups were identified in the latter. By the Toler method group A was composed by 4 genotypes, UFU-001, UFU-003, UFU-0010, and UFU-001. They showed a convex pattern of adaptability and stability. In contrast, the genotypes UFU-008 and UFU-0013 were classified in Group E with a concave pattern of adaptability and stability. Regarding results from the Centroid method, the Genotype UFU-002, with higher seed yield than average, was the only genotype in Ideotype VI with moderate adaptability to favorable environments. In contrast, 10 genotypes were included in the Ideotype V, of medium general adaptability. The genotypes UFU-001, UFU-002, UFU-006, UFU-0010, and UFU-0011 were recommended for use in the Brazilian Cerrado growing region. These genotypes had high seed yield potential in high quality environments.

Dilip Birla and Ramgiry (2015) The additive main effects and multiplicative interaction (AMMI) model was used to analysis the yield and yield component traits data of 25 soybean genotypes grown in three environments (Normal condition with rainfed condition, high plant population with rainfed condition and normal population with excess moisture). Main effects due to environments (E) and genotypes (G) were found significant for the all traits. The G× E interaction was significant for most of the traits, except days to 50% flowering, days to maturity and 100 seed weight (g). Gollob's test declared two components, Principal Component Analysis1 (PCA 1) and PCA 2, statistically significant ($P< 0.01$) for all the traits, except days to 50% flowering and days to maturity studied. The contribution of PCA 1 (99.6%) for G x E sum squares was greater for Days to maturity followed by Days to 50% flowering. The highest contribution for PCA 2 was (36.2%) for Grain yield per plant (g). In the present study, statistical analysis of yield trials of soybean under three environments with the AMMI model has revealed practical implications for plant breeding research towards in soybean.

Roshandel *et al.* (2016) The additive main effects and multiplicative interaction (AMMI) model was used to analysis the grain yield stability of 20 soybean genotypes in four locations (Karaj, Gorgan, Moghan and Shahre Kord) of Iran. Experiments were carried out based on randomized complete block design (RCBD), with three replications in 2014-2015. Result revealed that the grain yield was significantly influenced by environments (E), genotypes (G) and G × E interactions. Principal component analysis (PCA) declared three components which explained up to 90% of G × E sum square (IPCA1, IPCA2 and IPCA3 with 70.72%, 18.99% and 10.60%, respectively). AMMI multivariate method identified two genotypes (No.13 and No.8) with grain yield of 2789 and 2702 kg.ha-1 respectively, which were stable genotypes in different environments. The study concluded that the AMMI model is a practical and effective alternative for crop breeders to screen stability of soybean genotypes for different environments.

Birla *et al.* (2016) Twenty five newly developed strains of soybean were grown in three conditions (control, excess moisture and high plant population). Genetic parameters, inter-relationships and stability parameters for various yield and contributing traits were recorded. High heritability estimates coupled with high genetic advance was recorded for days to 50 per cent flowering, days to maturity and pods per plant under all three environments. Correlation studies showed that seed yield is positively related with harvest index (0.697*) followed by biological yield (0.586*). RVS 2007-1, RVS 2007-2, RVS 2007-4, JS20-53, JS 20-73 and JS 20-79 were identified as stable genotypes.

Anuradha *et al.* (2017) The analysis of variance revealed that environments (E), genotypes (G) and genotype × environment interactions (GEI) accounted about 19.61%, 26.18% and 40.71% of the total variation, respectively. GGE biplot graphically displayed inter-relationships between test locations as well as genotypes and facilitated visual comparisons through two-dimensional biplot between the first two principal components (PCI and PCII) which explained 74.40% variation for grain yield, 91.98% for days to 50% flowering, 83.27% for days to maturity and 84.68% for 100 seed weight.

Xavier *et al.* (2018) In this study, the genetic basis of soybean grain yield responsiveness to environmental factors was examined in a large soybean nested association population. For this, a genome-wide association to performance stability estimates generated from a Finlay-Wilkinson analysis and the inclusion of the interaction between marker genotypes and environmental factors was implemented. Genomic footprints were investigated by analysis and meta-analysis using a recently published multiparent model. Results indicated that specific soybean genomic regions were associated with stability, and that multiplicative interactions were present between environments and genetic background. Seven genomic regions in six chromosomes were identified as being associated with genotype-by-environment interactions.

Jandong *et al*. (2019) conducted trial in two distinct locations to assess the genotype –by-environment interaction (G*E) for specific traits such as number of pods, pod weight, seed yield and yield stability. The result revealed highly significant differences among the genotypes and locations for all the traits except for seed yield.

Raidas *et al.* (2020), the significant differences were observed among the genotypes for major growth physiological and yield attributes except number of branches, number of nodules and ascent of sap in the year. Further the result revealed that high magnitude of characters like plant height, dry weight of nodules, transpiration rate harvest index and yield per hectare were found in genotypes/varieties RVS2007-7, JS2069, RVS2007-1, RVS2001-4 and JS 2059 as stable genotypes.

Suhartina *et al.* (2022)evaluated 15 soybean genotypes consisted of 13 promising lines and 2 check varieties were evaluated in eight locations for seed yield trait and their adaptability during dry season II of 2017. Dering 1 and Grobogan varieties were used as check for drought tolerance and large seed size, respectively. Results of the study showed that 2 out of 13 soybean lines, AB-157-41-22 and DM-122-35-17, had the highest seed yield potential of 3.32 and of 2.99 t/ha, respectively. Average seed yield per ha of the two lines were 2.49 and 2.42 t/ha, respectively, which were higher than Dering 1 as check variety for drought tolerance (each 17.5 and 25.2%). Of the two selected lines, DM-122-35-17 showed stable adaptation across eight environments, while AB-157-41-22 was unstable adaptation. The two check varieties, Dering 1 and Grobogan, were both unstable across eight location with lower seed yield than AB-157-41-22 and DM-122-35-17. Therefore, soybean line DM-122-35-17 could be recommended as new variety possessing drought tolerance, high seed yield, large seed size, and stable in field performance.

CHAPTER- III

MATERIALS AND METHODS

The experimental material and the methods used during the course of present investigation have been described below:

3.1 Experimental site

The experiment was conducted in the experimental area of All India Coordinated Research Project on Soybean (AICRPS) at RAK College of Agriculture, Sehore (M.P.). The field was fairly uniform with gentle slope, adequate drainage and normal fertility status.

3.2 Experimental soil

The soil of field is clay loam vertisol with 52% clay,41.3% salt and 6.6% sand with pH ranging from 7.2 to 7.8. The soil was low in available nitrogen, medium in available phosphorous and moderate in available potassium.

3.3 Climate and season

Sehore is situated in the eastern part of Vindhyan Plateau in sub-tropical zone at the latitude of $23^{0}12'$ North and longitude of $77^{0}05'$ East at an attitude of 498.77 m above mean sea level in Madhya Pradesh. The annual rainfall varies from 1546.7 mm with major precipitation in the months of July and August. The weekly meteorological observations recorded during crop season (June 2021 to October 2021) have been presented in Table 3.1.1 The mean annual maximum and minimum temperature are 35.84^{0}C and 17.28^{0}C, respectively. The summer months are hot and May is the hottest month having a maximum temperature up to 45.60 ^{0}C, winter month experienced mild cold with an average temperature from 16.56^{0}C to 8.74^{0}C, December is the coldest moth as temperature reaches up to 5^{0}C. The weekly meteorological data viz., rainfall, temperature, relative humidity and number of rainy days during crop season were recorded in meteorological observatory of R.A.K. College of Agriculture, Sehore.

Meteorological data recorded during the period of experimentation in various locations under investigation are given in Table 3.1.1, 3.1.2, 3.1.3, 3.1.4.

Table 3.1.1-: Meteorological data during the crop season of 2021 at R.A.K. College of Agriculture (RVSKVV), Sehore (M.P.)

Month	**Standard week no.**	**Week**	**Temperature (°C)**			**Rainfall (mm)**	**No. of rainy days**
			Max	**Min.**			
June	23	07-13 June	38.3	23.4		112.8	3
	24	14-20	36.9	23.8		49.3	5
	25	21-27	34.3	22.7		126	4
	Average		**36.5**	**23.3**	**Total**	**288.1**	**12**
July	26	28-04	34.3	21.8		6.2	1
	27	05-11 July	36.5	26.3		11.5	1
	28	12-18 July	36.0	26.3		1.5	1
	29	19-25 July	32.2	23.2		98	3
	30	26-01 July	26.9	23.6		117.4	7
	Average		**33.18**	**24.24**	**Total**	**234.6**	**13**
August	31	02-08 aug	27.9	23.6		143.3	6
	32	09-15 Aug	35.1	25.7		10	2
	33	16-22 aug	30.1	24.9		67.4	5
	34	23-29 Aug	27.2	25.7		0	0
	Average		**30.07**	**24.97**	**Total**	**455.3**	**13**
September	35	30-05 sept	32.7	25.3		91	4
	36	06-12 sept	35.2	25.8		53.8	5
	37	13-19 sept	33.7	24.4		93	5
	38	20-26 sept	31.6	25		35.4	4
	Average		**33.3**	**25.12**	**Total**	**273.2**	**18**
October	39	27-03 oct	32.2	26.1		34	3
	40	04-10 0ct	34.4	25		0	0
	41	17-Nov	32.5	21.2		62.5	3
	Average		**33.03**	**24.1**	**Total**	**96.5**	**6**
					G.T.	**1347.7**	**62**

Source: Meteorological observatory, R.A.K.College of Agriculture, Sehore(M.P.) and all locations centers

The data in Table 3.1.1 indicates that during the crop season total rainfall was 1347.7 mm which was sufficient for the growth and development of soybean, with maximum and minimum rain, ranged from 143mm to 1.5 mm was observed in 26th and 23th meteorological standard week, respectively. The maximum temperature 38.3^{0}C was observed in 23rd meteorological standard week, and the minimum temperature 21.2^{0}C was observed in 40th meteorological standard week, while the maximum relative humidity of 94.76 per cent was observed in 31st meteorological week and the minimum relative humidity of 29 percent was recorded in 23rd meteorological week.

Table 3.1.2-: Meteorological data during the crop season of 2021-22 at Shivpuri

Month	Standard Week	Week	Temperature (^0C)		Rainfall in mm
			Max.	Min.	
July	26	25Jun-1Jul21	33.7	24.9	31.0
	27	2-8Jul21	34.9	27.5	0.0
	28	9-15Jul21	34.2	24.7	28.8
	29	16-22Jul21	32.1	24.9	84.8
	30	23-29Jul21	28.5	24.1	82.2
	Average		**32.7**	**25.2**	
Aug.	31	30Jul-5 Aug21	27.5	23.5	26.4
	32	6-12Aug21	30.2	23.8	1.4
	33	13-19Aug21	31.1	23.6	16.8
	34	20-26 Aug20	28.4	23.6	28.8
	Average		**29.8**	**23.6**	
Sept.	35	27Aug-2Sep21	31.0	23.2	68.2
	36	3-9Sep.21	31.8	24.0	9.6
	37	10-16Sep.21	29.9	23.3	62.2
	38	17-23Sep.21	28.1	22.6	73.0
	39	24-30Sep.21	30.6	22.4	156.8
	Average		**30.2**	**23.1**	
Oct.	40	1-7Oct.21	33.1	23.2	11.6
	41	8-14Oct.21	34.2	22.5	0.4
	42	15-21Oct.21	32.0	18.1	2.2
	43	22-28Oct21	31.0	16.7	0.0
	Average		**32.5**	**20.1**	

Source: Meteorological observatory, R.A.K.College of Agriculture, Sehore(M.P.) and all locations centers

Table 3.1.3-: Meteorological data during the crop season of 2021-22 at Dhar

Month	Standard Week	Week	Temperature (^{0}C)		Rainfall (mm)
			(Max)	(Max)	
July	26	25Jun-1Jul	32.8	25.8	72.1
	27	2-8Jul21	34.9	27.5	7.1
	28	9-15Jul	34.2	24.7	16.2
	29	16-22Jul	32.1	24.9	30.2
	30	23-29Jul	28.5	24.1	30.1
	Average		**32.7**	**25.2**	
Aug.	31	30Jul-5 Aug	27.5	23.5	5.6
	32	6-12Aug	30.2	23.8	6.0
	33	13-19Aug	31.1	23.6	1.1
	34	20-26 Aug	28.4	23.6	24.1
	Average		**29.8**	**23.6**	
Sep.	35	27Aug-2Sep	31.3	23.2	51.1
	36	3-9Sep	31.8	24.2	12.5
	37	10-16Sep	29.9	23.3	8.6
	38	17-23Sep	28.1	22.6	6.7
	39	24-30Sep	30.5	22.4	70.2
	Average		**31.2**	**24.1**	
Oct.	40	1-7Oct	32.1	22.3	46.1
	41	8-14Oct	35.2	21.5	1.5
	42	15-21Oct	30.0	17.12	3.9
	43	22-28Oct	33.0	15.6	1.1
	Average		**32.5**	**19.3**	

Source: Meteorological observatory, R.A.K.College of Agriculture, Sehore(M.P.) and all locations centers

Table 3.1.4 Meteorological data during the crop season of 2021-22 at Rajghar

Meteorological Week	**Standard Week**	**Week**	**Temperature C^o**		**Rainfall (mm)**
			Maximum	**Minimum**	
July	26	**25Jun-1Jul**	33.7	23.6	1.0
	27	**2-8Jul21**	36.5	24.6	-
	28	**9-15Jul**	35.4	24.3	20.2
	29	**16-22Jul**	33.2	25.0	9.3
	30	**23-29Jul**	29.3	23.2	26.5
August	**Average**		33.6	23.2	
	31	**30Jul-5 Aug**	29.6	21.3	13.5
	32	**6-12Aug**	31.4	23.3	15.5
	33	**13-19Aug**	32.1	23.4	16.5
	34	**20-26 Aug**	30.5	22.6	17.5
September	**Average**		30.9	22.6	
	35	**27Aug-2Sep**	31.6	21.2	72.0
	36	**3-9Sep**	32.6	23.7	86.0
	37	**10-16Sep**	31.4	23.4	35.5
	38	**17-23Sep**	30.2	24.1	31.0
	39	**24-30Sep**	31.6	23.2	40.5
Oct	**Average**		31.7	22.3	
	40	**1-7Oct**	35.1	25.2	13.0
	41	**8-14Oct**	35.7	24.5	-
	42	**15-21Oct**	34.3	18.9	20.5
	43	**22-28Oct**	34.0	18.1	-
	Average		34.7	21.6	

Source: Meteorological observatory, R.A.K.College of Agriculture, Sehore(M.P.) and all locations centers

3.4 Experimental material

The experimental material comprised of 15 advance breeding lines of soybean developed at All India Coordinated Research Project on Soybean (AICRPS) RAK College of Agriculture, Sehore, (M.P.).

3.3 Details of genotypes of present experiment material with their pedigree.

S. No .	Pedigree lines	Cross combinations
1.	RVS 14-1	RVS 2018 × JS20-34
2.	NRC 94	Source from NRC'S
3.	RVS 14-2	RVS 34×JS-335
4.	RVS 2011-35	JS 335 × PK1042
5.	NRC 137	Source from NRC'S
6.	JS 20-34	JS98-63×PK768
7.	RVS14-4	RVS 2001-4 × RVS 24
8.	NRC 136	JS97-52×NRC 37
9.	RVS 11-4	JS335xPK1042
10.	RVS 14-3	RVS 18 ×JS 20-16
11.	NRC 177	Source from NRC'S
12.	NRC 158	Source from NRC'S
13.	NRC 157	Source from NRC'S
14.	RVS 2013-7	JS97-52×JS 9305
15.	RVS 2013-15	ANKUR×JS 335

3.5 Experimental details

The experiment was laid out in Randomized Block Design with three replications. The genotypes were evaluated under four different environments created by growing them at four different locations viz.

