

**ASSESSMENT OF PARAMETRIC AND NON PARAMETRIC METHODS FOR  
SELECTING STABLE AND ADAPTABLE SOYBEAN GENOTYPES IN MULTI  
ENVIRONMENTS**

**M.Sc. (Ag) Thesis**

**by**

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**COLLEGE OF AGRICULTURE**

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**INDIRA GANDHI KRISHI VISHWAVIDYALAYA**

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**ASSESSMENT OF PARAMETRIC AND NON PARAMETRIC METHODS FOR  
SELECTING STABLE AND ADAPTABLE SOYBEAN GENOTYPES IN MULTI  
ENVIRONMENTS**

**Thesis**

**Submitted to the**

**Indira Gandhi Krishi Vishwavidyalaya, Raipur**

**by**

**Vibha Ramteke**

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**FOR THE DEGREE OF**

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**in**

**Agriculture Statistics**

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## CERTIFICATE-I

This is to certify that the thesis **entitled “Assessment of Parametric and Non Parametric methods for selecting stable and adaptable soybean genotypes in Multi environments”** Submitted in partial fulfilment of the requirements for the degree of Master of Science in Agriculture of the Indira Gandhi Krishi Vishwavidyalaya, Raipur is a record of the bonafide research work carried out by **Vibha Ramteke** under my guidance and supervision. The subject of the thesis has been approved by the Student’s Advisory Committee and the Director of Instructions.

No part of the thesis has been submitted for any other degree or diploma or has been published/published part has been fully acknowledged. All the assistance and help received during the course of the investigations have been duly acknowledged.

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Chairman

### THESIS APPROVED BY THE STUDENT’S ADVISORY COMMITTEE

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Member        (Dr. R. Lakpale)        .....

## **CERTIFICATE-II**

This is to certify that the thesis entitled “**Assessment of Parametric and Non Parametric methods for selecting stable and adaptable soybean genotypes in Multi environments** ” submitted by **Vibha Ramteke** to the Indira Gandhi Krishi Vishwavidyalya, Raipur, in partial fulfilment of the requirements for the degree of Master of Science in Agriculture in the Department of agricultural statistics and social science (L.) has been approved by the external evaluator and Student’s Advisory Committee after oral examination, under the chairmanship of Head of the Department.

Signature of Head of the Department

(Name.....)

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**Major Advisor** .....

**Faculty Dean** .....

**Approved/Not approved**

**Director of Instructions** .....

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*Date: .....*

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## LIST OF NOTATIONS/SYMBOLS

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% per cent

$b_i$  regression coefficient

$P_i$  Lin's and Binns

$W_i$  Wricke ecovalence

$\sigma_i^2$  Shukla's stability

$\overline{S_{di}^2}$  Eberhart & Russell's joint regression analysis

$S_i^{(1)}$  Mean of the absolute rank differences of a genotype

$S_i^{(2)}$  Variance among the ranks over the  $q$  environments

$S_i^{(3)}$  Mean of the absolute rank differences of a genotype

$S_i^{(6)}$  Variance among the ranks over the  $q$  environments

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## LIST OF ABBREVIATIONS

---

|          |   |
|----------|---|
| AEA      | Average-Environment Axis                            |
| AEC      | Average-Environment Coordination                    |
| AMMI     | Additive Main Effect and Multiplicative Interaction |
| ANOVA    | Analysis of Variance                                |
| ASV      | The AMMI stability value                            |
| CV       | Coefficient of Variability                          |
| DF       | Degree of freedom                                   |
| GE       | genotype by environment interaction                 |
| GEI      | Genotype x Environment Interaction                  |
| GGE      | G + GE  |
| ha-1     | Per hectare   |
| IPCA     | Interaction of Principal Component Analysis         |
| PB Tools | Plant Breeding Tools (IRRI)                         |
| PC       | Principal Component                                 |
| PCA      | Principal Component Analysis                        |
| Pi       | The Cultivar Performance Measure (by Lin & Binns)   |
| R        | Spearman's Rank Correlation                         |
| SS       | Sum of square                                       |

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## THESIS ABSTRACT

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- a) Title of the Thesis : “Assessment of Parametric and Non Parametric methods for selecting stable and adaptable soybean genotypes in Multi environments”
- b) Full Name of the Student : Vibha Ramteke
- c) Major Subject : Agricultural Statistics
- d) Name and Address of the : Dr. R. R. Saxena, Professor, Department of  
Major Advisor Agricultural Statistics and Social Science (L.),  
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- e) Degree to be Awarded : Master of Science in Agriculture  
(Agricultural Statistics)

Signature of Student

Signature of HOD

Signature of Chairman

Date :

---

## ABSTRACT

The statistical investigation of soybean crop in multi locations trials namely; Raipur, Jagdalpur, Kabirdham and Bemetara district was conducted on secondary data, collected



from Department of Genetics and Plant Breeding in Chhattisgarh during the years 2017-18 and having maximum number of genotypes in state. Comparison of the different stability parameters methods viz., Statistical methods such as conventional analysis of variance (ANOVA), stability parameters, ranking method and multivariate methods were identified for analysis of multi-location trials. Combined analysis of variance method used to identify the existence of Genotype x Environmental Interaction (GEI) from multilocation trials. This method describes the main effects of genotypes and location, effectively.

Parametric stability analysis gives an overall summary of the response patterns of genotypes to environmental different in choose soybean crop. The Genotypes RSC 11-05, RSC 11-02, CG Soya-1(c), and JS 97-52(c) were found to be the high yielding and most stable genotypes in different location of Chhattisgarh state. The multivariate method namely, principal component analysis describes the pattern in G x E Interaction and highlight the broad adaptability and specific adaptability of genotypes. The output is graphical and easy to understand and provide supporting evidence to confirm the result of other methods. The study has obviously demonstrated that the AMMI model can sum up patterns and connections of genotypes and environments effectively, just as give an important forecast appraisal that multivariate techniques are too complex to provide a simple measure of yield stability, which permits a positioning of genotypes. It is obviously indicating the transformation of genotypes to environments and can be utilized to distinguish the prevalent genotypes in connection with the environments and years.

GGE bi-plots are effective enough for analyzing and visualizing the patterns of G x E of the soybean multi-location data with respect to environment and genotype

evaluations. Non-parametric stability analysis simple to utilize and decipher and increments or erasures of one or a couple of genotypes don't cause a lot of variety of results. Thus, numerous scientists applied distinctive non-parametric statistics to assess stability. The relationship of parametric measures and non-parametric measures, among themselves, have been calculated. These, therefore, have to be judged by the rank correlation method. The results of the investigation would be quite useful to the plant breeder and geneticists who would be able to select genotypes simultaneously for crop yield and crop yield stability. The result showed that both the parametric and nonparametric methods gave a relatively similar result. The present study was an attempt in this direction, aiming the critical examination of stability in different location of soybean crop in Chhattisgarh.

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**Dr. Ravi. R. Saxena**  
Major Advisor

## शोध सारांश

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|                                    |  |
|------------------------------------|--|
| अ) शोध शीर्षक                      | बहुसंख्यकों में चयन करने योग्य स्थिर और अनुकूलन योग्य जननों के चयन के लिए पैरामैट्रिक और नॉन पैरामैट्रिक पद्धति का संयोजन।                             |
| ब) छात्रा का पूरा नाम              | विभा रामटेके   |
| स) मुख्य विषय                      | कृषि सांख्यिकीय एवं सामाजिक विज्ञान विभाग (एल.)  |
| द) मुख्य सलाहकार का नाम व पूरा पता | डॉ. रवि आर. सक्सेना<br>प्राध्यापक, कृषि सांख्यिकीय एवं सामाजिक विज्ञान विभाग (एल.) कृषि महाविद्यालय, इंदिरा गांधी कृषि विश्वविद्यालय, रायपुर छत्तीसगढ़ |
| ई) उपाधि का नाम                    | एम.एस.सी. (कृषि) कृषि सांख्यिकीय एवं सामाजिक विज्ञान विभाग (एल.)   |

छात्रा का हस्ताक्षर

मुख्य सलाहकार के हस्ताक्षर

दिनांक

विभागाध्यक्ष के हस्ताक्षर

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## सारांश

सोयाबीन फसल में मुख्य 10 जीनोटाइप की बहुस्थानों परीक्षण की सांख्यिकीय विश्लेषण रायपुर, जगदलपुर, कबीरधाम एवं बेमेतरा जिले में वर्ष 2017–18 में उपज आँकड़े पर आधारित आँकड़े पादप प्रजनन एवं जेनेटिक्स विभाग द्वारा एकत्रित किया गया था। विभिन्न स्थिरता मापदंडों के विधियों का तुलनात्मक अध्ययन जैसे प्रसरण विश्लेषण, स्थिरता मापदंड, रैंकिंग विधि तरीकों के द्वारा **G x E Interaction** के प्रमुख प्रभावों का वर्णन करती है।

**Parametric Stability analysis** चयनित सोयाबीन फसल के पर्यावरण परिवर्तन के जीनोटाइप के प्रतिक्रिया पैटर्न का एक सामान्य सारांश प्रदान करता है। जीनोटाइप आरएससी 11–05 आरएससी 11–02, सीजी सोया–1 (सी), और जेएस 97–52 (सी) छत्तीसगढ़ राज्य के विभिन्न स्थानों में उच्च उपज और सबसे स्थिर जीनोटाइप पाए गए। **Principal Component analysis, GXE interaction** में पैटर्न का वर्णन करता है और जीनोटाइप के व्यापक अनुकूलनशीलता और विशिष्ट अनुकूलन शीलता को उजागर करता है। आउटपुट अन्य तरीकों के परिणाम की पुष्टि करने के लिए ग्राफिकल और समझने में आसान है और सहायक साक्ष्य प्रदान करता है। अध्ययन ने स्पष्ट रूप से दिखाया है कि **AMMI Model** जीनोटाइप और वातावरण के पैटर्न और संबंधों की सफलतापूर्वक

सारांशित कर सकता है, साथ ही एक मूल्यवान भविष्यवाणी मूल्यांकन प्रदान कर सकता है कि उपज स्थिरता का एक सरल उपाय प्रदान करने के लिए बहु विभिन्न रूपी तरीके बहुत परिपक्व है, जो जीनोटाइप की रैंकिंग की अनुमति देता है । यह स्पष्ट रूप से वातावरण में जीनोटाइप के अनुकूलन को दिखा रहा है और इसका उपयोग वातावरण और वर्षों के संबंध में बेहतर जीनोटाइप की पहचान करने के लिए किया जा सकता है ।

पर्यावरण और जीनोटाइप मूल्यांकन के संबंध में सोयाबीन बहु-स्थान डेटा के **GXE interaction analysis** और कल्पना करने के लिए **GGE bi-plot** काफी प्रभावी है ।

**Non Parametric Method** का उपयोग करना आसान है और एक या कुछ जीनोटाइप के परिवर्धन या विलोपन परिणाम के बहुत भिन्नता का कारण नहीं बनते हैं । परिणाम स्वरूप कई शोध कर्ताओं ने स्थिरता का मूल्यांकन करने के लिए विभिन्न **Non Parametric** आंकड़े लागू किए **Parametric** उपायों और **Non Parametric** उपायों के संबंध में आपस में की गणना की गई है । इसलिए उन्हें रैंक सह संबंध विधि द्वारा आंका जाना चाहिए । जाँच के परिणाम उपज स्थिरता के लिए किए साथ जीनोटाइप का चयन करने में सक्षम होंगे । वर्तमान अध्ययन इस दिशा में एक प्रयास था, जिसका उद्देश्य छत्तीसगढ़ में सोयाबीन की फसल के विभिन्न स्थानों में स्थिरता की जांच की गई ।

कृषि सांख्यिकीय एवं सामाजिक विज्ञान विभाग एल.  
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प्रमुख मार्गदर्शक

## CHAPTER-I INTRODUCTION

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Soybean (*Glycine max* L. Merrill) is the world's most important seed legume, which adds to 25% of the worldwide edible oil and about two-thirds of the world's protein concentrate for livestock feeding. Soybean is the world's leading source of oil protein. It has the most elevated protein content (40%) of all food crops and is second just to groundnut as far as oil content (20%) among food legumes. In the recent past, soybean cultivation has expanded complex with some other oilseed crop in India and stands next just to groundnut, however commercial production of soybean started distinctly in 1971-72. India is world's second biggest merchant of vegetable oil after China. India is overwhelmed by palm gathering of oils followed by soybean oil. Production of soybean in India is commanded by Maharashtra and Madhya Pradesh which contribute 89 per cent of the all out production. Rajasthan, Andhra Pradesh, Karnataka, Chhattisgarh and Gujarat contribute the staying 11 per cent production.

Stability analysis aims to characterize the performance of genotypes in various environments. Cultivar stability isn't only important for breeders but also important for farmers since a cultivar should be able to adapt different growing conditions so as to diminish the risk of variance of yield due to unpredictable environmental changes (Baihaki and Wicaksana, 2005). A number of statistical methods are now known for estimation of phenotypic stability. For this purpose the multi-locations trials over a number of years are conducted. An ideal variety always combines high yield with the stability of performance (Eberhart & Russell, 1966) in spite of the fact that it is hard to track down such high yielding and stable assortment over a wide scope of variable conditions.