(1) R.A.K. College of Agriculture, Sehore
(2) K.V.K. Rajgarh
(3) K.V.K. Shivpuri
(4) K.V.K. Dhar

Experiment was sown on 29 June 2021. Each genotype was planted three rows of 3m long, with row to row spacing and plant to plant spacing of 40cm and 30cm respectively. Fertilizer dose 20:60:20:20 NPKS Kg/ha was applied uniformly over the soil and recommended package of practices were adopted for optimum crop growth and development with proper plant protection measure under rainfed condition.

A random selection of five plants in each plot was made and various observations were recorded on each selected plant. The mean values of each character under study were computed on the basis of five plants for each genotype from each replication.

3.6 Characters studied

Following observations were recorded on five randomly selected competitive plants from each genotype and each replication. The detailed procedure adopted for recording two phenological and ten agronomic traits are given below:

3.6.1 Phenological traits:

Based on developmental stages of soybean, observations on following two phenological phases were recorded:

i. Days to 50% flowering:

Data were recorded on days to flowering when 50 percent of plants in each replication showed flowering initiation from the date of sowing.

ii. Days to maturity:

Numbers of days from sowing to 80 percent plants per plot attaining maturity were counted.

3.6.2 Agronomic traits:

i. Plant height (cm):

Height of the plants was measured in centimeter from the ground level to the top of the plants at the time of maturity.

ii.Number of primary branches per plant:

The number of primary branches per plant directly arising from main stem counted at maturity and averaged.

iii. Internode length (cm):

Length of five randomly selected plant internodes from each selected five plants per plot was measured and averaged.

iv. Pod length (cm):

Length of five randomly selected pods from each selected five plants per plot was measured and averaged.

v. Number of pods per plant:

Total number of fully matured pods of five plants were counted and averaged to obtain pods per plant.

vi. Number of Seeds per pod:

Total number of seed present in per pod were counted to mature pods.

vii. 100-seed weight (g):

The weight of 100-seeds from the produce of each entry in each replication was recorded on Electronic Single Pan Balance in grams.

viii. Biological yield per plant (g):

The total biomass was estimated by weighing whole plant (cut roots) at maturity and recorded in grams.

ix.Seed yield per plant (g):

The seed yield of the sample plants were recorded in grams on Top Pan Digital Balance and averaged for each genotype.

x. Harvest index (%):

It is a ratio of seed yield to biological yield per plant and expressed in percentage as:

$$\text{H.I. (\%)} = \frac{\text{Seed yield per plant (g)}}{\text{Biological yield per plant (g)}} \times 100$$

3.7 Statistical methodology:

3.7.1 Analysis of variance

Analysis of variance (ANOVA) for different characters was carried out the procedure of randomized block design can be expressed as follows.

$$Pij = \mu + gi + rj + eij$$

Where,

Pij = phenotypic effect of i^{th} genotype in the j^{th} replication.

μ = general population mean

gi = effect of j^{th} replication

eij = error associated with the experiment.

The skeleton for analysis of variance for randomized block design is given below.

Source of variation	**D.F**	**Sum of squares**		**Mean sum of squares**
Replication	(r-1)	SSr		σ^2r
Genotypes	(g-1)	SSg	Mst	$\sigma^2e+r\ \sigma^2g$
Error	(r-1)(g-1)	Sse	Mse	σ^2e
Total	(rg-1)			

Where,

r = number of replications

g= number of genotypes

σ^2g= genotypic variance (MSt, MSe/r)

σ^2e= error variance

A. Test of significant

The mean sum of squares for genotypes and replications were tested against the error mean sum of square for calculating F values which were compared with tabulated F value at 5 and 1 percent level of significance.

B. Standard error of mean

It was calculated using formula given below

$$\text{SEm} \pm = \sqrt{MSe/r}$$

Where,

SEm ± = standard error of mean

MSe = mean sum of square due to error

r = number of replication.

C. Standard error of differences

It was calculated using formula given below

$$\text{SEm} \pm = \sqrt{2MSe/r}$$

Where,

SEm ± = standard error of differences

MSe = mean sum of square due to error

r = number of replications.

D. Critical difference

It was measured using formula mentioned below.

CD= SEd X t value at 5% level of significance.

Where,

CD = critical difference

SEd= standard error of difference

t = table value of 5% probability level of error df.

3.7.2 Genetic analysis

The mean, range components of variance, genotypic and phenotypic coefficient of variation and heritability in broad sense, genetic advance and expected genetic advance were calculated as per procedure mentioned below. (Johnson *et al.* ,1955)

A. Mean

Mean was calculated using following conventional formula

$$\overline{X} = \frac{\Sigma X}{N}$$

Where,

$\overline{X}$= simple mean

ΣX = summation of all the observation.

N = number of observation

B. Range

It is the range of lowest and highest values of each trait taken in the observations.

C. Genotypic variance ($\sigma^2 g$)

$$\sigma^2 g = \frac{MSt - MSe}{r}$$

Where,

MSt = treatment mean sum of square MSe = error mean sum of squares

r = number of replications.

D. Phenotypic variance ($\sigma^2 p$)

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

$\sigma^2 g$ = genotypic variance

$\sigma^2 e$ = environmental variance

E. Heritability

Heritability in board sense was estimated by the formula proposed by Singh and Choudhary (1985).

$$h^2 = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

h^2 = Heritability in broad sense.

F. Coefficient of variance

The formula given by Burton (1952) was used for computation of genotypic and phenotypic coefficient of variation as mentioned below.

a) Genotypic coefficient of variation

It was calculated by using the following formula

$$GCV = \frac{\sqrt{\sigma^2 g}}{\overline{X}} \times 100$$

Where,

GCV = genotypic coefficient of variation $\sigma^2 g$ = genotypic variance

● = general mean of the characters

b) Phenotypic coefficient of variation

It was calculated by using the following formula.

$$PCV = \frac{\sqrt{\sigma^2 p}}{\overline{X}} \times 100$$

Where,

PCV = phenotypic coefficient of variation $\sigma^2 p$ = phenotypic variance

$\overline{X}$= general mean of the characters

G. Genetic advance

The genetic advance was calculated in per cent by the formula suggested by Johnson *et al.* (1955).

a) $GA = \frac{\sigma^2 g}{\sigma^2 p} \times \sigma p \times k$

b) GA as percentage of mean (GAM) = $\frac{GA}{\bar{x}} \text{x} 100$

Where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

σp = Phenotypic standard deviation

K = Selection differential at 5 per cent selection intensity (2.06)

$\bar{x}$ = Mean of the character

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

Low :< 10 (%)

Moderate : 10 – 20 (%)

High : > 20 (%)

3.7.3 Correlation Coefficient

Phenotypic, genotypic and environmental correlation coefficient between characters were computed utilizing respective components of variance and co-variance, by following formulae suggested by Miller *et al*. (1958).

$$r_{xy} = \frac{\text{Cov}(x,y)}{[V(x) \times V(y)]^{1/2}}$$

Where,

r_{xy} = Correlation coefficient between character x and y,

Cov (x.y) = Co- variance of character x and y,

V(x) = Variance of character x, and

V(y) = Variance of character y.

To test the significance of correlation coefficient, the calculated values were compared with the tabulated values of Fisher and Yates (1938) at t-2 d.f at two levels of probability, viz., 5% and 1%.

3.7.8 Stability Analysis

Statistical procedure:

Pooled analysis of data:

Since 15 varieties were grown in four environments, the data were combined separately over environments to get information on genotype × environment (g×e) interaction. The form of analysis of variance for pooled data is given as under:

Prior pooling the data, the test of homogeneity for error variance was applied by utilizing the Barlletts method (Panse and Sukhatme, 1967).

The test of homogeneity of variance was carried out as follows:

Let there be n mean squares S_1^2, S_2^2,……, S_n^2 based on K_1, K_2,……, K_nd.f., respectively. From these values a pooled estimated of variance, $\bar{S}^2$, was calculated by-

$$\bar{S}^2 = \left[\frac{1}{\sum_{r=1}^{n} Kr} \left(\sum_{r=1}^{n} KrS^2r \right) \right]$$

$$X^{1^2} = \left\{ \left(\sum_{r=1}^{n} Kr \right) \log_e \bar{S}^2 - \sum_{r=1}^{n} Kr \ \log_e S^2r \right\}$$

The quantity X^{1^2} is distributed approximately as X^2 with (n-1) d.f. but it is slightly biased upwards.

It can be effectively corrected by dividing it by the C.F. (C)

$$C = 1 + \frac{1}{3(n-1)} \left\{ \sum_{r=1}^{n} \frac{1}{Kr} - \frac{1}{\left(\sum_{r=1}^{n} Kr \right)} \right\}$$

The quantity X^{1^2}/C was compared with the table value of chi-square (X^2) with (n-1) degrees of freedom at p=0.05.

The mean of individual variety over all replications for each environment was calculated and data obtained were analysed, dividing the total variability in to variance.

1. Due to environment on genotypes
2. Due to genotypes over environments
3. Due to genotypes × environments

The structure of analysis of variance is presented below:

Analysis of variance

Source of variation	**D.F.**	**MSS**	**Expected M.S.S.**
Environment	(n-1)		
Varieties	(t-1)	M_1	$\delta^2e + \delta^2l + n\delta^2g$
Variety X Environment	(n-1)(t-1)	M_2	$\delta^2e + \delta^2l$
Pooled Error	(nt-1)	M_e	δ^2e
Total	**r(t-1)**		

Where,

n = Total number of environments

t = Total number of varieties

The mean sum of squares due to varieties and environments were tested against mean sum of squares due to varieties × environments. The sum of squares due to varieties × environments was tested against pooled error.

Estimation of pooled error:

The pooled error was computed using the mean sum of squares due to error obtained in individual environments as follows:

$$\text{Pooled error} = \frac{(n_1-1)(\text{M.S. error } E_1) + \ldots\ldots + (n_n-1)(\text{M.S. error } E_n)}{(n_1-1) + \ldots\ldots\ldots\ldots\ldots\ldots + (n_n-1)}$$

Where,

(n_1-1) = d.f. for error in environment 1, and

M.S. error E_1 = mean sum of squares due to error for environment I.

(n_n-1) = d.f. for error in environment n_n and

M.S. error E_n = Mean sum of square due to error for environment n.

In case the mean sum of squares due to varieties × environments was found significant, the analysis had been further proceeded for the estimation of stability parameters.

Analysis for stability parameters:

Eberhart and Russell (1966) model was used for estimation of stability parameters.

$y_{ij} = \mu_i + \beta_i I_j + \delta_{ij}$

where,

y_{ij} = The mean of i^{th} variety in j^{th} environment (I= 1, 2,……, v & j= 1, 2,……, n)

μ_i = The mean of i^{th} variety over all the environments

β_i = Regression coefficient that measures the response of the i^{th} variety to varying environments.

I_j = Environmental index which is defined as the deviation of the mean of all the varieties for given environment from the overall mean.

$$= \frac{\sum_i y_{ij}}{t} - \frac{\sum_i \sum_j y_{ij}}{ts} \quad \text{with} \quad \sum_j I_j = 0$$

δ_{ij} = The deviation from regression of the i^{th} variety in j^{th} environment.

The model provides a mean of partitioning the variety × environment interaction of each variety into two parts.

1. The variation due to the response of the varieties to varying environmental indexes (S.S. due to regression), and,
2. The unexplainable deviation from the regression on the environmental index.

Analysis of variance structure for stability is presented in the Table below:

Analysis of variance for stability parameters:

Source	**d.f.**	**S.S.**	**M.S.**
Total	nv-1	$\sum_i \sum_j y_{ij}^2$ - C.F.	
Varieties (V)	v-1	$\frac{1}{n}\sum_i y_i^2$ - C.F.	M.S.$_1$
Environment (Env.)	n-1	$\frac{\sum_i \sum_j y_{ij}^2 - y_i^2}{n}$	
V×Env.	(v1I)(n1I)v(n-1)		
Env. (linear)	1	$\frac{\frac{1}{v}\left(\sum_j y_j I_j\right)^2}{\sum_j I_j^2}$	
V×Env. (linear)	v-1	$\sum_{ij}\left\{\frac{\left(\sum_j y_{ij} I_j\right)^2}{\sum_j I_j^2}\right\}$ -(Env. linear) S.S.	M.S.$_2$
Pooled deviation	v(n-2)	$\sum_i \sum_j \delta_{ij}^2$	M.S.$_3$
Variety I	n-2	$\left(\sum_j y_{ij}^2 - \frac{y_i^2}{n}\right) - \frac{\left(\sum_j y_{ij} I_j\right)^2}{\sum_j I_j^2}$	
Variety V	n-2	$\left(\sum_j y_v^2 - \frac{y_v^2}{n}\right) - \frac{\left(\sum_j y_{vi} I_j\right)^2}{\sum_j I_j^2} = \sum_j \delta_v^2$	
Pooled error	n(r-1)(v-1)		

Stability parameters: The two parameters of stability were calculated as follows:

(a) The regression coefficient: Which is the regression of the performance of each variety under different environment on the environmental means over all the varieties. This was estimated as follows

$$\beta_i = \frac{\sum_j y_{ij} I_j}{\sum_j I_j^2}$$

where,

$\sum_j y_{ij} I_j$ was the sum of products of variety environmental index and $\sum_j I_j^2$ was the sum of square of all the environmental indexes.

(b) Mean square deviation $\left(\bar{S}_d^2\right)$ from linear regression

$$\bar{S}_{di}^2 = \left(\frac{\sum_j \delta_{ij}^2}{n-2} - \frac{S_e^2}{r} \right)$$

where,

$$\sum_j \delta_{ij}^2 = \left(\sum_j y_{ij}^2 - \frac{y_i^2}{t} \right) - \frac{\left(\sum_j y_{ij} I_j \right)^2}{\sum_j I_j^2}$$

And S_e^2 = The estimate of pooled error.

The various computational steps involved in the estimation were as follows

Computation of environmental index (I_j):

The I_j was calculated as

$$I_j = \frac{\text{Total of all the varieties at } j^{th} \text{ location}}{\text{Number of varieties}} - \frac{\text{G.T.}}{\text{Total number of observation}}$$

$$I_j = \frac{\sum_j y_{ij}}{t} - \frac{\sum_i \sum_j y_{ij}}{ts}$$

Computation of regression coefficient (β_i) for each variety

$$\beta_i = \frac{\sum_j y_{ij} I_j}{\sum_j I_j^2}$$

(a) It was obvious that for each value of regression coefficient, $\sum_j I_j^2$ was common.

(b) But $\sum_j y_{ij} I_j$ for each variety was the sum of products of environmental index (I_j) with the corresponding mean ($\bar{x}$) of that variety at each location.

Computation of $\bar{S}_d^2$:

(b)Deviation from regression

In a regression analysis it is possible to partition the variance of the dependent variable (y) into two parts the one which explains the linearity between dependent and independent variable (variances due to regression) and the other which explain the variance due to deviation + δ^2 deviation from regression.

By subtracting the variance due to regression from δ^2y, one can get the variance due to deviations from regression, which in turn can be used, for estimating $\bar{S}_d^2$ values. The variance of mean over different locations with regard to individual varieties may be obtained as below:

$$\delta^2 vi = \sum_j y_{ij}^2 - \left(\frac{y_i^2}{t}\right)$$

Test of hypothesis:

(a) In order to test the significance of the difference among the variety means i.e. Ho = $\mu_1 = \mu_2 = \ldots\ldots = u_n$, the appropriate 'F' test defined below was applied.

$$F = \frac{MS_1}{MS_3}$$

(b) The hypothesis that variance did not differ for their regression on the environment index i.e.