Multi location trials are conducted to understand the adaptability and the performance of the genotypes or the varieties under different situations. A genotype would be stable one when its performance remains almost same over the different situations. There are different genotypes which require to study their suitability under different situations trials are conducted to oversee the consistency in performance of the genotypes.

The genotype x environment interaction (GEI) is a phenomenon that cultivars perform differently across diverse environment. Thus, G x E Interaction will make the selection ineffective and cause difficulties in the selection of ideal and stable genotypes for all environments. In such broadly factor situations, the event of critical genotype x environment interaction (GEI) is to a great extent conceivable. Such event of critical G x E Interaction in crop is both a chance and a test. The procedure of recognizable proof of steady and high yielding genotype under various growing environments like the soybean growing regions of Chhattisgarh is troublesome as a result of the event of G x E Interaction.

The parametric strategy includes the methods which are based on variance components and joint regression, while non-parametric approaches are based on the ranks of genotypes in each environment. Although a few parametric models for the statistical measurement of the stability have been proposed, everyone of which reflects various part of stability and no single technique can sufficiently clarify genotype execution across environments. Regression technique was first talked about by Yates and Cochran (1938) and later by Finlay and Wilkinson (1963) to measure stability and afterward was improved by Eberhart and Russell (1966) . Some other parametric stability statistics are: Shukla's (1972) stability variance, genotype grouping technique based on Francis and Kanenberg's (1978) coefficient of variation (CV<sub>i</sub>), Lin and Binn's (1988) and Cultivar superiority index (P<sub>i</sub>).

Nonparametric methods also give viable alternate options which are based on the ranks of genotypes in each environment and use the idea of environmental resistance as a measure of the stability. Nonparametric dependability estimates dependent on positions give a practical choice to introduce parametric estimates dependent on supreme information (Nassar and Huehn, 1987). There is plentiful legitimization for the utilization of nonparametric measures of crop varieties in the assessment of yield stability. As per Huehn (1990) nonparametric methodology have the accompanying favourable circumstances over parametric stability methods: (i) they decrease the bias cause of outliers, (ii) No presumptions are required about the dispersion of watched values. (iii) They are anything but difficult to utilize and interpret. (iv) Addition or cancellation of at least one genotypes doesn't cause a lot of variety in results. The nonparametric are less ground-breaking than their parametric counterpart. The force productivity of the nonparametric measures will be very near those of parametric measures. There are an increasing number of stability measures for genotypes grown in different environments. It is therefore, useful to study the statistical statistics to find relations between the parametric and nonparametric stability the best and appropriate parameters for testing genotypes in breeding programs. One approach is to calculate the rank correlation coefficient (Spearman's correlation) between different stability parameters on the basis of empirical data sets. Another approach is using the principle component analysis to study the relationship between stability statistics (Piepho and Lotito, 1992).

Hence, the present study is mainly focused "Assessment of Parametric and Non Parametric methods for selecting stable and adaptable soybean genotypes in Multi environments" and keeping the above focuses in see the current examination is defined with following objectives:

## **OBJECTIVES**

- To compare the various Parametric and Non parametric statistical methods to describe soybean genotype performance in the soybean producing areas of Chhattisgarh.
- To determine the most suitable method for describing soybean genotype  $\times$  environments in Chhattisgarh.
- To apply multivariate techniques AMMI and GGE bi-plot statistical model for determination of the magnitude and pattern of  $G \times E$  interaction impacts and performance stability of grain yield in choosing genotypes.



## CHAPTER-II

### REVIEW OF LITERATURE

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The review of literature in the work done on the past is essential to understand fully the problem in depth. This chapter deals with the review of studies on research to the objective of present study. The literature pertaining to the present investigation entitled “**Assessment of Parametric and Non Parametric methods for selecting stable and adaptable soybean genotypes in Multi environments**”

Afzalet *al.* (2001) evaluated 10 genotypes of chick pea along with two local checks in Uttar Pradesh. Yields' being a polygenic character is influenced by genotypes, environment and GEI; normal agronomic practices were followed at each location. Stability parameters measured were regression coefficient and variance due to deviation from regression. The joint regression methods such as Finlay and Wilkinson, Eberhart & Russell's, Perkins-Jinks and Freeman-Perkins used to analysis the cultivar yield stability due to environment.

Sumith and Abeysiriwardena (2001) evaluated the stability analysis of multi-location trials using the different parametric methods of on farm trials for testing adaptability of rice crop in developing countries. They studied the Lin and Binns regression methods to measure the superiority of varieties tested in multi-location yield trials.

Kaya and Taner (2003) estimated the non-parametric stability analysis in wheat crop across eleven locations in Turkey. Experimental was conducted in Randomized Block Design with four replications during 2002-03 developing season. SAS statistical software used for the statistical analysis. Two non-parametric stability measures namely, mean of unquestionably the rank  $S_i^{(1)}$  difference, fluctuation among the positions over the environments  $S_i^{(2)}$  were used for the stability analysis. They determined that non-parametric estimates dependent on positions gave a

valuable option in contrast to parametric measures. For every genotype  $Z_1^{(1)}$  and  $Z_2^{(2)}$  value were determined dependent on positions of the adjusted information and summed up over genotypes. Both of these insights were not exactly basic worth and no essentialness contrast found in dependability measures among the 9 genotypes in eleven situations.

Letta (2007) compared the several biometrical methods for analysis of GE interaction and yield stability. The experiment was conducted to assess the nature and magnitude of GEI and to determine correlation among some stability parameter of grain yield. The stability analysis of genotypes 3 and genotype 4 as more stable and recommended for commercial production in the South East Ethiopia. Stability analyses were used by MSTAT-C and IRRI stat computer programs (IRRI Stat), Spearman's coefficient of rank relationship was processed for each pair of the conceivable pair-wise correlation of the stability parameter by MINITAB and AMMI was calculated by Purchase (1997).

Anandanet *et al.* (2009) evaluated in multi-environment trials ,to analyzed the performance and adoption for specific or general environment. To analyzed the pattern of genotype x environment interaction for grain yield of 46 genotypes by using Additive Main effects and Multiplicative Interaction (AMMI) model from three saline stress environment conditions.

Kabir *et al.* (2009) estimated dependability measures on wheat crop for grain yield, genotype x environment interaction (GEI) as influenced by different environment. different wheat genotypes were planted in eight distinct dates at Bangladesh over two consecutive years 2007-08 and 2008-09 under watered condition utilizing RBD with three replications. They were analyzed by linear regression techniques (Eberhart & Russell's Stability method). It was discovered that November 29 is the most ideal time of planting of wheat crop in Bangladesh.

Choukan (2010) evaluated yield stability on multi-environment trials (METs ) based on principal component analysis (PCA), GGE bi-plot analysis. The METs data of 14 maize genotypes were used to identify the stable genotypes by AMMI and GGE bi-plot analysis. He studied the Additive main effects and multiplicative interaction (AMMI) which were effective alternative method for assessing the suitable genotype. GGE bi-plot is effective tool for the Mega-environment analysis (which-won-where pattern), genotype evaluation (mean performance and stability) and environment evaluation (to discriminate among genotypes in targeted environment).

Farshadfar *et al.* (2011) determined stable wheat genotypes with high grain yield with single parameter, field experiment were conducted with 14 genotypes for 3 consecutive years under completely randomized design with three replications in two different conditions. The statistical method used to describe the stability by coefficient of determination, coefficient of variability and the genotype variances across environment, agronomic concept of stability, regression coefficient method and AMMI stability method. To better understand the relationship, similarities and dissimilarities among the yield stability statistics, principal component analysis (PCA) based on the rank correlation matrix was used.

Hidayat *et al.* (2011) contemplated the exhibition of mungbean genotypes and assessed in multi-environmental trials utilizing the GGE bi-plot technique. Experiments were conducted Randomized Block Design with three replications for two years at three areas in Pakistan. Combined analysis of variance exhibited significant effect for genotype (G), environment (E) and genotype x environment interaction (GEI) effect on grain yield. The graphical demonstration proposed by the bi-plot analysis provided an effective overview of average performance and environmental stability of mungbean genotypes in multi-condition preliminaries.

Jandonget *et al.* (2011) studied the combined effects of genotypes; environment and genotype x environment interaction (GEI) on the crop yield of soybean. They studied the adaptation and stability of soybean varieties over six locations. The experiments were conducted in a factorial design laid out CRD design with 3 replications. The GGE biplot statistical method applied to determination the suitable genotypes across diverse soil pH levels.

Ngeve and Boukamp (2011) compared the various statistical methods to identify the best genotype on the basis of yield parameter in Sweet potato. Twenty seven trials were conducted with 20 Sweet potato clones in seven locations over 4 year. Four stability methods were used namely; Eberhart& Russell's model, Perkins and Jinks methods, Shukla's method and Francis and Kannenberg. They studied the Francis and Kannenberg was very convenient, easy to use and was appropriate for grouping clone of greater and lesser stability.

Asfaw *et al.* (2012) analyzed multi-environment grain yield trials in Mungbean based on GGE bi-plot in Ethiopia. They evaluated to quantify the magnitude of the genotype x environment interaction (GEI) effect on Mungbean grain yield and determined the best genotype for the tested in varied environment.

Atif *et al.* (2012) evaluated sixteen genotypes of rice during 2008-09 growing season at two locations in Sudan, suitable genotype performance, and identified high yielding genotypes. The experiment was conducted in randomized block design with three replications in each location. They compared the performance of breeding lines developed for various ecosystems and identify stable genotypes with wide adoptability. Three stability parameters such as Finlay and Wilkinson model, Eberhart& Russell's model and mean yield , coefficient of regression were used as measure of yield response of adoption pattern.

Parmar *et al.* (2012) studied the non-parametric methods for interpreting genotype X environment (GEI) interaction of 21 rice genotypes in different agro-ecological regions of Gujrat state. Multi-location trials were conducted in Randomized Block Design with two replications with follow the standard cultural practices applied. Stability analysis by non-parametric methods was applied based on ranks of genotypes within environments. Four non-parametric stability measures namely, mean of the absolute rank  $S_i^{(1)}$  difference, variance among the ranks over the environments  $S_i^{(2)}$ , mean of the absolute rank difference  $S_i^{(3)}$  and variance among the ranks over the environments  $S_i^{(6)}$  were applied for the comparison of genotype x environmental interaction. They concluded that the uncorrected and corrected ranks of yield consideration of both stability measures. Conclude that correction eliminated the genotypic effects from data.

Kahramet *al.* (2013) determined suitable wheat genotypes in the moderate areas of Iran, 18 durum wheat genotypes were assessed along with commercial bread wheat and Dena cultivars as control. The study was directed in randomized block design with 3 replications in two successive years (2008 to 2009). To assessed the genotype x environment interaction (GEI) and distinguish the stable genotype, analysis of stability was performed. Some stability parameters such as the new parameter AMMI stability value (ASV) and graphical strategy for AMMI were considered.

Hegazyet *al.* (2013) studied the genotype x environment interaction (GEI) and stability parameter for yield and its components in Lentil crop. The regression model and Wricks'covalence method were utilized to break down and select the best genotype in varied environment over different years. Result were indicated that both natural conditions and considered genotypic increase impacted fundamentally on the presentation of yield and yield segments.

Ferreira *et al.* (2016) examined the hypothetical determinations of non-parametric techniques, which utilize direct relapses dependent on rank request, for stability analysis. The non- parametric stability methods were effective for the evaluation of phenotypic stability. The first method adopted by simple linear regression based on rank order  $R_{ij}$ , and second technique utilized Lin and Binns was then determined with the end goal that every genotype was contrasted with the most extreme presentation in every condition based position  $P_i$ , Wricke covalence ( $W_i$ ) technique was additionally summed up for non-parametric cases, once these normalized qualities were acquired, the mean value ( $\bar{V}_i$ ) and variance of the positions ( $S_{v_i}^2$ ) of the  $i^{\text{th}}$  genotype over the  $q$  situations were evaluated. Two non-parametric stability measures namely, mean of the absolute rank  $S_i^{(1)}$  difference, variance among the ranks over the environments  $S_i^{(2)}$  were used for the study. For each genotype  $Z_1^{(1)}$  and  $Z_2^{(2)}$  value were calculated based on ranks of the corrected data and summarized over genotypes. This outcome showed that most techniques utilized may not contain a similar data, yet are viewed as corresponding.

Goksoy *et al.* (2018) seed yield of 15 soybean genotypes were evaluated in three locations *i.e.* Bursa, Samsun and Konya under main crop conditions through summer seasons from 2014 to 2016. Experiment conducted in Randomized complete block design with four replications. They estimated the stability parameters of seed yield of 15 soybean genotypes by different stability analysis methods over nine environmental conditions and interrelationship among these stability methods. The result of most parametric and non parametric stability analysis showed that genotypes BDUS 04, KASM 02, KASM 03, KAMD 03 and BDSA 05 were stable genotypes. These genotypes were demonstrated superior adaptability with high yield performance in many environments. Result of correlation analysis indicated that seed yield was significantly correlated

with  $R_i^2$  ( $P < 0.05$ ),  $S_i^{(3)}$  ( $P < 0.05$ ), Di ( $P < 0.01$ ),  $S_i^{(6)}$  ( $P < 0.01$ ), TOP ( $P < 0.01$ ) and showed a negative and significant correlation with Pi and RS ( $P < 0.01$ ). The coefficient of regression ( $b_i$ ) had positively significant associated with  $CV_i$ , and  $S_i^{(6)}$  with superiority parameter.