Ho = $b_1 = b_2 = \ldots\ldots\ldots\ldots = b_n$ was tested as below:

$$F = \frac{MS_2}{MS_3}$$

(c) Individual deviation from linear regression was tested as follows:

$$F = \frac{\left(\sum_j \delta_{ij}^2\right) / (S - 2)}{\text{Pooled error}}$$

To test the hypothesis that individual b_1^s did not differ significantly from unity 't' test was applied to test the hypothesis

$$\text{'t'} = \frac{(1 - b)}{\text{SE of b}}$$

SE of b was computed by the formula:

$$\text{SE (b)} = \sqrt{\frac{\text{M.S. due to pooled deviation}}{\sum_j I_j^2}}$$

Where,

$\sum_j I_j^2$ = Summation of squared values of environmental indices

Calculated t value was tested against table 't' value at (t-2) d.f.

CHAPTER-IV
RESULTS

The experimental findings of the present study entitled **"Stability analysis for yield and its traits in Newly Developed Breeding Lines of soybean (*Glycine max* (L.) Merrill)"** are reported in this chapter under following heads:

1. Genetic variation
2. Heritability
3. Genetic advance
4. Correlation coefficient
5. Stability analysis

1. Genetic variation:

Analysis of variance:

The analysis of variance (Table 4.1) was computed for seed yield and its components viz., days to 50% flowering, days to maturity, plant height, number of primary branches per plant, internode length, pod length, number of pods per plant, number of seed per pods, 100 seed weight, biological yield per plant and harvest index for each environment separately.

The analysis of variance revealed that there were highly significant differences among genotypes for all the traits except biological yield per plant under in E-3 environment.

Population mean:

Estimates of population mean of 12 characters under each of 4 environments are presented in Table 4.2. The highest number of days (43.22) taken to 50% flowering was recorded in E-2 and lowest in E-4 (42.76). Highest number of days (104.4) taken to physiological maturity was observed in E-3 and lowest (103.5) in E-4. plant height was highest (52.01 cm) in E-2 and lowest (50.95 cm) in E-4, Number of primary branches per plant was highest (8.51) in E-2 and lowest (7.67) in E-3,Internode length was highest observed (6.32) in E-2 and lowest (6.04) in E-4, Pod length was highest found (3.38) in E-2 and closely related with E-3and lowest (3.14) in E-4, number of pods per plant was highest (69.45) in E-2 and lowest (69.07) in E-1, number of seeds per pod was highest (2.71) in E-3 and lowest (2.54) in E-4, 100 seed weight was highest (11.65 g) in E-3 and lowest (11.21 g) in E-4, biological yield per plant was highest (35.55 g) in E-2 and lowest (34.64 g) in E-4, seed yield per plant was highest (17.05 g) in E-3 and lowest (16.78 g) in E-4, and harvest index was highest (51.53%) in E-3 and lowest (50.16%) in E-2 was recorded.

Table 4.1 Analysis of Variance for each Environment: (Mean sum of squares)

Environment	**E-1**		**E-2**		**E-3**		**E-4**	
Source of variation	**Genotype**	**Error**	**Genotype**	**Error**	**Genotype**	**Error**	**Genotype**	**Error**
d.f.	**14**	**28**	**14**	**28**	**14**	**28**	**14**	**28**
Days to 50% flowering	21.707**	1.307	16.507**	1.336	18.800**	0.938	17.593**	1.446
Days to maturity	73.069**	3.350	61.619**	1.985	74.009**	2.290	72.803**	3.326
Plant height (cm)	537.22**	9.688	511.8**	14.88	536.744**	11.578	535.162**	5.180
Number of primary branches /plant	10.691**	0.157	13.586**	0.859	9.978**	0.121	9.088**	0.100
Internode length (cm)	5.306**	0.259	4.634**	0.297	5.349**	0.305	4.473**	0.066
Pod length (cm)	0.480	0.055	0.443	0.145	0.722**	0.143	0.492	0.046
Number of pods/plant	506.573**	21.382	509.636**	24.44	502.242**	25.642	519.371**	12.778
Number of seeds/pod	0.140	0.087	0.146	0.083	0.372**	0.198	0.166	0.075
100 seed weight (g)	15.436**	0.398	14.536**	0.880	13.605**	1.441	15.362**	0.374
Biological yield/Plant (g)	628.297**	12.460	624.931**	15.79	632.329**	14.402	616.116**	12.611
Seed yield/plant (g)	98.966**	5.073	92.722**	6.260	88.525**	7.123	97.034**	3.464
Harvesting index(%)	205.49**	33.284	232.273**	39.838	285.66**	53.935	219.067**	35.527

Table 4.2. Population mean for different characters

Characters	Environment			
	E-1	**E2**	**E3**	**E-4**
Days to 50% flowering	43.18	43.22	42.87	42.76
Days to maturity	104.36	104.00	104.4	103.51
Plant height (cm)	51.24	52.01	51.55	50.95
Number of primary branches/plant	7.68	8.51	7.67	7.69
Internode length (cm)	6.10	6.32	6.12	6.04
Pod length (cm)	3.20	3.38	3.38	3.14
Number of pods/plant	69.07	69.45	68.45	69.09
Number of seed/pods	2.59	2.59	2.71	2.54
100 Seed weight (g)	11.30	11.55	11.65	11.21
Biological yield/plant (g)	34.94	35.55	35.09	34.64
Seed yield/plant (g)	16.81	16.91	17.05	16.78
Harvesting index (%)	50.30	50.16	51.53	50.86

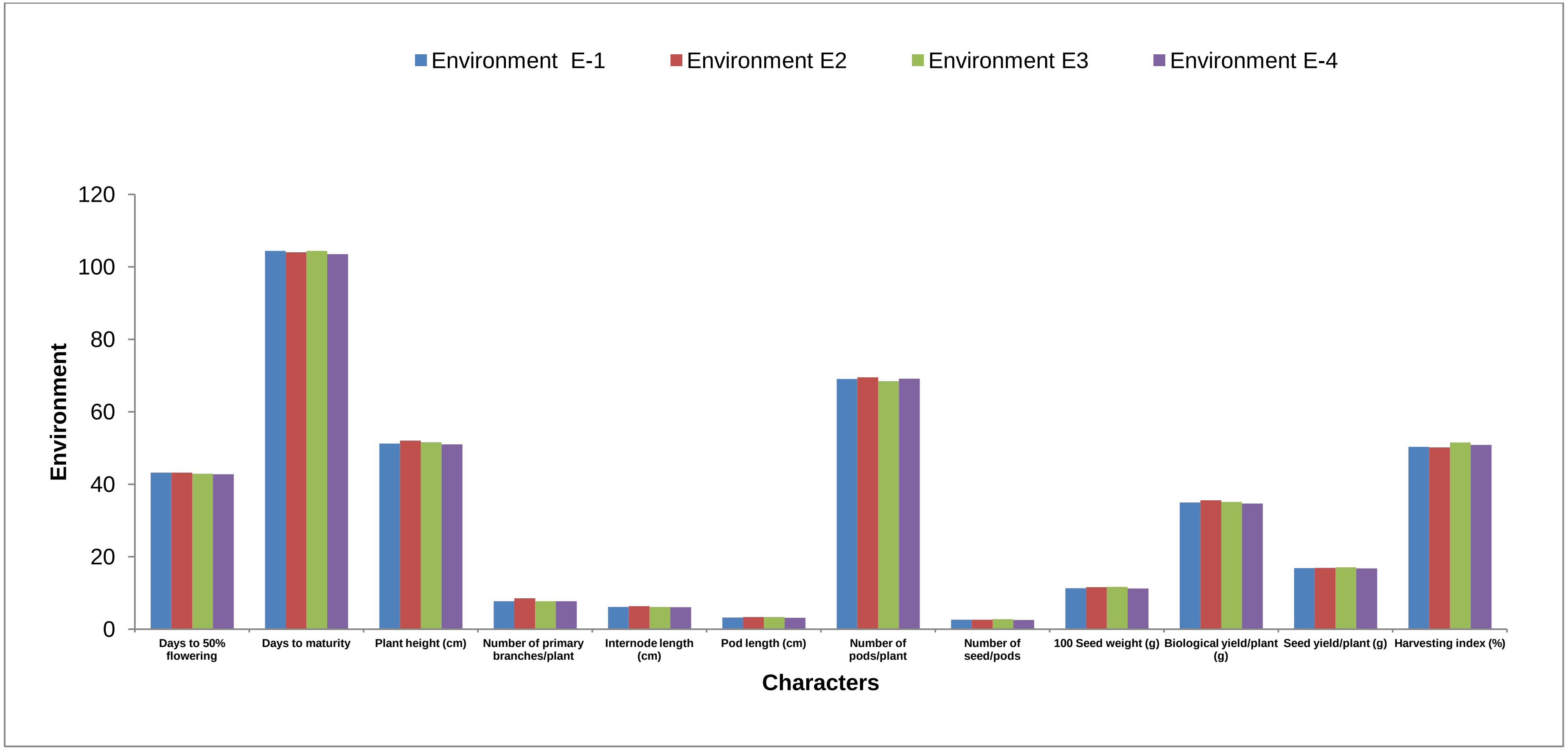

Fig 1 : . Population mean for different characters

Range:

Ranges of values for 12 characters under each of four environments are reported in Table 4.3. Maximum range for number of days taken to 50% flowering (40.00-52.00 days) was recorded in E-3 and lowest (39.67-50.00 days) in E-4, for number of days taken to maturity highest (96.00-111.00 days) was found in E-2 and lowest (94.00-111.00 days) in E-4, for plant height highest (28.04- 85.81cm) was in E-2 and lowest (26.73-85.27 cm) in E-3 followed by in E-1 (26.70-85.44 cm), for number of primary branches per plant highest (4.53-12.73) was observed in E-2 and lowest (4.07-11.00) in E-4, for internode length highest (4.60-8.87cm) was noticed in E-2 and lowest (3.67-8.83cm) in E-3, for pod length highest (2.73-4.38 cm) was found in E-3 and lowest (2.49-4.03 cm) in E-2, for number of pods per plant the highest (22.86-171.19) was noticed in E-2 and lowest (19.93-173.67) in E-4, for number of seeds per pod the highest value (2.37-3.67) was showed in E-3 and lowest (2.27-3.03) in E-1, for 100 seed weight the highest (8.93-15.82 g) was recorded in E-4 and lowest (8.00-14.35 g) in E-2, for biological yield per plant highest (20.27-63.47 g) was in E-1 and lowest (17.33-62.87 g) in E-4, for seed yield per plant highest (11.45-26.85 g) was in E-3 and lowest (10.95-26.00 g) in E-2, and for harvest index highest (30.22-67.05%) was in E-3 and lowest (28.99-63.00 %) in E-2.

Table 4.3. Range for different characters

Characters	Environment			
	E1	**E-2**	**E-3**	**E-4**
Days to 50% flowering	41.00-51.00	40.00-50.00	40.00-52.00	39.67-50.00
Days to maturity	95.00-111.00	96.0-111.00	94.00-111.00	94.00-111.00
Plant height (cm)	26.70-85.44	28.04-85.81	26.73-85.27	27.00-85.47
Number of primary branches/plant	4.73-11.87	4.53-12.73	4.73-11.63	4.77-11.00
Internode length (cm)	3.73-8.70	4.60-8.87	3.67-8.83	3.90-8.27
Pod length (cm)	2.66-4.03	2.49-4.03	2.73-4.38	2.48-4.12
Number of pods/plant	21.78-170.67	22.86-171.19	21.05-171.18	19.93-173.67
Number of seeds/pod	2.27-3.03	2.30-3.10	2.37-3.67	2.30-3.03
100 Seed weight (g)	8.11-14.18	8.00-14.35	8.67-14.47	8.93-15.82
Biological yield/plant (g)	20.27-63.47	18.47-63.38	17.81-63.37	17.33-62.87
Seed yield/plant (g)	10.74-27.21	10.95-26.61	11.45-26.85	10.77-27.25
Harvesting Index (%)	30.42-65.83	28.99-63.00	30.22-67.05	30.68-63.30

Phenotypic coefficient of variation (P.C.V.):

Phenotypic coefficient of variation estimates, in percent, in each of the four environments are presented in Table 4.4.

For days to 50% flowering PCV was the highest found value (6.59%) in environment E-1 and lowest (5.85%) in E-2, for days to maturity the highest value observed (4.972%) in E-4 and lowest(4.496%) in E-2, for plant height highest (26.58%) in E-1 closely followed byE-4(26.50%) and lowest (25.83%) in E-2, for number of primary branches per plant the highest value of (26.54%) in E-2 and lowest (22,87%) in E-4, for internode length highest value observed (23.01%)in E-3and lowest value (20.50%) in E-4, for pod length the highest value found (17.18%) in E-3 and lowest (13.89%) in E-1,for number of pods per plant the highest value noticed (60.37%) in E-4 and lowest (59.21%) in E-13, for number of seed per pods the highest figure exhibited (18.70%) in E-3 and lowest (12.49%) in E-2, for 100 seed weight the highest noticed (20.66%) in E-4 and lowest (20.12%) in E-3, for biological yield per plant the highest estimate recorded (42.30%) in E-3 and lowest (41.85%) in E-2,for seed yield per plant the highest found value (35.88%) in E-1 and lowest (34.33%) in E-3, for harvest index the highest value observed (22.22%) was in E-3 and lowest (18.93%)in E-1.

Table 4.4. Estimates of phenotypic coefficient of variation

Characters	Environment			
	E1	**E2**	**E3**	**E4**
Days to 50% flowering	6.59	5.85	6.12	6.11
Days to maturity	4.94	4.49	4.90	4.97
Plant height (cm)	26.58	25.83	26.50	26.46
Number of primary branches/plant	24.92	26.54	24.05	22.87
Internode length (cm)	22.86	20.90	23.06	20.50
Pod length (cm)	13.89	14.62	17.18	14.08
Number of pods/plant	59.74	59.63	59.21	60.37
Number of seed/pods	12.54	12.49	18.70	12.81
100 seed weight (g)	20.58	20.18	20.12	20.66
Biological yield per plant (g)	42.23	41.85	42.30	42.20
Seed yield per Plant (g)	35.88	35.01	34.33	35.08
Harvesting index(%)	18.93	20.33	22.22	19.33

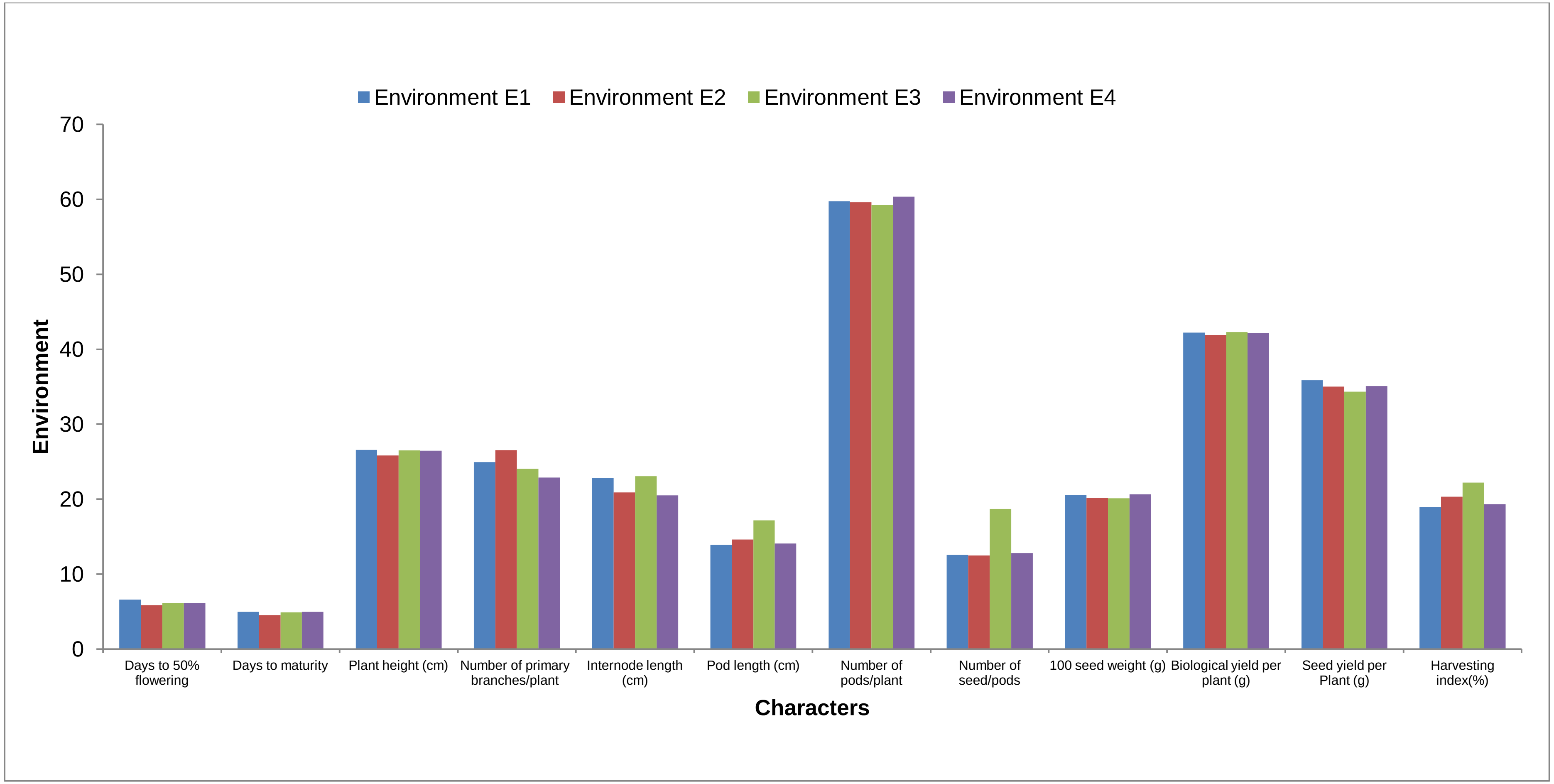

Fig 2 Estimates of phenotypic coefficient of variation

Genotypic coefficient of variation (G.C.V.):

Genotypic coefficient of variation estimates, in percent, in each of the four environments are presented in Table 4.5.

Genotypic coefficient of variation for days to 50% flowering was the highest found value(6.03%) in environment E-1 and lowest (5.20%) in E-2,for days to maturity the highest value noticed (4.68%) in E-3 and lowest (4.28%) in E-2, for plant height the highest estimate recorded (26.08%) in E-4 closely followed by E-1(25.877%) and lowest (24.74%) in E-2, for number of primary branches per plant the highest value observed (24.38%) in E-1 and lowest (22.49%) in E-4,for internode length the highest value observed (21.27%) in E-1 and lowest (19.04%) in E-2, for pod length the highest value found (13.00%) in E-3 and lowest (9.31%), for number of pods per plant the highest value noticed (60.14%) in E-4 and lowest (59.20%) in E-2, for number of seeds per pods the highest (8.88%) in E-3 and lowest (5.13%) in E-1, for 100 seed weight the highest value of (19.93%) in E-4 and lowest (17.28%) in E-3 and for biological yield per plant the highest found value (41.01%) in E-1 and lowest (40.31%) in E-2, for seed yield per plant the highest value observed (33.28%) in E-1 and lowest (30.55%) in E-3,for harvest index the highest found value (17.05%) in E-3 and lowest (15.06%) in E-1.

Table 4.5. Estimates of genotypic coefficient of variation

Characters	Environment			
	E1	**E2**	**E3**	**E4**
Days to 50% flowering	6.03	5.20	5.69	5.42
Days to maturity	4.62	4.28	4.68	4.64
Plant height (cm)	25.87	24.74	25.66	26.08
Number of primary branches/plant	24.38	24.20	23.62	22.49
Internode length (cm)	21.27	19.04	21.17	20.05
Pod length (cm)	11.78	9.31	13.00	12.27
Number of pods/plant	59.37	59.20	58.76	60.14
Number of seeds/pod	5.13	5.59	8.88	6.85
100 seed weight (g)	19.82	18.47	17.28	19.93
Biological yield per plant (g)	41.01	40.31	40.90	40.94
Seed yield/plant (g)	33.28	31.74	30.55	33.28
Harvest index (%)	15.06	15.96	17.05	15.38

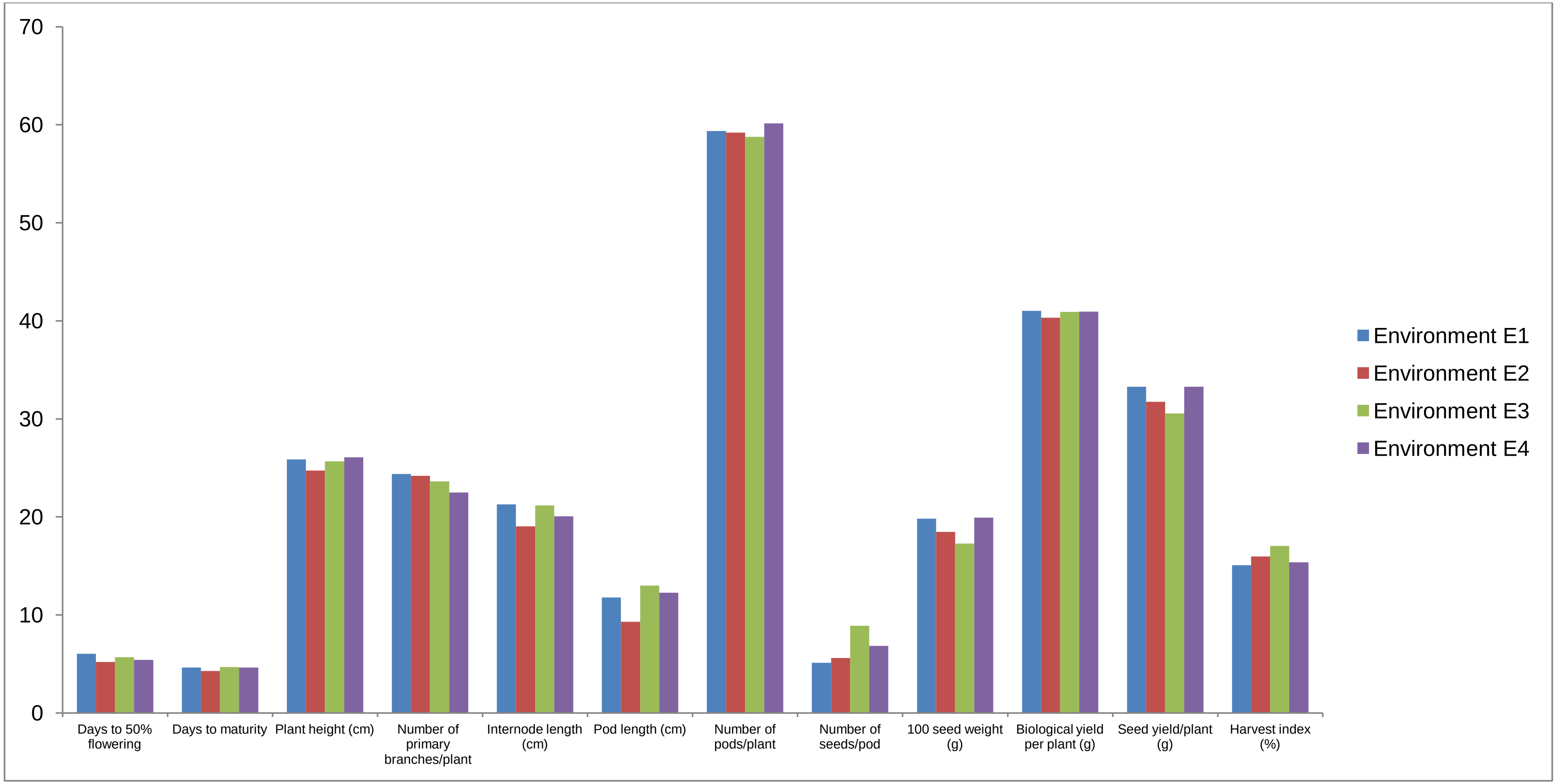

Fig 3 Estimates of genotypic coefficient of variation

Heritability:

Estimates of heritability in broad sense for different traits under the all four environments are reported in Table 4.6.

Number of days to 50% flowering showed the highest heritability (86.38%) in E-3 and lowest (78.82%) in E-4, days to maturity found the highest (91.25%) in E-3 and lowest (87.39%) in E-1,plant height showed the highest (97.15%) in E-4 and lowest (91.75) in E-2,number of primary branches per plant recorded the highest (96.76%) in E-4 and lowest (83.14%) in E-2, internode length the highest value observed (95.64%) in E-4 and lowest (82.92) in E-2, pod length the highest found (75.97%) in E-4 and lowest (in E-2 40.53%), number of pods per plant the highest (99.26%) in E-4 and lowest (98.48%) in E-3, number of seed per pods found the highest (28.65%) in E-4 and lowest (16.73%) in E-1, 100 seed weight exhibited the highest (93.03%) in E-4 and lowest (73.76%) in E-3, similarly biological yield per plant noticed highest (94.27%) in E-1 and lowest (92.78%) in E-2, seed yield per plant the highest (90.00%) in E-4 and lowest (82.15%) in E-2 and harvest index showed highest heritability (63.28%) in E-1 and lowest (58.88%) in E-3.

Table 4.6. Estimates of heritability (%) in broad sense

Characters	Environment			
	E1	**E2**	**E3**	**E4**
Days to 50% flowering	83.86	79.09	86.38	78.82
Days to maturity	87.39	90.91	91.25	87.43
Plant height (cm)	94.77	91.75	93.79	97.15
Number of primary branches/plant	95.71	83.14	96.42	96.76
Internode length (cm)	86.62	82.92	84.61	95.64
Pod length (cm)	71.90	40.53	57.28	75.97
Number of pods/plant	98.74	98.57	98.48	99.26
Number of seed/pods	16.73	20.06	22.55	28.65
100 seed weight (g)	92.72	83.80	73.76	93.03
Biological yield/plant (g)	94.27	92.78	93.46	94.10
Seed yield/plant (g)	86.04	82.15	79.20	90.00
Harvest index (%)	63.28	61.68	58.88	63.26

Genetic advance:

Genetic advance estimates in percent’ expect. all the four environments are reported in Table 4.7.

For days to 50% flowering the highest value noticed (4.91%) genetic advance was expected in from E-1 and lowest (4.12%) from E-2, for days to

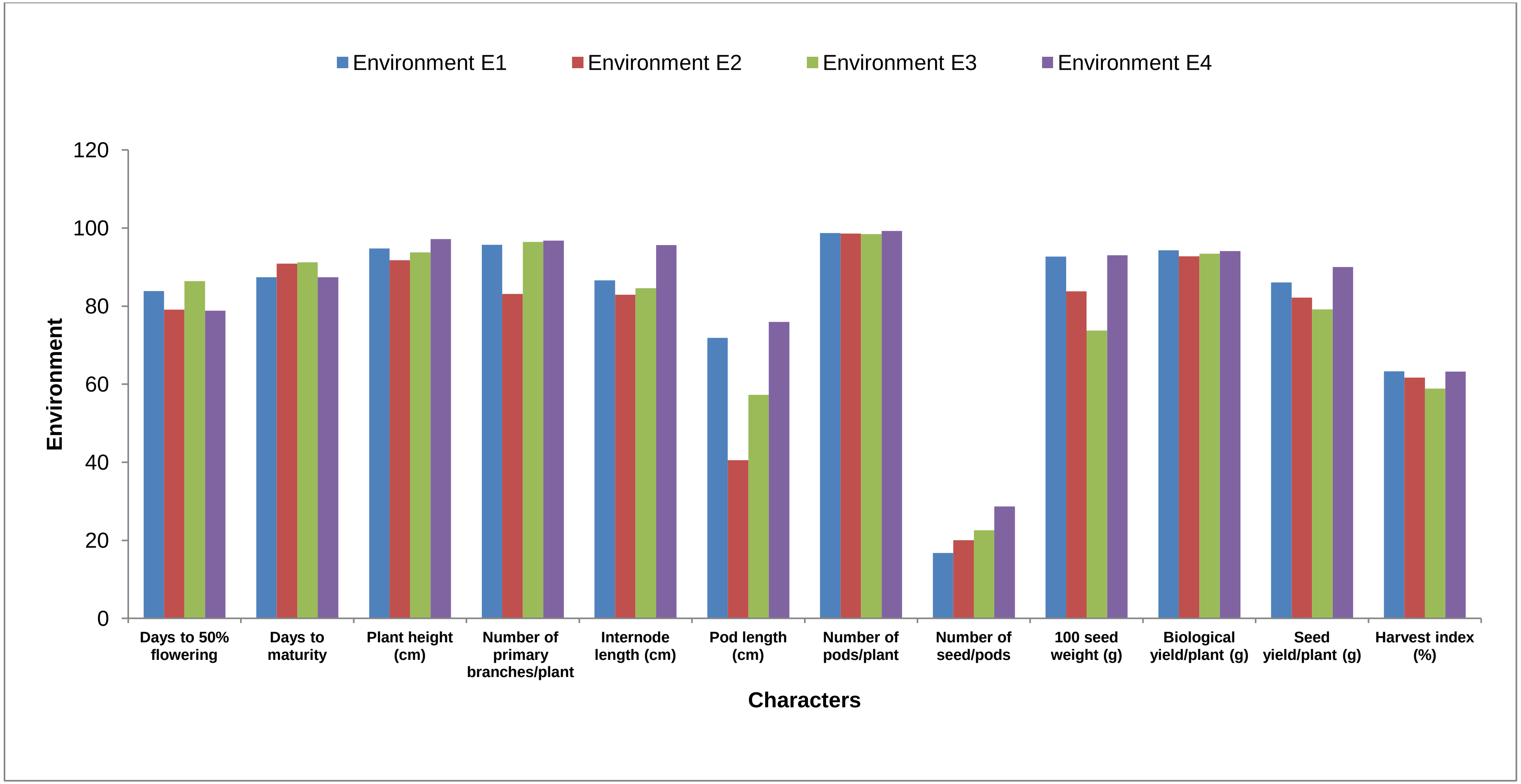

Fig 4 Estimates of heritability (%) in broad sense

maturity the highest value found (9.62%) from E-3 and lowest (8.75%) from E-2, for plant height the highest (26.98%) from E-4 and lowest (25.39%) from E-2, for number of primary branches per plant the highest figure observed (3.86%) from E-2 and lowest (3.50%) in E-4, for internode length the highest value observed (2.48%) from E-1 and lowest (2.25%) from E-2, for pod length the highest value found (0.69%) from E-4 and lowest (0.41%) from E-2,for number of pods per plant the highest magnitude recorded (85.29%) from E-4 and lowest (83.43%) from E-3, for number of seed per pods the highest value noticed (0.23%) from E-3 and lowest (0.11%) from E-1, for 100 seed weight the highest value found (4.44%) from E-1, closely related with E-4 and lowest (3.56%) from E-3, for biological yield per plant the highest value found (28.65%) from E-1 and lowest (28.27%) from E-2, for seed yield per plant the highest value observed (10.91%) from E-4 and lowest (9.55%) from E-3 and for harvest index the highest value recorded (13.89%) from E-3 and lowest (12.41%) from E-1.