Manjubala *et al.* (2018) evaluated the stable genotypes by different nonparametric measures and studied association among nonparametric methods. Nine nonparametric techniques were utilized for recognizable proof of stable genotype and relationship among these measures were checked by correlation. As indicated by principal component analysis (PCA), nonparametric measures were partitioned into three gatherings Group 1 included Kamgranksum,  $NP_i^{(1)}$ ,  $NP_i^{(2)}$ ,  $NP_i^{(3)}$ ,  $NP_i^{(4)}$ , Group 2 included  $S_i^{(3)}$  and  $S_i^{(6)}$ . Group 3 included  $S_i^{(1)}$  and  $S_i^{(2)}$ . Parametric and nonparametric methods used to quantify crop yield stable.

Alemu *et al.* (2019) deciphered genotype fundamental impact and GEI got by AMMI investigation and gathering the genotype having comparative reaction design over all situations. Fifteen bread wheat genotypes were assessed by RBD utilizing four replications at six areas in Ethiopia. One of the multivariate techniques is the AMMI model. The AMMI model joins the examination of difference for the genotype and environment main effects with principal components analysis of the  $G \times E$  interaction. The methods used in mean grain yield, AMMI stability value, yield stability index, Rank sum, and interaction principal component. Results of AMMI analysis of mean grain yield for the six areas showed significant differences among the genotypes, the situations and GEI. The environment had the greatest effect of the environmental sum of squares (35.28%) than the genotypes (33.46%) and GEI (31.45%) effect.

Hashash *et al.* (2019) investigated stable genotypes among sixteen genotypes dependent on various non-parametric stability statistics across four areas during the 2016, 2017 and 2018 developing seasons in Egypt. Experiment conducted in a Randomized block design (RBD) with

three replications. The AMMI analysis demonstrated an exceptionally note worthy impact of genotyped (G), environment (E) and  $G \times E$  interaction (GEI). Based on the static and dynamic ideas, the results of spearman's rank correlation and PCA indicated that stability measures could be characterized into three gatherings. While the other non-parametric stability statistics ( $S_i^{(1)}, S_i^{(2)}, S_i^{(3)}$ ) and ( $S_i^{(6)}, NP_i^{(1)}, NP_i^{(2)}, NP_i^{(3)}$  and  $NP_i^{(4)}, \delta r, MID, LOW$ ) represented the concept of static stability statistics, the genotype G6 and G11 were progressively stable combined with high seed yield. Genotypes may be utilized for hereditary improvement of soybean and they should be discharged in contemplated district and other areas in Egypt.

Singh *et al.* (2019) evaluated fifty wheat genotypes from nine assorted areas in India and distinguished high-yielding and stable genotypes. The analysis of variance based on additive main effects and multiplicative interaction (AMMI) indicated significant genotype, environment and genotype - environment (GEI) interactions, with an all out variety of 5.99, 20.23 and 73.77%, separately. Regression analysis, sum of squared deviations from regression, Principal Component Analysis (PCA), cluster analysis and Additive Main effects and Multiplicative Interaction models (AMMI) utilized for the analysis of stable genotypes. The genotype stability index (GSI) considered the positions of the genotype yields across environments and AMMI stability values. The AMMI and GGE bi-plot package in R programming was utilizes for the analyses. Approaches, AMMI and GGE bi-plot, permitted the recognizable proof of basic genotypes (G129, G111, G131, G135 and G112) that are stable and high yielding over all areas.

Raiger *et al* (2019) studied based on rank of genotypes by different yield stability measures our 7 environments that the 8 stability measure would be divided into four distinct groups. The test of significance for genotype x environment (GE) interaction and eight non-parametric measures of stability analysis were used to identify high seed yield stable genotype



across the seven environments. Non-parametric methods namely; mean of the absolute rank  $S_i^{(1)}$  difference, variance among the ranks over the environments  $S_i^{(2)}$ , mean of the absolute rank difference  $S_i^{(3)}$ , and variance among the ranks over the environments  $S_i^{(6)}$  and Thennarasu's stability measures  $NP^{(1)}$ ,  $NP^{(2)}$ ,  $NP^{(3)}$  and  $NP^{(4)}$  were used for the studied. The eight stability measures have been taken in this study for stable varieties in terms of high yield and stability. Simultaneous selection of genotype for high yield and stability is useful effect of genotype x environment interaction and selection genotype can be selected in refined manner. Eight non-parametric measures had been employed, based on low value of non-parametric measures, H-2279 was identified most stable as well as high yielding genotype.

Abate (2020) analyzed the magnitude of GxE interaction and evaluates the versatility and stability of open pollinated maize genotypes for grain yield, utilizing AMMI (Additive Main Effects and Multiplicative Interaction) model. The field analyze was directed for two back to back a long time during the slow times of year of 2016/17 and 2017/18 at three areas to be specific, Awra, Dalifage and Dubti. The test in every areas was spread out utilizing RCBD with three replications. The pooled analysis of variance over environments for AMMI model was exceptionally critical. He found that the genotypes and the environments for grain yield, showing the differential execution of genotypes over the situations. In light of the AMMI model genotypes Melkassa-2 and Melkassa-7 were the most stable varieties with lower Interaction (IPCA) score and least ASV rank. The results of AMMI bi-plots were additionally in found with the consequences of ASV. Heinfers that maize grain yield was exceptionally affected by situations and G x E association

Baraki et al. (2020) studied the multi-location trials and identify the genotype x environment interaction (GEI) and yield stability analysis of mung bean genotypes in Northern

Ethiopia. The analysis was led RBD with three replication from 2009–2011 cropping seasons with six mung bean genotypes and assessed to early maturing and high yielding genotypes. The combined analysis of variance, AMMI and Bi-plot graphical measures were used for the stability analysis. ANOVA revealed that there was highly significant of grain yield among the genotypes, environments and genotype by environment interaction. The genotypic, environmental and the genotype x environment interaction (GIE) accounted about 30.47%, 45.01% and 11.59% of the total variation. The AMMI bi-plot additionally portrayed that, SML-668 and SML-32 were the high yielding and low yielding genotype, respectively. Like the AMMI bi-plot, the GGE bi-plot also confirmed that SML-668 was the winning genotype in most of the environments; whereas, SML-32 and local 2-sheraro, were the low yielding genotypes in few or all of the situations.