Table 4.7.Estimates of genetic advance in percent

Characters	Environment			
	E1	**E2**	**E3**	**E4**
Days to 50% flowering	4.91	4.12	4.68	4.24
Days to maturity	9.28	8.75	9.62	9.27
Plant height (cm)	26.59	25.39	26.39	26.98
Number of primary branches/ plant	3.77	3.86	3.66	3.50
Internode length (cm)	2.48	2.25	2.45	2.44
Pod length (cm)	0.65	0.41	0.68	0.69
Number of pods/plant	83.93	84.09	83.43	85.29
Number of seeds/pod	0.11	0.13	0.23	0.19
100 seed weight (g)	4.44	4.02	3.56	4.44
Biological yield/plant (g)	28.65	28.27	28.58	28.34
Seed yield/plant (g)	10.69	10.02	9.55	10.91
Harvesting index (%)	12.41	12.95	13.89	12.81

Genetic advance value % means

Genetic advance estimates in percent mean expect. all the four environments are reported in Table 4.8.

For days to 50% flowering the highest value noticed (11.39%) genetic advance in percent mean was expected in from E-1 and lowest (9.92%) from E-4, for days to maturity the highest value found (9.21%) from E-3 and lowest (842%) from E-2, for plant height the highest (52.97%) from E-4 and lowest (48.82%) from E-2, for number of primary branches per plant the highest figure observed (49.14%) from E-1 and lowest (45.46%) in E-4, for internode length the highest value observed (40.79%) from E-1 and lowest (35.75%) from E-2, for pod length the highest value found (22.04%) from E-4 and lowest (12.21%) from E-2,for number of pods per plant the highest magnitude recorded (123.45%) from E-4 and lowest (120.13%) from E-3, for number of seed per pods the highest value noticed (8.69%) from E-3 and lowest (4.32%) from E-1, for 100 seed weight the highest value found (39.60%) from E-4, closely related with E-1 and lowest (30.58%) from E-3, for biological yield per plant the highest value found (82.02%) from E-1 and lowest (79.98%) from E-2, for seed yield per plant the highest value observed (65.04%) from E-4 and lowest (56.02%) from E-3 and for harvest index the highest value recorded (26.96%) from E-3 and lowest (24.68%) from E-1.

Table 4.8.Estimates of genetic advance in percent means

Characters	Environment			
	E1	**E2**	**E3**	**E4**
Days to 50% flowering	11.39	9.53	10.89	9.92
Days to maturity	8.89	8.42	9.21	8.95
Plant height (cm)	51.89	48.82	51.21	52.97
Number of primary branches/plant	49.14	45.46	47.78	45.59
Internode length (cm)	40.79	35.75	40.11	40.39
Pod length (cm)	20.54	12.21	20.27	22.04
Number of pods/plant	121.53	121.09	120.13	123.45
Number of seeds/pod	4.32	5.16	8.69	7.56
100 seed weight (g)	39.31	34.84	30.58	39.60
Biological yield/plant (g)	82.02	79.98	81.46	81.81
Seed yield/plant (g)	63.59	59.26	56.02	65.04
Harvest index (%)	24.68	25.83	26.96	25.20

Correlation coefficient:

Phenotypic correlation:

Estimates of phenotypic correlation coefficients for different traits with seed yield per plant noted in four environments are presented in Table 4.9 and with all the other traits were given in 4.9.1.

Seed yield per plant was observed positively and significantly correlated with number of pods per plant and biological yield per plant under all the environments. It was significantly and positively correlated with number of primary branches per plant under E-1 and significantly and negatively correlated with pod length under E-1,E-3 & E-4. Similarly seed yield also showed significant and negative correlated with 100 seed weight under E-1,E-2,E-4.

1. **Days to 50% flowering:** Days to 50% flowering revealed negative significant correlation with pod length (-0.397**) and positive non-significant with days to maturity (0.242) number of primary branches per plant (0.079), number of pods per plant (0.059), biological yield per plant (0.122), seed yield per plant (0.051) it also shows negative non-significant correlation with plant height (-0.281), internode length (-0.198) harvesting index (-0.209), number of seeds per pod (-0.040) and with 100 seed weight (-0.106).
2. **Days to maturity:** Days to maturity exhibited positive significant correlation with plant height (0.477**), biological yield per plant (0.436**), number of pods per plant (0.676**), number of primary branches per plant (0.729**) and positive non-significant with internode length (0.169) and seed yield per plant (0.214) while it shown significant negative correlation with pod length (-0.510**), harvesting indexand (-0.485*). It was negatively non-significant correlated only with number of seeds per pod (-0.121) and 100 seed weight (-0.039).
3. **Plant height:**Plant height was observed positively significant correlated with biological yield per plant (0.439**), number of pods per plant (0.772**), number of primary branches per plant (0.764**) and with internode length (0.482**). It was negatively significant correlated with harvesting index (-0.349*) while it shows non-significant negative correlation withdays to 50% flowering (-0.281), 100 seed weight (-0.143), pod length (-0.122) and with number of seeds per pod (-0.055) mean while positively non-significant with seed yield per plant (0.270).
4. **Number of primary branches per plant:** Number of primary branches per plant was recorded significant positively correlated with number of pods per plant (0.827**) biological yield per plant (0.527**) and seed yield per plant (0.311*)while it observed that number of primary branches per plant was negatively significant correlated with pod length (0.510**) and harvesting index (0.472*). It was observed positively non-significant correlated with internode length (0.263) and it shows negatively non-significant correlation with 100 seed weight (0.274) and with number of seeds per pod (0.108).
5. **Internode length:** Internode length noticed significant negatively correlated

with harvesting index (-0.509**). Internode length found positive non-significant with pod length (0.099) and with number of pods per plant (0.159), biological yield per plant (0.189**) and 100 seed weight (0.059).itwas also observed negatively non-significant correlated with number of seeds per pod (-0.078) and seed yield per plant (-0.119).

6. **Pod length:** Pod length revealed positive significant correlation with 100 seed weight (0.409*). It was shown negatively significant correlation with number of pods per plant (-0.488**), seed yield per plant (-0.374*)and biological yield (-0.458**) while it was observed positively non-significant correlated with number of seeds per pod (0.124) and harvesting index (0.279).
7. **Number of pods per plant:** Number of pods per plant was analyzed positive significantly correlated with biological yield per plant (0.689**) and seed yield per plant (0.593) although it was negatively significant correlated with 100 seed weight (-0.316**) and harvest index (-0.361*). It was shown positively non-significant correlation with number of seeds per pod (0.062).
8. **Number of seeds per pod:** Number of seeds per pod was recorded positive significant correlation with harvesting index (0.300*). Whereas it was observed positively non-significant correlated with 100 seed weight (0.141) and seed yield (0.044) whereas negatively non-significant biological yield per plant (-0.097).
9. **100 seed weight:** 100 seed weight exhibited negative non-significant correlated with harvesting index (-0.049) while it was negative significant correlated with biological yield per plant (- 0.314*) and seed yield per plant (-0.361*).
10. **Biological yield per plant:** Biological yield per plant was observed significant negatively correlated with harvesting index (-0.582**) meanwhile positively significant with seed yield per plant (0.868**).

Phenotypic Correlations Matrix

	Day of 50 % Flowering	Days to Maturity	Plant Height (cm)	Number of Primary branches per Plant	Inter node length (cm)	Pod length (cm)	Number of pods per plant	Number of seeds per Pod	100 Seed weight (g)	Biological Yield per Plant (g)	Seed Yield per Plant (g)	Harvesting index (%)
Day of 50 % Flowering												
Days to Maturity	0.242^{NS}											
Plant Height (cm)	-0.281^{NS}	0.477^{**}										
Number of Primary branches / Plant	0.079^{NS}	0.729^{**}	0.764^{**}									
Inter node length (cm)	-0.198^{NS}	0.169^{NS}	0.482^{**}	0.263^{NS}								
Pod length (cm)	-0.397^{**}	-0.510^{**}	-0.122^{NS}	-0.510^{**}	0.099^{NS}							
Number of pods per plant	0.059^{NS}	0.676^{**}	0.772^{**}	0.827^{**}	0.159^{NS}	-0.488^{**}						
Number of seeds per Pod	-0.040^{NS}	-0.121^{NS}	-0.055^{NS}	-0.108^{NS}	-0.078^{NS}	0.124^{NS}	0.062^{NS}					
100 Seed weight (g)	-0.106^{NS}	-0.039^{NS}	-0.143^{NS}	-0.274^{NS}	0.059^{NS}	0.409^{**}	-0.316^{*}	0.141^{NS}				
Biological Yield per Plant (g)	0.122^{NS}	0.436^{**}	0.439^{**}	0.527^{**}	0.189^{NS}	-0.458^{**}	0.689^{**}	-0.097^{NS}	-0.314^{*}			
Seed Yield per Plant (g)	0.051^{NS}	0.214^{NS}	0.270^{NS}	0.311^{*}	-0.119^{NS}	-0.374^{*}	0.593^{**}	0.044^{NS}	-0.361^{*}	0.868^{**}		
Harvesting index (%)	-0.209^{NS}	-0.485^{**}	-0.349^{*}	-0.472^{**}	-0.509^{**}	0.279^{NS}	-0.361^{*}	0.300^{*}	-0.049^{NS}	-0.582^{**}	-0.135^{NS}	

Table 4.9. Estimates of coefficient of phenotypic correlation with seed yield per plant

Characters	Environment			
	E1	**E2**	**E3**	**E4**
Days to 50% flowering	0.051	0.142	-0.007	0.055
Days to maturity	0.214	0.189	0.053	0.194
Plant height (cm)	0.270	0.257	0.272	0.277
Number of primary branches/plant	0.311*	0.206	0.266	0.272
Internode length (cm)	-0.119	-0.244	-0.135	-0133
Pod length (cm)	-0.374*	-0.273	-0.357*	-0.402**
Number of pods/plant	0.593**	0.596**	0.566**	0.575**
Number of seeds/pod	0.044	0.120	0.152	0.027
100 seed weight (g)	-0.361*	-0.319*	-0.243	-0.360*
Biological yield/plant (g)	0.868**	0.848**	0.843**	0.867**
Harvest index (%)	-0.135	-0100	-0.179	-0.195

*** - Significant at p = 0.05 ** - Significant at p = 0.01**

Genotypic correlation:

Estimates of genotypic correlation coefficients for different traits with seed yield per plant under all the four environments are presented in Table 4.10

The seed yield per plant was found positively correlated with plant height, number of pods per plant and biological yield per plant under all environments, while it was significantly positively correlated with number of primary branches per plant under E-2 & E-3 and it exhibited significant and negative correlation with pod length, 100 seed weight, harvesting index under all the environment.

Table 4.10. Estimates of coefficient of genotypic correlation with seed yield per plant

Characters	Environment			
	E1	**E2**	**E3**	**E4**
Days to 50% flowering	0.076	0.204	0.032	0.071
Days to maturity	0.203	0.225	0.031	0.184
Plant height (cm)	0.316*	0.296**	0.328*	0.296*
Number of primary branches/plant	0.373*	0.284	0.307*	0.283
Internode length (cm)	-0.139	-0.331*	-0.123	-0.163
Pod length (cm)	-0.507**	-0.623**	-0.599**	-0.479**
Number of pods/plant	0.627**	0.641**	0.616**	0.592**
Number of seeds/pod	0.027	0.240	0.237	-0.023
100 seed weight (g)	-0.401**	-0.407**	-0.318*	-0.409**
Biological yield/plant (g)	0.909**	0.890**	0.892**	0.900**
Harvest index (%)	-0.367*	-0.363*	-0.497**	-0.361*

*** - Significant at p = 0.05 ** - Significant at p = 0.01**

Genotypic Correlations Matrix

	Day of 50 % Flowering	Days to Maturity	Plant Height (cm)	Number of Primary branches per Plant	Inter node length (cm)	Pod length (cm)	Number of pods per plant	Number of seeds per Pod	100 Seed weight (g)	Biological Yield per Plant (g)	Seed Yield /Plant (g)	Harvesting index (%)
Day of 50 % Flowering												
Days to Maturity	0.245^{NS}											
Plant Height (cm)	-0.345*	0.523**										
Number of Primary branches per Plant	0.107^{NS}	0.817**	0.806**									
Inter node length (cm)	-0.225^{NS}	0.186^{NS}	0.516**	0.279^{NS}								
Pod length (cm)	-0.451**	-0.582**	-0.092^{NS}	-0.647**	0.155^{NS}							
Number of pods per plant	0.070^{NS}	0.719**	0.795**	0.849**	0.171^{NS}	-0.580**						
Number of seeds per Pod	0.000^{NS}	-0.393**	-0.081^{NS}	-0.299*	-0.486**	0.176^{NS}	0.098^{NS}					
100 Seed weight (g)	-0.108^{NS}	-0.029^{NS}	-0.174^{NS}	-0.290^{NS}	0.031^{NS}	0.503**	-0.333*	0.538**				
Biological Yield per Plant (g)	0.115^{NS}	0.437**	0.461**	0.565**	0.222^{NS}	-0.557**	0.703**	-0.246^{NS}	-0.338*			
Seed Yield per Plant (g)	0.076^{NS}	0.203^{NS}	0.316*	0.373*	-0.139^{NS}	-0.507**	0.627**	0.027^{NS}	-0.401**	0.909**		
Harvesting index (%)	-0.228^{NS}	-0.646**	-0.403**	-0.553**	-0.692**	0.356*	-0.460**	0.643**	-0.029^{NS}	-0.705**	-0.367*	

Environmental correlation:

Estimates of environmental correlation coefficients for different traits with seed yield per plant under all the four environments are presented in Table 4.11.

Seed Yield was found positively correlated with number of pods per plant, biological yield per plant and harvest index under all environments similarly it was shown negative significant relationship with number of primary branches per plant only under E-1.

Table 4.11. Estimates of coefficient of environmental correlation with seed yield per plant

Characters	Environment			
	E1	**E2**	**E3**	**E4**
Days to 50% flowering	-0.093	-0.117	-0.197	-0.032
Days to maturity	0.288	-0.044	0.194	0.281
Plant height (cm)	-0.175	-0.001	-0.098	-0.007
Number of primary branches/plant	-0.355*	-0.163	-0.021	0.138
Inter node length (cm)	0.007	0.169	-0.191	0.279
Pod length (cm)	0.128	0.264	0.156	-0.040
Number of pods/plant	0.368*	0.388**	0.389**	0.586**
Number of seeds/pod	0.098	0.059	0.130	0.144
100 seed weight (g)	-0.029	0.114	0.002	0.171
Biological yield/plant (g)	0.556**	0.626**	0.647**	0.509**
Harvest index (%)	0.601**	0.603**	0.550**	0.401**

*** - Significant at p = 0.05 ** - Significant at p = 0.01**

6.Stability analysis:

In the development of improved varieties genotype x environment interaction had been of great importance to the plant breeder. When varieties are compared over a series of environment relative ranking usually differ which causes difficulty in demonstrating the significance superiority of one variety over the other. For reducing the impact of varieties x environment interaction, breeder selects stable genotype,which will interact less with the environment in which they are to be grown.