Rahayu (2020) yield stability analysis of rice mutant lines using AMMI method in high-elevations regions of Indonesia. He state that the information on the stability of rice genotypes to be adapted in highland across three different high-elevations. The AMMI analysis revealed KN10-111; KN-20-124 and RB-10-98 mutant lines were the most stable genotypes across environments evaluated. KK-10-249 mutant line was explicit in 900 m above sea level area, C4-30-21, RB-10-95 and KN-20-127 mutant lines adapted in 700 m above sea level area (dry season) whereas B-30-82, IPB117-F-20 and C3-10-171 lines specified in the rainy season. The stable and promising mutant lines could be discharged and built up another assortment to improve the yield of rice good country adjusted.

## **CHAPTER-III**

### **MATERIALS AND METHODS**

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The present investigation entitled “Assessment of Parametric and Non Parametric methods for selecting stable and adaptable soybean genotypes in Multi environments” was carried out at the Department of Agriculture Statistics and Social Science, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur during 2019-20. The point of this chapter is to give a brief description of the materials and methods which give the analysis.

The methodology is presented under the following heads.

3.1 Description of the study area, period and crop.

3.2 Analytical tools and techniques applied.

#### **3.1 Description of the study area, period and crop**

Data on different environment trials on soybean was chosen from the Chhattisgarh state for the present study. The test environments were Raipur, Jagdalpur, Bemetara and Kabirdham district for the multi environmental trials. Secondary yield data of ten traditional as well as newly developed genotypes of soybean crop namely; CG Soya-1(c), JS 93-05(c), JS 97-52(c), RSC 10-52, RSC 10-71, RSC 11-02, RSC 11-03, RSC 11-04, RSC 11-05, RSC 11-06, collected from Department of Genetics and Plant Breeding in Chhattisgarh during the years 2017-2018.

#### **3.2 Analytical tools and techniques applied**

Keeping in view the objectives set out for the study, following statistical tools and methods have been deployed. The data are analysed by using software like R-Package 3.5.1, Statistical Package for Agricultural Research Works (OPSTAT), PB tools 1.5 and MS-EXCEL.

##### **3.2.1 Statistical methods to measure G x E Interaction**

A combined analysis of variance procedure is the most widely recognized technique used to distinguish the presence of G x E Interaction from replication multi-area preliminaries. On the

off chance that the G x E Interaction change is seen as critical, at least one of the various methods for measuring the stability of genotypes can be utilized to distinguish the stable genotype (s). A wide scope of techniques is accessible for the analysis of G x E Interaction and can be extensively characterized into four gatherings: The analysis of segments of fluctuation, stability analysis, multivariate techniques and subjective techniques.

### 3.2.2 Conventional analysis of variance

Consider a trail in wherein the yield of  $G$  genotypes is estimated in  $E$  environments each with  $R$  replicates. The classic model for analyzing all out yield variety contained in  $G \times E \times R$  perceptions is the analysis of variance (Fisher, 1918, 1925). The within-environment residual mean square measures the error in estimating the genotype implies, the  $G \times E$  perceptions are divided into two sources: (a) additive main effect for genotype and environments and (b) non additive effects due to  $G \times E$  Interaction. The analysis of change of the consolidated information communicates the watched ( $Y_{ij}$ ) mean yield of the  $i^{th}$  genotype at the  $j^{th}$  environments as

$$Y_{ij} = \mu + G_i + E_j + GE_{ij} + e_{ij}$$

Where  $\mu$  is the overall mean;  $G_i, E_j$  and  $GE_{ij}$  represent the effect of the genotype, environment, and the genotype x environment interaction, individually; and  $e_{ij}$  is the average of the random errors associated with the  $r^{th}$  plot that gets the  $i^{th}$  genotype in the  $j^{th}$  environment.

### 3.2.3 Stability analysis

Stability analysis gives a overall summary of the response patterns of genotypes to environmental change. Freeman (1973) named the fundamental kind of stability analysis, joint regression analysis or joint linear regression (JLR). It includes the regression of the genotype

implies on an environmental index. Joint regression analysis gives a methods for testing whether the genotypes have characteristic linear responses to change in conditions.

### 3.2.4 Francis and Kannenberg's (1978) coefficient of variability ( $CV_i$ )

The mean  $CV_i$  analysis presented by Francis (1977) was intended to help in concentrates on the yield stability. He acquainted a basic graphical methodology with evaluate execution and stability simultaneously. It quantifies the exhibition and  $CV_i$  for every genotype general conditions and the mean yield plotted against the  $CV_i$ .

$$s_i^2 = \sum_{j=1}^q (X_{ij} - \bar{X}_{i.})^2 / (q - 1)$$

$$CV_i = \frac{s_i}{\bar{X}_i} \times 100$$

The stability method employed was the genotype grouping technique of Francis and Kannenberg (1978), which groups genotypes on the basis of their mean yields and their coefficients of variation relative to the grand mean and average  $CV_i$ . (Groups: I high yield, small variation; II high yield, large variation; III low yield, small variation; IV low yield, large variation.)

### 3.2.5 Wricke's Ecovalence ( $W_i$ )

Wricke's (1962, 1964) characterized the idea of ecovalence as the contribution of every genotype to the Genotype x Environment interaction (GEI) sum of square. The ecovalence ( $W_i$ ) or stability of the  $i^{th}$  genotype is its interaction with the environments, squared and summed across environments, and express as:

$$W_i = \sum_{j=1}^e [\bar{Y}_{ij} - \bar{Y}_i - \bar{Y}_j - \bar{Y}_{..}]^2$$

Where,  $Y_{ij}$  is the mean execution of genotypes  $i^{th}$  genotype in the  $j^{th}$  environment and  $Y_i$  and  $Y_j$  are the genotype and environment mean deviation separately, and  $Y_{..}$  is the general mean. For this reason, genotypes with a low  $W_i$  value have smaller deviations from the mean across environments and are thus more stable.

### 3.2.6 Finlay and Wilkinson's joint regression analysis ( $b_i$ )

Finlay and Wilkinson (1963) defined a genotype with  $b_i = 0$  as stable. One the genotype x environment interaction in usual analysis of variance is found significant, next by taking genotype means of any genotype at different environments as dependent variable and environment means as independent variable one can frame regression equations for different genotypes on environmental means. Thus, the sum of squares due to interactions is partitioned in to two components viz. sum of square due to regression and deviation from regression ( $b_i$ ).

Let there be  $i$  ( $i=1,2,\dots v$ ) number of genotypes to be tested in  $j$  ( $j= 1,2,\dots s$ ) number of environment, then

$$\bar{g}_i = \frac{1}{s} \sum_{j=1}^s \bar{y}_{ij} = \text{Mean of } i^{th} \text{ genotype}$$

$$\bar{e}_j = \frac{1}{v} \sum_{i=1}^v \bar{y}_{ij} = \text{Mean of } j^{th} \text{ environment}$$

$b_i$  = regression coefficient of  $i^{th}$  genotype on environmental means

$$b_i = \frac{\sum_{i=1}^v \sum_{j=1}^s \bar{y}_{ij} \times \bar{e}_j}{\sum_j (\bar{e}_j)^2} = \frac{Cov(\bar{y}_{ij}, \bar{e}_j)}{Var(\bar{e}_j)}$$

Where,  $\bar{y}_{ij}$  is the mean response of  $i^{th}$  genotype in  $j^{th}$  environment. Where,  $(\bar{g}_i)$  is the mean of the  $i^{th}$  genotype and  $b_i$  is the regression coefficient of the  $i^{th}$  genotypes on environmental means. According to Finlay and Wilkinson model, the regression coefficient is the stability parameter. Decision with respect to stability and suitability of different genotypes under different is taken on the basis of the following guidelines.

### 3.2.7 Lin and Binns cultivar performance measure ( $P_i$ )

Lin and Binns (1988) characterized the prevalence measure ( $P_i$ ) of the  $i^{th}$  test genotypes as the MS of distance between the  $i^{th}$  test genotype and the maximum response as

$$P_i = \sum_{j=1}^n (X_{ij} - M_j)^2 / 2n$$

$$P_i = \frac{[n(\bar{X}_i - \bar{M})^2 + (\sum_{j=1}^n (X_{ij} - \bar{X}_i - M_j + \bar{M}))^2]}{2n}$$

Where,  $\bar{X}_i = \sum_{j=1}^n \frac{X_{ij}}{n}$

And  $\bar{M} = \sum_{j=1}^n \frac{M_j}{n}$

Where,  $X_{ij}$  is the average response of the  $i^{th}$  genotype in the  $j^{th}$  environment,  $\bar{X}_i$  is the mean deviation of  $i^{th}$  genotype,  $M_j$  is the genotype with maximum response among all genotypes in the  $j^{th}$  environment, and  $n$  is the number of environment. The smaller the value of  $P_i$ , the less is the distance to the genotype with most extreme yield and the better the genotype.

### 3.2.8 Eberhart & Russell's joint regression analysis

In order to improve the method of assessing stability through the method of Finlay and Wilkinson, in the year 1966, Eberhart and Russell proposed a model with the following modifications additions:

- (a) Instead of using environment al mean, an index called environmental index called

environmental index was formulated for each and every environment.

- (b) A new parameter in the form of non-linear response was introduced in the model. As a result the variance due to environment and Genotype x Environment Interaction (GEI) were further partitioned due to linear and deviation from linearity components.

Let there be  $t$  genotypes whose performance are to be tested in  $l$  environments.

Then according to this model:

$$Y_{ij} = \mu_i + \beta_i E_j + \delta_{ij} \quad (i= 1,2,\dots,t) \text{ and } (j= 1,2,\dots,l)$$

Where,  $Y_{ij}$  = Mean of  $i^{th}$  variety in  $j^{th}$  situation

$\mu_i$  = Mean of the variety over all the situation

$\beta_i$  = Regression coefficient  $i^{th}$  variety on the environmental indices

$E_j$  = Environmental index for  $j^{th}$  situation

$\delta_{ij}$  = Deviation of the regression of  $i^{th}$  variety on the environmental indices.

Once the G x E Interaction effect becomes significant then comes the question of using suitable stability model. Before the analysis of the stability parameter, a parameter called environmental index is required to be worked out.

The Environmental Index is defined as the deviation of the average performance of all the varieties at a given environment from the overall average performance. That is,

$$E_j = \frac{\sum_{i=1}^t Y_{ij}}{t} - \frac{\sum_{i=1}^t \sum_{j=1}^l Y_{ij}}{tl} \text{ or } \sum_{j=1}^l E_j = 0$$

The environmental index is a type of arrangement to measure the performances of different environments overall the genotypes and accordingly the environments can be ranked also. According to Eberhart and Russell model there are two stability parameters viz. (i) regression coefficient and (ii) the mean squared deviation from the regression.



- (i) The regression coefficient ( $b_i$ ) is the regression of the performance of every genotype under various environments on environmental average over all the genotypes and is estimated as

$$b_i = \frac{\sum_{j=1}^l Y_{ij} E_j}{\sum_{j=1}^l E_j^2}$$

where,  $\sum_{j=1}^l Y_{ij} E_j$  is the sum of products of average performance of  $j$ th location and  $j$ th environmental index, and  $\sum_{j=1}^l E_j^2$  is the sum of square of due to environmental index.

- (ii) The mean square deviation  $S_{di}^2$  from the regression is given as

$$S_{di}^2 = \frac{\sum_{j=1}^l \delta_{ij}^2}{(l-2)} - \frac{S_e^2}{r}$$

$$\text{Where, } \sum_{j=1}^l \delta_{ij}^2 = \left[ \sum_{j=1}^l Y_{ij}^2 - \frac{Y_{i..}^2}{t} \right] - \frac{\left( \sum_{j=1}^l Y_{ij} E_j \right)^2}{\sum_{j=1}^l E_j^2}$$

And  $S_e^2$  is the estimate of pooled error.

Eberhart and Russell (1966) proposed pooling the sum of squares for conditions and G x E Interaction and partitioning it into a linear effect between situations (with 1 df), a direct impact for genotype x environment (with  $E-2$  df). In actuality the remaining mean squares from the regression model across situations is utilized as an index of stability, and a stable genotype is one in which the deviation from regression mean squares ( $S_{di}^2$ ) is small.

$$S_{di}^2 = \frac{1}{E-2} \left[ E_j (X_{ij} - \bar{X}_i - \bar{X}_{.j} + \bar{X}_{..})^2 - (b_i - 1)^2 E_j (\bar{X}_{.j} - \bar{X}_{..})^2 \right]$$