Under present investigation adoptive potential and relative stability of 15 genotype of soybean for yield and its contributing traits have been determined. The pooled analysis of variance was carried out and presented in Table 4.11 which indicated that the genotypes significantly differed for all the characters taken under study. The interaction of genotype × environment (G×E) mean sum of squares were found significant for days to 50% flowering, days to maturity, plant height, number of primary branches per plant, internode length, number of pods per plant, biological yield per plant, seed yield per plant and 100 seed weight and harvesting index Verma *et al.*(2011),Nagalamu *et al.*(2013), Roshandel,M. et al(2016),Bhartiya *et al.*(2017), Wedajoet *et al.*(2018), Jandong *et al.(2019),Raidas et al.(2020)* also reported significant GXE interaction for most of the yield and yield attributing characters.

The response of genotypes to changing environment was measured by the environment linear effect, which was significant for all the characters except harvest index. The regression or V×E (linear) mean sum of squares were significant for most of the characters except pod length and number of seed per pods.

The stability parameters, viz., regression coefficient (b) and mean deviation from regression S^2d for all the characters of each genotype, were computed and are presented in Table 4.12 to Table 4.21.The magnitudes of deviation from linearity for all the characters were observed suggesting large fluctuations in the expression of all the characters over environments. Mean sum of squares due to pooled deviation were found significant for most of the characters except number of primary branches per plant, internode length, pod length, number of seeds per pod.

Days to 50% flowering:

Stability analysis regarding days to 50 per cent flowering revealed that all the genotypes except NRC-94,NRC-137,NRC-177 had regression coefficient near unity and mean deviation from regression equivalent to zero (Table 4.12). The genotype RVS14-1, JS 20-34,RVS11-4,NRC-158,NRC-157 showed more than one regression coefficient value and deviation from regression equivalent to zero.

Days to maturity:

15 Out of 6 genotypes showed less than one regression coefficient value and deviation from regression equivalent to minimum. (Table 4.13).

Genotype NRC-94,RVS14-4,NRC-177,NRC-158,NRC-157 showed near to one regression coefficient figure and deviation from regression equivalent to zero.

Genotype RVSM2011-35, RVS11-4, RVS2013-15,RVS14-3 showed more than one regression coefficient figure and deviation from regression equivalent to minimum. .

Plant height:

Out of 15 genotypes, 5 genotypes had b=1 and deviation from regression equivalent to zero (Table 4.14).

Genotypes RVS14-2,RVS2011-35,NRC-177,RVS14-1 showed more than one regression coefficient estimate and deviation from regression equivalent to zero.

Genotypes NRC-94,NRC-137,NRC-136,NRC-157,RVS2013-7, RVS 2013-15 showed less than one regression coefficient estimate and deviation from regression equivalent to zero.

Number of primary branches per plant:

Nine genotypes had showed b=1 and deviation from regression equivalent to zero. Table(4.15.)

The genotypes NRC-158,RVS11-4s howed more than one regression coefficient estimate and deviation from regression equivalent to zero.

Internode length

Out of 15 genotypes, 7 genotypes had b=1 and deviation from regression equivalent to zero (Table 4.16). Genotypes NRC-157,RVSM 2011-35,RVS2013-15 showed more than one regression coefficient estimate and deviation from regression equivalent to minimum.

Genotypes RVS14-1, RVS14-2,NRC-136, RVS11-4,NRC-158 showed less than one regression coefficient estimate and deviation from regression equivalent to zero.

Pod length

Out of 15 genotypes, 7 genotypes(RVS14-1 ,NRC-94,RVS14-4,NRC-136,RVS11-4,RVS14-3,NRC-177) had b=1 and deviation fromregression equivalent to zero (Table 4.17).

Genotypes RVSM2011-35,,NRC-157, RVS2013-15 showed more than one regression coefficient estimate and deviation from regression equivalent to zero.

Number of pods per plant:

Five genotypes had b=1 and deviation from regression equivalent to minimum (Table 4.18). In case of the genotypes NRC-94,JS 20-34, RVS11-4, NRC-177,RVS14-3 the deviation from regression was found significant, while most of these genotypes had b=1.

Number of seeds per pod:

Out of 15 genotypes, 3 genotypes had b=1 and deviation from regression to minimum. Varieties RVS14-1, JS20-34 and RVS11-4,RVS14-4,NRC-137 showed regression coefficient more than one and deviation from regression equivalent to zero (Table 4.19). Genotypes NRC-94,RVSM2011-35, NRC-136, NRC-158,RVS 14-3, RVS 2013-7,RVS2013-15 showed regression coefficient less than one and deviation from regression equivalent to minimum.

100 Seed weight

Five genotypes had b = 1 and deviation from regression equivalent to zero (Table 4.20).

Genotypes NRC-94, RVS14-4, RVS14-3,NRC-158 and RVS2013-15, showed regression coefficient more than one and deviation from regression near to zero. three genotypes, viz.,RVS14-2,NRC-137 ,NRC-177, NRC-157,RVS2013-7 showed regression coefficient less than one and deviation from regression equivalent to zero. All genotype deviated nonsignificantly from regression near to zero.

Biological yield per plant:

Seven genotypes had b=1 and deviation from regression equivalent to zero (Table 4.21).

Genotypes JS20-34, RVS11-4,NRC-177 and NRC-157 had regression coefficient greater than one and deviation from regression equivalent to zero.

The genotypes RVS14-1,RVS14-4,RVS2013-7,RVS2013-15 had regression coefficient less than one and deviation from regression equivalent to zero.

Seed yield per plant:

Seven genotypes had b=1 and deviation from regression equivalent to minimum (Table 4.22).

Five genotypes RVS14-1,RVS11-4,NRC-158,RVS2013-7, RVS2013-15 showed regression coefficient more than one and deviation from regression equivalent to zero.

While, three genotypes, NRC-137, JS20-34, RVS 14-3 showed regression coefficient less than one and deviation from regression equivalent to minimum.

Harvest index:

Four genotypes had b=1 and deviation from regression to zero.

Genotypes,RVS14-2,RVS14-4,NRC-158. NRC-157 and RVS2013-15 showed regression coefficient more than one and deviation from regression equivalent to minimum (Table 4.23).

The genotypes NRC-94,NRC-137,JS20-34, NRC-136,RVS14-3, NRC-177 showed regression coefficient less than one and deviation from regression equivalent near to zero..

Stability of all the 15 varieties for yield and components traits was worked out and reported in Table (4.24) which showed that genotypes NRC-94, NRC-177 were suitable for 7 characters, RVS14-4 was found stable for 6 characters including seed yield per plant.

Genotype NRC-136, RVS14-2 recorded stable performance for 5 characters including seed yield per plant. Genotypes RVSM2011-35,NRC-157 exhibited stability for 4 characters including seed yield per plant.

In respect of stability of different traits it was found that number of primary branches per plant in (9) genotypes, seed yield per plant in (7) genotypes, biological yield per plant in (7) genotyoes, were the most stable characters, Internode length (7), pod length(7), days to maturity in genotyoes (5) and plant height (5), number of pods per plant(5), 100 seed weight in (5) genotypes, and harvest index in (4) genotypes, days to 50% flowering (3) and number of seed per plant was found least stable character, which was stable only in 3 genotypes.

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Table 4.12. Estimates of stability parameters for days to 50% flowering

Characters	**Days to 50% flowering**		
	Mean	**Reg. Coeff. (b)**	**S^2d**
RVS 14-1	43.750	2.747**	-0.309
NRC-94	43.500	1.052	3.993
RVS 14-2	41.750	-0.292	-0.384
RVSM 2011-35	44.250	-0.970	-0.008
NRC-137	50.250	1.087	-0.138
JS 20-34	43.500	2.455**	-0.396
RVS 14-4	42.000	-0.000	-0.419
NRC-136	40.167	-0.070	1.081
RVS 11-4	44.750	2.280**	1.544
RVS 14-3	40.583	-0.316	-0.052
NRC-177	43.167	1.894	-0.203
NRC-158	41.250	3.332**	0.077
NRC-157	42.500	2.455**	-0.396
RVS 2013-7	41.750	-1.087	-0.138
RVS 2013-15	41.917	0.433	-0.281
Mean	**43.01**	**1.00**	
S.Em	**0.48**	**2.078**	

Table 4.13. Estimates of stability parameters for days to maturity

Characters	**Days to maturity**		
	Mean	**Reg. Coeff. (b)**	**S^2d**
RVS 14-1	102.750	0.306	0.438
NRC-94	110.167	0.934	-0.634
RVS 14-2	101.833	0.730	-0.881
RVSM 2011-35	107.000	1.751**	-0.691
NRC-137	110.667	0.642	0.983
JS 20-34	94.750	0.306	0.438
RVS 14-4	104.083	1.386	-0.692
NRC-136	108.500	-1.430	1.290
RVS 11-4	106.583	2.699**	1.279
RVS 14-3	105.250	1.620**	-0.204
NRC-177	102.167	1.342	2.019
NRC-158	96.917	1.211	-0.799
NRC-157	97.750	1.094	-0.842
RVS 2013-7	104.750	-0.073	-0.761
RVS 2013-15	107.833	2.481**	-0.641
Mean	**104.07**	**1.00**	-
S.Em (±)	**0.56**	**1.356**	-

Table 4.14 Estimates of stability parameters for plant height

Characters	Plant height		
	Mean	Reg. Coeff. (b)	S^2d
RVS 14-1	46.043	1.665**	-3.384
NRC-94	69.426	-0.683	-3.217
RVS 14-2	59.333	2.364**	-2.402
RVSM 2011-35	47.749	2.153**	-1.426
NRC-137	47.493	0.450	-3.403
JS 20-34	27.117	1.007	-3.168
RVS 14-4	46.892	1.505	-3.192
NRC-136	85.498	0.297	-3.394
RVS 11-4	56.568	1.444	-0.825
RVS 14-3	51.025	1.492	-3.415
NRC-177	42.638	1.874**	-3.436
NRC-158	53.678	1.504	-2.596
NRC-157	49.498	-0.861	-1.737
RVS 2013-7	48.561	0.007	-3.097
RVS 2013-15	40.042	0.781	-2.881
Mean	**51.44**	**1.00**	
S.Em (±)	**0.47**	**1.04**	

Table 4.15. Estimates of stability parameters for number of primary branches per plant.

Characters	Number of primary branches per plant		
	Mean	Reg. Coeff. (b)	S^2d
RVS 14-1	6.503	0.345	-0.081
NRC-94	10.549	1.420	-0.099
RVS 14-2	6.381	1.033	-0.074
RVSM 2011-35	7.774	0.568	0.015
NRC-137	10.568	0.928	-0.079
JS 20-34	4.691	-0.259	-0.103
RVS 14-4	6.427	-0.091	0.084
NRC-136	11.807	1.473	0.107
RVS 11-4	8.481	1.583**	-0.046
RVS 14-3	7.663	1.218	-0.101
NRC-177	6.631	1.276	0.002
NRC-158	7.917	2.236**	-0.099
NRC-157	6.925	1.036	-0.103
RVS 2013-7	8.452	1.224	-0.063
RVS 2013-15	7.586	1.010	-0.100
Mean	**7.89**	**1.00**	
S.Em (±)	**0.12**	**0.289**	

Table 4.16. Estimates of stability parameters for Internode length (cm)

Characters	Internode length		
	Mean	**Reg. Coeff. (b)**	**S^2d**
RVS 14-1	5.317	0.072	-0.070
NRC-94	7.642	0.846	-0.071
RVS 14-2	7.875	0.047	-0.075
RVSM 2011-35	8.667	1.650**	-0.020
NRC-137	5.475	0.915	-0.077
JS 20-34	4.692	0.883	-0.075
RVS 14-4	6.192	1.408	-0.064
NRC-136	6.692	-0.165	-0.065
RVS 11-4	4.775	-1.092	-0.074
RVS 14-3	5.832	0.827	-0.056
NRC-177	5.483	0.853	-0.077
NRC-158	6.425	-0.734	-0.067
NRC-157	6.242	3.978**	-0.012
RVS 2013-7	6.833	1.412	-0.027
RVS 2013-15	4.033	4.100**	0.011
Mean	**6.14**	**1.00**	
S.Em (±)	**0.09**	**0.739**	

Table 4.17. Estimates of stability parameters for Pod length (cm)

Characters	Pod length(cm)		
	Mean	**Reg. Coeff. (b)**	**S^2d**
RVS 14-1	3.403	1.168	-0.027
NRC-94	2.762	0.959	-0.014
RVS 14-2	4.139	0.506	0.003
RVSM 2011-35	3.333	1.746**	0.016
NRC-137	2.457	0.174	-0.030
JS 20-34	2.928	-0.219	-0.029
RVS 14-4	3.391	0.961	-0.006
NRC-136	2.849	1.139	-0.026
RVS 11-4	3.636	1.228	-0.032
RVS 14-3	3.459	0.808	-0.006
NRC-177	3.403	1.302	-0.028
NRC-158	3.476	0.697	-0.026
NRC-157	3.532	1.580**	-0.028
RVS 2013-7	3.171	0.779	-0.008
RVS 2013-15	3.169	2.172**	-0.025
Mean	**3.27**	**1.00**	
S.Em (±)	**0.07**	**0.566**	

Table 4.18. Estimates of stability parameters for number of pods per plant

Characters	Number of pods per plant		
	Mean	**Reg. Coeff. (b)**	**S^2d**
RVS 14-1	82.538	0.330	-7.017
NRC-94	135.708	1.867**	-5.695
RVS 14-2	46.139	0.502	-6.648
RVSM 2011-35	46.960	-3.302	-5.608
NRC-137	110.021	-2.128	-6.771
JS 20-34	21.700	4.375**	-5.963
RVS 14-4	57.057	1.454	-6.832
NRC-136	171.676	-2.379	-4.677
RVS 11-4	74.276	5.044**	-5.201
RVS 14-3	69.599	1.881**	-6.376
NRC-177	62.944	5.582**	-6.703
NRC-158	39.284	1.553	-6.441
NRC-157	43.333	0.719	-6.787
RVS 2013-7	31.958	-1.263	-5.382
RVS 2013-15	45.750	0.765	-6.363
Mean	**69.26**	**1.00**	
S.Em (±)	**0.53**	**2.49**	

Table 4.19. Estimates of stability parameters for number of seed per pods

Characters	Number of seeds per plant		
	Mean	**Reg. Coeff. (b)**	**S^2d**
RVS 14-1	3.208	4.152	-0.026
NRC-94	2.633	-0.630	-0.037
RVS 14-2	2.375	0.711	-0.023
RVSM 2011-35	2.392	0.144	-0.037
NRC-137	2.467	1.623**	-0.037
JS 20-34	2.508	2.221**	-0.033
RVS 14-4	2.683	1.662**	-0.029
NRC-136	2.392	-0.012	-0.033
RVS 11-4	2.658	2.915**	-0.036
RVS 14-3	2.775	-0.046	-0.035
NRC-177	2.875	1.224	-0.035
NRC-158	2.783	0.073	-0.036
NRC-157	2.692	1.068	-0.017
RVS 2013-7	2.317	-0.347	-0.033
RVS 2013-15	2.358	0.242	-0.033
Mean	**2.61**	**1.00**	
S.Em (±)	**0.04**	**0.592**	

Table 4.20. Estimates of stability parameters for 100 seed weight

Characters	100 seed weight		
	Mean	**Reg. Coeff. (b)**	**S^2d**
RVS 14-1	11.363	1.140	-0.219
NRC-94	9.572	2.980**	-0.216
RVS 14-2	11.031	-0.846	-0.072
RVSM 2011-35	13.344	0.621	-0.193
NRC-137	9.209	0.350	-0.018
JS 20-34	8.176	1.193	-0.176
RVS 14-4	12.246	2.377**	-0.235
NRC-136	8.819	1.702	-0.181
RVS 11-4	14.295	0.680	-0.256
RVS 14-3	12.860	2.619**	-0.251
NRC-177	15.517	-1.508	-0.210
NRC-158	13.010	1.843**	-0.217
NRC-157	8.697	0.418	-0.151
RVS 2013-7	11.901	-1.052	-0.254
RVS 2013-15	11.355	2.481**	-0.240
Mean	**11.43**	**1.00**	
S.Em (±)	**0.15**	**0.071**	

Table 4.21. Estimates of stability parameters for biological yield per plant

Characters	Biological yield per plant		
	Mean	**Reg. Coeff. (b)**	**S^2d**
RVS 14-1	35.083	-0.392	-4.551
NRC-94	57.198	1.384	-4.435
RVS 14-2	23.492	1.324	-4.505
RVSM 2011-35	47.770	0.988	-4.507
NRC-137	39.783	1.101	-3.851
JS 20-34	49.388	2.202**	-4.330
RVS 14-4	23.118	0.309	-4.303
NRC-136	63.272	0.687	-4.555
RVS 11-4	40.216	1.676**	-4.574
RVS 14-3	35.396	0.829	-4.543
NRC-177	30.208	1.670**	-4.569
NRC-158	21.106	1.284	-4.245
NRC-157	17.737	1.662**	-4.528
RVS 2013-7	19.227	0.068	-3.531
RVS 2013-15	22.065	0.209	-3.989
Mean	**35.00**	**1.00**	
S.Em (±)	**0.30**	**1.021**	

Table 4.22. Estimates of stability parameters for seed yield per plant(g)

Characters	**Seed yield per plant(g)**		
	Mean	**Reg. Coeff. (b)**	**S^2d**
RVS 14-1	20.394	3.210**	-1.826
NRC-94	23.934	0.769	-1.789
RVS 14-2	11.610	0.919	-1.367
RVSM 2011-35	14.306	0.875	-1.709
NRC-137	16.357	-2.705	-1.491
JS 20-34	26.355	-2.336	-1.744
RVS 14-4	12.295	0.975	-1.785
NRC-136	26.981	1.755	-1.757
RVS 11-4	20.973	3.125**	-1.808
RVS 14-3	17.594	-0.964	-1.536
NRC-177	15.954	0.775	-1.540
NRC-158	11.427	3.846**	-1.706
NRC-157	11.405	1.545	-1.752
RVS 2013-7	11.364	2.953**	-1.780
RVS 2013-15	12.356	3.512**	-1.820
Mean	**16.89**	**1.00**	
S.Em (±)	**0.21**	**1.75**	

Table 4.23. Estimates of stability parameters for harvest index(%)

Characters	**Harvesting Index (%)**		
	Mean	**Reg. Coeff. (b)**	**S^2d**
RVS 14-1	58.074	0.620	-12.182
NRC-94	41.898	0.255	-13.501
RVS 14-2	49.633	4.473**	-12.380
RVSM 2011-35	30.077	0.571	-12.894
NRC-137	41.143	-3.252	-13.175
JS 20-34	53.148	0.127	-9.512
RVS 14-4	53.218	3.604**	-10.770
NRC-136	42.663	0.069	-12.958
RVS 11-4	52.163	0.941	-13.382
RVS 14-3	50.403	-1.378	-13.390
NRC-177	52.703	-1.573	-13.524
NRC-158	54.586	3.919**	-11.856
NRC-157	64.553	2.341**	-8.883
RVS 2013-7	60.023	0.850	8.808
RVS 2013-15	56.373	3.435**	-11.654
Mean	**50.71**	**1.00**	
S.Em (±)	**0.97**	**1.55**	

4.24 Estimate of Stable genotypes with stable trait

s.no.	Stable lines	Stable character	Stable traits
1	RVS 14-1	Pod length,100 seed weight,Harvesting index.	03
2	NRC-94	Days to 50% flowering, Days to maturity, Number of primary branches pre plant, Internode length, Pod length, Biological yield per plant, Seed yield per plant	07
3	RVS11-4	Plant height, pod length, 100 seed weight, Harvesting index.	04
4	RVS14-2	Number of primary branches per plant, number of pods per plant, number of seed per pods, Biological yield per plant, Seed yield per plant.	05
5	RVSM2011-35	100 seed weight, Biological yield per plant, Harvesting index , seed yield per plant.	04
6	NRC-137	Days to maturity, Number of primary branches per plant, Internode length, Biological yield per plant.	04
7	JS20-34	Plant height, Internode length, 100 seed weight.	03
8	RVS14-4	Days to maturity, plant height, internode length, Pod length, number of pods per pods, Seed yield per plant.	06
9	NRC-136	No. of primary branches per plant, Pod length, 100 seed weight, Biological yielg per plant, Seed yield per plant.	05
10	RVS14-3	Plant height, Number of primary branches per plant, Internode length, pod length, Biological yield per plant.	05
11	NRC-177	Days to 50% flowering, Days to maturity, No. of primary branches per plant, Internode length, pod length, No. of seed per pods, Seed yield per plant,	07
12	NRC-158	Days to maturity, Plant height, No. of pods per plant, Biological yield per plant.	04
13	NRC-157	Days to maturity, no. of primary branches per plant, No. of seed per pods, Seed yield per plant.	04
14	RVS2013-7	Number of primary branches per plant, internode length, No. of pods per plant, Harvesting index.	04
15	RVS2013-15	No. of primary branches per plant, number of pods per plant.	02

CHAPTER-V

DISCUSSION

The findings of the present investigation have been interpreted and discussed in this chapter in the light of the similar research work carried out by other research workers.

The discussion is confined to the relevant topics, viz. genetic variation, heritability, genetic advance, correlation and stability. Variation was estimated through variance, phenotypic and genotypic coefficients of variation and by determining the range. Estimates of heritability and expected genetic advance were obtained which are prerequisite for selection. The association between seed yield and its eleven component characters were estimated to establish potential of each character as a component of index to selection. Similarly stability parameters were worked out to identify consistent performance of genotypes over environments.

The experimental results on above aspects have been discussed as under:-

Genetic variation: Genetic variation in any crop is an essential pre requisite for an efficient crop improvement program. The technique for adopting any breeding program depends upon the nature and magnitude of variation present in the available genotype studied. Assessment of genetic variation of yield and its contributing traits in the available population was an important purpose of the present investigation. Phenotypic of an individual reflects the genotypic contribution interacting with the environment. Phenotypic and genotypic variances, coefficient of phenotypic and genotypic variation play a very important role in understanding the extent and nature of genetic variation in the population studied. The analysis of variance revealed significant differences among genotypes for most of the traits under study however, in environment E-1,E-2 and E-4 pod length, number of seeds per pod did not show significant variation. It could be due to least genotype × environment interaction for this trait present in the material studied. The genotypic coefficient of variation was found high for number of pods per plant followed by biological yield, seed yield and plant height in all environments as also reported by several researchers (Bhushan *et al.*2006,Sharma *et al.*2011, Patel 2012, Baraskar *et al.* 2014 Mofokeng *et al.* 2018, Kuswantoro *et al.* 2018, Kumar *et al.*2020, Goonde *et al.*2021)

Heritability:

Heritability estimates in broad sense, include variances due to all types of gene expression. Heritability, which measures the relationship between genotype and phenotype, is an important criterion for success in breeding program, since selective capacity in a population depends upon the amount of heritable variability present.

The high heritability was observed for most of the characters in all the environments except number of seed per pods in E-1. Selection of genotypes for these traits may be effective in aforesaid environments. Hence these characters were highly heritable and less affected by the environment. Sharma *et al.*(*2005*),Bhushan *et al*.(2006)*,*Costa *et al*.(2008) and Karnwal and Singh (2009), Singh *et al.*(2010), Bhat *et al.*(2012), Hunde (2017), Neelima *et al.*(2018), Bianchi *et al.*(2020), W.G.Fufa(2021) have also reported similar findings.

The low heritability was observed for number of seeds per pod in E-1 environment. This trait may be avoided while selecting genotypes in above environments.

Genetic advance:

Genetic advance is the product of selection intensity, heritability and the phenotypic standard deviation. It is an important parameter to evaluate the success of selection program. Greater advance couldbe expected from a population with high mean and wide range of phenotypic variability.

Estimates of genetic advance under different environments revealed appreciable variation for all the traits. However trend was not found similar. Under E-4 high genetic advance through selection could be expected for number of pods per plant followed by biological yield per plant, plant height and harvest index. It is suggested that variable magnitude of genetic advance could be expected under different environments for different traits. Similar findings in respect of plant height, number of pods per plant, biological yield, harvest index were also reported by several researchers namely Shrivastava *et al.* (2005),Karthika and Lakshmi (2006), Yadav(2007),Borah(2009), Rajkumar *et al.* (2010), Amrita *et al.*(2014), Mehbub *et al.*(2016),Mofokeng *et al*.(2018), Baria(2019), Kumar *et al*.(2020), Shruthi *et al.*(2021) and Dhaka(2021).

Correlation:

Knowledge of correlation is of great significance as all the biological attributes are the inter play of several factors among themselves and their individual and combined interactions with the environmental factors. It also provides opportunity to estimate the correlated response to directional selection to predict genetic gain and thus could be utilized as selection parameter for formulating effective breeding program. Correlation could be at phenotypic, genotypic or environmental levels. Phenotypic correlation, which includes genetic and non-genetic effects, is computed from values measured directly on individuals. A positive correlation between desirable characters is favorable to the plant breeder because it helps in simultaneous improvement of both the characters. A negative correlation, on the other hand, will hinder the simultaneous expression of both the characters with high values. In such situations, some economic compromise has to be made. The genetic improvement in yield can be achieved by applying strong selection to character, which is genetically correlated with the yield, called correlated response.

Some times a character has low heritability. Under such situation another character having high heritability and high correlation with the former traits is chosen to make selection more effective. Thus genetic improvement is achieved using indirect selection through component characters with high heritability.

In the present study the estimates of phenotypic correlation of seed yield per plant with number of pods per plant, biological yield per plant in all environments, with number of primary branches in E-1. This suggested that yield contributing characters could play a significant role as selection parameters for isolating a high yielding suitable genotype. Above traits could be used prominently for making selection for high yielding genotypes. It was also revealed that yield was not correlated with internode length and harvest index at in all the environments suggesting that these trait could be manipulates without affecting seed yield.

Saharan *et al.* (2006), Yadav *et al.* (2007), Karnwal *et al.* (2009), Parmar *et al.* (2014), Jain and Ramgiry (2015) and Balla *et al.* (2017) reported positive correlation of these yield attributing characters with seed yield per plant. The estimates of genotypic correlation coefficient of seed yield per plant were positive with number of pods per plant, biological yield per plant and plant height in all environments. Which is in conformity the findings of a Suneeta *et al.* (2010), Aditya *et al.* (2011), Shree *et al.* (2018), Pawar *et al.* (2020), Karyawati *et al.* (2021).

However, the seed yield per plant showed negative association with pod length ,100 seed weight and harvest index in all four environments is accordance to results obtained by Singh *et al.*(2010).

The estimates of environmental correlation coefficients of seed yield per plant were positive correlated with number of pods per plant, biological yield per plant and harvest index while negative non significant correlation observed with days to 50% flowering, plant height, days to maturity under E-2,number of primary branches per plant under E-2 & E-3,internode length under E-3, pod length under E-4,100 seed weight under E-1. It suggested that environment played negligible role in determining phenotypic correlation between seed yield and aforesaid characters.

However estimates were positive with days to maturity under E-1,E-2 and E-3,with number of primary branches per plant and 100 seed weight under E-4, with number of pods per plant, biological yield per plant and number of seeds per pod under all environment and with harvest index under all environment. It indicates that environmental factors contribute considerably to the phenotypic correlation and need to be taken into account while formulating selection indices.

Stability:

In the development of improved varieties genotype × environment interaction had been of great importance to the plant breeder. When varieties are compared over a series of environments relative ranking usually differ which causes difficulty in demonstrating the significant superiority of one variety over the other. For reducing the impact of variety × environment interaction, breeder selects stable genotypes, which will interact less with the environment in which they are to be grown.

Under present investigation adoptive potential and relative stability of 15 genotypes of soybean for yield and its contributing traits have been determined. The pooled analysis of variance carried out to know the response of different characters. Various environmental factors, revealed that genotype × environment interactions were significant for days to 50% flowering, days to maturity, plant height, number of primary branches per plant, internode length, number of pods per plant, 100 seed weight ,biological yield per plant, , seed yield per plant and harvest index. This suggested that these characters were highly sensitive to the changes in the environmental conditions.

Whereas interactions for pod length and number of seed per plant were non-significant which indicated that these traits showed least effect to the changes in the environmental conditions. Joshi *et al.* (2005), Mahajan *et al.* (2006), Ramana and Satyanarayana (2006), Pan *et al.* (2007) and Holkar *et al*.(2008), Verma *et al.*(2011), Roshandel *et al.*(2016), Bhartiya *et al*.(2017), Jandong *et al*.(2019) and Novita(2022) also reported significant G×E interaction for most of the yield and yield attributing characters.

Variances due to genotype x environment (linear) was significant for days to 50% flowering, days to maturity, plant height, number of primary branches per plant, internode length, number of pods per plant, 100 seed weight biological yield per plant, seed yield per plant, and harvest index. It indicated the differential response of genotypes to various agro-climatic conditions.

According to Eberhart and Russell (1966) an ideal genotype is one having high mean (X), unit regression coefficient (b =1) and least deviation (S^2d)around the regression slope i.e. mean deviation square from regression not significantly different from zero. Therefore, it implies that while selecting varieties, predicting rate of seed yield in a given environment, mean values, regression slope of the genotypes and deviation from regression should be considered.

The stability analysis has two major objectives in plant breeding program. To identify the varieties with greater stability and wider adaptability for yield and its components, secondly to identify the potential varieties i.e. variety with high mean performance under wider range of environments. Such variety can be utilized in hybridization program. Hence an attempt was made to identify the high yielding and widely adapted varieties. The stability performance of different genotypes for yield and yield components is discussed below:

Genetic parameters:

Information on variability is essential to a plant breeder to decide a breeding procedure to develop and identify superior genotypes. The efficacy of selection mainly depends upon the extent of genetic variability present in a population. Wide range of variability for all characters is also necessary to isolate significantly superior variety for release as well as to be used as parent in a breeding programmes

The analysis of variance revealed significant differences among genotypes for most of the traits, however, number of primary branches per plant under E-3 and E-4 ,100 seed weight did not show significant difference in E-1 and E-4. These traits also exhibited narrow range. This trait also exhibited low GCV number of primary branches per plant(23.62%)in E-3,(22.49%) in E-4 and for 100 seed weight (19.82%) in E-1,(19.93%) in E-4.

The nature of variability and magnitude of environmental influence on it was examined by estimating standardized statistics-phenotypic and genotypic coefficient of variation.

1. Days to 50% flowering:

Genotypes having early 50% flowering are preferred because they require minimum moisture to complete their life cycle.

Genotypes NRC-136 required less mean number of days to 50% flowering, had regression coefficient near unity (b=1) and mean deviation from regression equivalent to minimum. These genotypes could be recommended for wide range of cultivation as they had early 50% flowering as well as stable performance.

Genotype NRC-158 could specifically be recommended to good management conditions because its regression coefficient was more than unity; mean deviation square was equivalent to zero. It look medium duration for 50% flowering, as it required about 41 days for 50% flowering.

In according to these result Nagalamu *et al.*(2013), Bhartiya *et al.* (2017) also identified stable genotype for days to 50 % flowering in soybean.

2. Days to maturity:

Short duration varieties are desirable, as they require less input to produce economic yield apart from their ability to escape heat as well as moisture stress, which results in poor development of seeds. Genotypes JS 20-34, NRC-158,NRC-157 took less number of days to physiological maturity, had regression coefficient near unity i.e. $b = 1$ and mean deviation from regression near zero ($S^2d= 0$). Hence these genotypes were found to be more stable than the other genotypes and could perform relatively better in wide range of environments, with early maturity.

Genotype NRC-137 required more number of days to maturity and showed regression coefficient less than one and deviation from regression near to zero. This genotype may be suitable for good management condition where availability of moisture is in plenty.

In contrary to this result Verma *et al.*(2011), Kamaluddin et.*al.* (2012) and Bhartiya *et al.* (2017) identified stable genotype for days to maturity in soybean.

3. Plant height:

Dwarf genotypes are desirable as these are high yielding and lodging resistant.

Genotypes JS20-34,RVS14-4 had short height, regression coefficient near unity and deviation from regression coefficient equivalent to zero. These genotypes are stable in varying environmental conditions.

Genotypes,RVS11-4,RVS14-3,NRC-158 showed unit regression coefficient, deviation from regression near zero but these are taller.

Genotypes NRC-94 and NRC-157 were dwarf had regression coefficient less than one and deviation from regression nearly zero. Therefore, these genotypes may be suitable for poor management conditions.

Genotype RVSM2011-35 and RVS14-2 was dwarf and had regression coefficient more than one and deviation from regression nearly zero. Therefore, the genotypes may be suitable for good management conditions.In accordance to these result Kamaluddin *et al.* (2012), Raidas *et al*.(2020) also identified stable genotype for plant height in soybean.

4. Number of primary branches per plant:

Number of primary branches per plant is an important yield-contributing attribute. It is positively correlated with yield. Genotypes NRC-94,NRC-136,NRC-137 and RVS11-4 showed regression coefficient near unity, deviation from regression equivalent to zero and had higher mean number of primary branches per plant over general mean. These, therefore, showed high stability. These genotypes are better suited to a wide range of environments.

In contrary to this result Nagalamu *et al.*(2013),Jandong *et al.*(2019), Raidas *et al*. (2020) identified stable genotype for number of primary branches per plant in soybean.

5. Internode length

Internode length is an important yield-contributing attribute. It is positively correlated with yield. Genotypes NRC-94,NRC-137,JS20-34, RVS14-4, RVS 14-3, NRC-177,RVS2013-7 showed regression coefficient near unity, deviation from regression equivalent to zero and had higher mean internode length over general mean. These, therefore, showed high stability.

Similar to this result Nagalamu *et al.*(2013) identified stable genotype for internode length in soybean.

6. Pod length

Pod length is an important yield-contributing attribute. It is positively correlated with yield. Genotypes RVS14-1, NRC-94,RVS14-4,NRC-136,RVS11-4,RVS14-3 and NRC-177 showed regression coefficient near unity, deviation from regression equivalent to zero and had higher mean pod length over general mean. These, therefore, showed high stability. These genotypes are better suited to a wide range of environments for pod length. Kamaluddin *et al. (2012)*and Nagalamu *et al.*(2013) also identified stable genotype for pod length in soybean.

7. Number of pods per plant:

Number of pods per plant is an important yield attribute as it is positively correlated with yield. Therefore, varieties having more number of pods per plant, regression coefficient of unity and deviation from regression near to zero, could be considered as stable and high yielding. One genotypes, NRC-94 had regression coefficient near unity, deviation from regression equivalent to zero and higher mean, genotypes NRC-136,NRC-137 had regression coefficient less than one and genotypes RVS11-4,NRC-177 had regression coefficient more than one deviation from regression equivalent to zero and higher mean number of pods per plant than general average number of pods per plant. Thus these genotypes exhibited high stability. These genotypes are better suited for a wide range of environments.

In accordance to these result Solanki *et al.* (2014) Verma *et al.* (2011) and Kamaluddin *et al.(2012)* Jandong *et al.(2019).* also identified stable genotype for number of pods per plant in soybean.

8 Number of seeds per pod:

Genotype NRC-157, NRC-177 and RVS14-2 showed regression coefficient near unity, deviation from regression equivalent to zero and higher number of seed per pods (desirable). therefore, these showed high stability. These varieties are better suited to a wide range of environments. Genotype RVS14-1, RVS11-4 and RVS14-4 may give better and stable yield under good management conditions, since these exhibited regression coefficient more than one, deviation from regression equivalent to zero and had more number of seed per pods.

Genotype JS20-34 and NRC-137 showed regression coefficient more than one, deviation from regression near to zero but had less number of seeds per plant (not desirable). Therefore these varieties may not be suited for cultivation.

Genotype NRC-94,NRC-136,RVSM2011-35,NRC-158,RVS14-3, RVS 2013-7, RVS2013-15 exhibited less than one regression coefficient, deviation from regression near zero but poor performance for number of seeds per plant i.e. had less number of seeds per plant.

9 100 seed weight:

Seed weight is an important yield component as it is highly positively associated with seed yield.

Five varieties, RVSM2011-35,NRC-158,NRC-136, JS20-34 and RVS14-1 having high seed weight, regression coefficient of one and deviation from regression near to zero were more stable under wide range of environment and therefore desirable for cultivation over a wide range of environment.

Genotype NRC-94,RVS14-4,RVS14-3,NRC-158 and RVS2013-15 may give better and stable performance under good management conditions, since it exhibited regression coefficient more than one, deviation from regression equivalent to zero and had more 100 seed weight.

Genotype RVS14-2,NRC-137,NRC-177,NRC-157 and RVS2013-7 had regression coefficient less than one and deviation from regression nearly zero and more 100 seed weight. Therefore, this genotype may be suitable for poor management conditions.

In accordance to these result, Joshi *et al.(2005),*Pan *et al.*(2007) and Verma *et al.* (2011), Solanki *et al.* (2014) also identified stable genotype for 100 seed weight in soybean for this trait.

10 Biological yield per plant:

Biological yield is another important attribute of a variety. High biological yield is highly desirable because, seed yield, straw yield is almost equally important to the farmers.

Genotypes, NRC-94,RVS14-2,RVSM2011-35,NRC-137,NRC-136,14-3 and NRC-158 had regression coefficient near unity, deviation from regression equivalent to zero and more biological yield per plant. Hence these exhibited high stability. These genotypes are better suited for a wide range of environments.

Genotype JS20-34,RVS11-4,NRC-177 and NRC-157 may give better and stable biological yield under good management conditions, since it exhibited regression coefficient more than one, deviation from regression equivalent to zero and had more biological yield per plant.

Genotype RVS14-4 and RVS2013-7 had regression coefficient less than one and deviation from regression nearly zero and more biological yield per plant. Therefore, these genotypes may be suitable for poor management conditions or stress environmental condition.

11 Seed yield per plant:

Seed yield is the most important attribute of a variety. Only the varieties, which have high, mean seed yield are desirable for commercial cultivation as well as to be used as parents in breeding programmes.

Genotypes NRC-94,RVS14-2,RVSM2011-35,RVS14-4,NRC-136NRC-177 and NRC-157 showed substantially higher seed yield per plant, regression coefficient of near to one and genotypes RVS14-1,RVS11-4,NRC-158,RVS2013-7, RVS2013-15 showed more than one regression coefficient and deviation from regression near to zero. It indicated that these varieties were suitable for cultivation on a wide range of environments as these had greater stability along with high seed yield.

Genotype NRC-137,RVS14-3 and JS20-34 exhibited regression coefficient less than unity, deviation from regression near to zero but had average mean seed yield per plant. Therefore, though this genotype had above average stability but is not suitable for cultivation due to average seed yield per plant. Verma *et al.* (2011), Kamaluddin *et al.* (2012), Nagalamu *et al.* (2013), Roshandel *et al.* (2016) and Jandong *et al.(2019),* Raidas *et al.(*2020),Novita (2022*)* also reported variable stability for seed yield per plant. Genotypes RVS14-1 and RVS11-4 may give better and stable yield under good management conditions, since it exhibited regression coefficient more than one, deviation from regression equivalent to zero and had more seed yield per plant.

12 Harvest index:

Harvest index is an important yield component as it had positive correlation with seed yield. Therefore, varieties having more harvest index, regression coefficient of unity and deviation from regression near zero could be recommended as stable and high yielding varieties.

Four genotypes, had higher harvest index, regression coefficient near unity and deviation from regression equivalent to zero, exhibited high stability. These varieties were better suited for a wide range of environment.

Genotypes RVS14-2,RVS14-4,NRC-158,NRC-157 and RVS2013-15 showed regression coefficient more than one, deviation from regression near to zero but had high harvest index .

Genotype NRC-137,NRC-136 and JS20-34 had regression coefficient less than one and deviation from regression nearly zero and more harvest index. Therefore, this genotype may be suitable for poor management conditions.

Genotypes NRC-94,RVS14-3 and NRC-177 exhibited less than one regression coefficient, deviation from regression near zero but poor performance for harvest index. Hence it is not suitable for poor management conditions.

Selection of better parents for hybridization had always been a problem for plant breeders. Stability in performance of different traits indicate number of genes involved in its control. Monogenic or Oligogenic traits are least influenced by the environmental conditions and therefore, better suited for selection. Genotypes having such traits may easily be chosen as parents for hybridization.

The stability of yield and yield components revealed that number of primary branches per plant and seed yield were most stable trait as these remained stable in most of the genotypes , followed by biological yield per plant, internode length and pod length which was stable in 7,days to maturity,plant height, number of pods per plant,100 seed weight stable in 5. It indicated that these traits are governed by few genes and therefore, can be given due weight age while selecting parents for hybridization. Harvest index in 4 and days to 50% flowering was the least stable trait because this was stable only for 3 genotypes. It suggested that days to 50% flowering was least stable and selection of genotypes based on these traits in different environments would be unpredictable.

Over all stability parameters revealedthat among genotypes, NRC-94and NRC-177 was observed most stable, as this was stable for 7 traits followed by RVS14-4 which were stable for 6 traits including seed yield per plant.

Genotypes NRC-136,RVS14-2 were found stable for 5 traits including seed yield per plant, other variety RVSM2011-35 and NRC-157 which was stable for 4 traits including seed yield per plant. Stable genotypes may be used as parents in breeding programmes for wider adaptability traits.

CHAPTER – VI

SUMMARY , CONCLUSION AND SUGGESTIONS FOR FURTHER WORK

The present investigation entitled " Stability analysis for Major Yield Traits in Newly Developed Breeding Lines of Soybean (Glycine max (L.) Merrill.)" was carried out at Research area of All India Co-ordinate Research Project on soybean, R.A.K. College of Agriculture, Sehore (M.P.) to assess the stability of genotype with regard to yield and its contributing characters in soybean and to estimate genetic parameters and variability for different traits and their association. Fifteen genotypes of soybean developed projectAICRP on Soybean, Sehore, were grown in four environment in complete randomized block design with three replications during Kharif (2021-22). Observations were recorded on days to 50 % flowering, days to maturity, plant height, number of primary branches per plant, itnernode length, pod length, number of pods per plant,number of seed per pods, 100 seed weight, biological yield per plant, seed yield per plant and harvest index.

Analysis of variance for all the twelve characters for each environment and on pooled basis indicated substantial amount of variability for most of the yield and yield contributing characters except for biological yield per plant under in E-3 and pooled environments.

Estimates of variance , genotypic and phenotypic coefficient of variation and range revealed large variability for most of the traits. Trend of variability at genotypic level was similar to that at phenotypic level for most of the characters.

High estimate of heritability was recorded for most of the characters under each environment except number of seed per pods in E-1.

Variation in expected genetic advance under different environments was studied. High genetic advance obtained for number of pods per plant, biological yield per plant, plant height and harvest index was expected under all the environments.

Correlation of seed yield with several other traits was observed in different environments. Internode length and harvest index did not show association with seed yield while number of primary branches per plant was found positively correlated in one environments. It was concluded that internode length and harvest index could be manipulated independently without affecting yield. Number of pods per plant, biological yield per plant, plant height was found positively and significantly correlated with seed yield per plant in all four environments. Trend of correlation was similar at genotypic level also.

Variety x environment interactions were found significant for days to 50%flowering, days to maturity, plant height, number of primary branches per plant, internode length, number of pods per plant, biological yield per plant, 100 seed weight, seed yield per plant , and harvest index. The regression and Genotypes x Environment (Linear) mean sum of squares were found significant for all the characters except for pod length and number of seed per pods.

Genotypes NRC-94, NRC-177 were suitable for 7 characters, RVS14-4 was found stable for 6 characters including seed yield per plant. Genotypes NRC-136, RVS14-2 recorded stable performance for 5 characters including seed yield per plant. Genotypes RVSM2011-35,NRC-157 exhibited stability for 4 characters including seed yield per plant.

In respect of stability of different traits it was found that number of primary branches per plant in (9) genotypes, seed yield per plant in (7) genotypes, biological yield per plant in (7) genotyoes, were the most stable characters, Internode length (7), pod length(7), days to maturity in genotyoes (5) and plant height (5), number of pods per plant(5), 100 seed weight in (5) genotypes, and harvest index in (4) genotypes, days to 50% flowering (3) and number of seed per plant was found least stable character, which was stable only in 3 genotypes.

The following genotypes were found desirable and stable for different characters in all four environments.

NRC-136 was the best performer among all the four different locations. It’s seed yield was very high in good soil conditions and rain fall (Sehore).`

NRC-94,RVS14-2,NRC-13,NRC-177,NRC-157 For number of primary branches per plant, RVS14-4 for plant height, RVS14-2 and RVS14-4 for number of pods per plant, NRC-94,RVS14-2, RVSM2011-35 and NRC-136 for biological yield per plant, RVS14-2,NRC-177 and NRC-157 for number of seed per pods, NRC-94,RVS14-2,NRC-136 and NRC-177 for seed yield per plant, JS20-94 and RVS14-1,RVSN2011-35 and JS20-34 for 100 seed weight.

Conclusion:

High estimates of heritability accompanied by high genetic advance were recorded for plant height, number of pods per plant, biological yield per plant over environments suggested that direct selection on these traits can improved the seed yield.

Stability performance furnished information about the adaptation of genotypes in different environments. Genotypes , NRC-94,NRC-177, RVS14-2 and RVS14-4 Showed stability for seed yield and yield components and could be recommended for cultivation in western part of the Vindhyan Plateau of Madhya Pradesh during kharif season.

The traits viz days to 50% flowering, days to maturity, plant height ,number of branches per plant and number of seed per pods have been identified as major yield contributing traits through association analysis.

Suggestions for further works :

The following **suggestions are given to widen the scope of present investigations.**

- Further evaluation under wide range of environments is needed to find out the adaptive potential and phenotypic stability of the genotypes.
- The variability present in the soybean genotypes could be exploited for the development of stable and high yielding varieties.
- Identified genotypes need to be exploited for commercial growing and as parents for developing better varieties.
- Further study of correlation at phenotypic and genotypic levels is required for better understanding of true relationships among traits through path analysis.
- Assessment of other minor yield and qualitative traits of genotypes be carried out over the seasons and years to judge their consistence performance.

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