**Table 3.1 Stability parameter from Eberhart & Russell regression**

| S.N. | Means                 | Regression coefficient (b <sub>i</sub> ) | $S_{di}^2$  | Inference  |
|------|-----------------------|--|-------------|--|
| 1    | $\bar{g}_i > \bar{y}$ | $b_i = 1$                                | Non-Sign.   | Genotype is stable for all environment                                   |
| 2    | $\bar{g}_i > \bar{y}$ | $b_i > 1$                                | Do          | Genotype is above average stable and adapted for rich environment        |
| 3    | $\bar{g}_i > \bar{y}$ | $b_i < 1$                                | Do          | Genotype is stable and adapted for poor environment                      |
| 4    | $\bar{g}_i > \bar{y}$ | $b_i = 1$                                | Significant | Genotype is average responsive and less stable for all environment       |
| 5    | $\bar{g}_i < \bar{y}$ | $b_i = 1$                                | Significant | Genotype is below average responsive and less stable for all environment |
| 6    | $\bar{g}_i < \bar{y}$ | $b_i < 1$                                | Significant | Genotype is unstable   |

### 3.2.9 Perkins and Jinks' Model (1968)

An attempt to improve the stability model Eberhart and Russell opined that G x E Interaction is more important from stability point of view. As such they proposed to regress G x E Interaction on environmental indices rather than the mean performances of genotypes over the environments ( $Y_{ij}$ ). They proposed the following model:

$$Y_{ij} = \mu + a_i + e_j + g_{ij} + \varepsilon_{ij}, i = 1, 2, \dots, t \text{ and } j = 1, 2, \dots, l$$

Where,  $Y_{ij}$  = mean effect of  $i^{\text{th}}$  genotype in  $j^{\text{th}}$  environment

$$\mu = \frac{1}{sxt} \sum_j Y_{ij} = \text{Mean of all genotypes over the environment}$$

$$a_i = \bar{Y}_i - \mu = \text{Additive genotype effects of the } i^{\text{th}} \text{ genotype}$$

$$e_j = \bar{Y}_j - \mu = \text{Additive effects due to } j^{\text{th}} \text{ environment}$$

$$g_{ij} = Y_{ij} - \mu - a_i - e_j = \text{Interaction effect of } i^{\text{th}} \text{ genotype in } j^{\text{th}} \text{ environment}$$

$\varepsilon_{ij}$  = Error associated with  $i^{th}$  genotype in  $j^{th}$  environment

Again,

$$g_{ij} = \beta_i e_j + \delta_{ij}$$

Where,  $\beta_i$  = Regression coefficient  $i^{th}$  variety on the environmental indices

$\delta_{ij}$  = Deviation of the regression of  $i^{th}$  variety on the environmental indices

Thus the Perkins and Jinks' Model turn out to be

$$\begin{aligned} Y_{ij} &= \mu + a_i + e_j + g_{ij} + \varepsilon_{ij} \\ &= \mu + a_i + e_j + \beta_i e_j + \delta_{ij} + \varepsilon_{ij} \\ &= \mu + a_i + (1 + \beta_i) e_j + \delta_{ij} + \varepsilon_{ij} \end{aligned}$$

So the basic structure of the model remains the same, even the deviation from regression. But the regression coefficient  $b_i$  in Eberhart-Russell model becomes  $b_i = (1 + \beta_i)$ .

### 3.2.10 Principal component analysis

Principal component analysis (PCA) is the most often utilized multivariate technique (Crossa, 1990; Purchase, 1997). Its point is to change the information from one set of coordinate axes to another, which preserves, however much as could reasonably be expected, the original configuration of the arrangement of focuses and thinks the greater part of the information structure in the first principal component axis.

### 3.2.11 Principal coordinates analysis

Principal coordinate analysis is a generalization of the PCA analysis where any proportion of similitude between individuals can be utilized' this kind of analysis was first utilized by Gower (1996). Its destinations and restrictions are like those of PCA, and furthermore has the following advantages as pointed out by Crossa (1990); (1) it is reliable when utilized for information that incorporate very low or high yielding locales; (2) it doesn't depend on the

arrangement of genotypes incorporated the analysis; and (3) it is easy to distinguish stable varieties from the sequence of graphic displays.

### **3.2.12 Additive main effects and multiplicative interaction (AMMI)**

The additive main effect and multiplicative interaction (AMMI) technique incorporates analysis of fluctuation and principal components analysis into a brought together methodology (Gauch, 1988). The three conventional models, analysis of variance (ANOVA) neglects to recognize a significant interaction component, principal component analysis (PCA) neglects to distinguish and separate the significant genotype and environment main effects, linear regression models account for only a small portion of the interaction sum of squares Zobel *et al.* (1988).

The AMMI technique is utilized for three primary purposes. The first is model judgments, AMMI is more proper in the initial statistical analysis of yield preliminaries, since it gives a scientific device of diagnosing different models as sub situations when these are better for particular data sets (Gauch, 1988). furthermore, AMMI explains the G x E Interaction. AMMI sum up patterns and relationship of genotypes and environments (Zobel *et al.*, 1988; Crossa *et al.*, 1990). The third use is to improve the precision of yield estimates. Gains have been obtained in the accuracy of yield estimates that are equivalent to increasing the number of replicates by a factor of two to five (Zobel *et al.*, 1988; Crossa *et al.*, 1990). Such gains might be utilized to decrease testing cost by diminishing the number of replications, to remember more treatments in the analyses, or to improve efficiency in choosing the best genotypes.

The AMMI model consolidates the analysis of variance for the genotype and environment main effects with principal component analysis of the genotype environment interaction. It has demonstrated valuable for understanding complex G x E Interaction. The

outcome can be graphed in a helpful biplot that show both fundamental and interaction effects for both the genotypes and environments.

AMMI consolidates analysis of variance (ANOVA) into a single model with additive and multiplicative parameters.

The model equation is:

$$Y_{ij} = \mu + G_i + E_j + \sum_{k=1}^n \lambda_k \alpha_{ik} \gamma_{jk} + e_{ij} \dots \dots \dots$$

Where  $Y_{ij}$  is the yield of the  $i$ th genotype in the  $j$ th environment;  $\mu$  is the grand mean;  $G_i$  and  $E_j$  are the genotype and environment deviations from the grand mean, separately;  $\lambda_k$  is the eigen value of the PCA analysis axis  $k$ ;  $\alpha_{ik}$  and  $\gamma_{jk}$  are the genotype and environment principal component scores for axis  $k$ ;  $n$  is the number of principal components retained in the model and  $e_{ij}$  is the error term.

The association is clarified as a bi-plot show where, PCA scores are plotted against one another and it gives visual assessment and understanding of the G x E Interaction segments. Incorporating bi-plot show and genotypic stability statistics enable genotypes to be grouped dependent on similitude of execution across diverse environments.

### 3.2.13 The AMMI stability value (ASV)

The AMMI model doesn't make arrangement for a particular stability measure to be resolved, such a measure is fundamental so as to rank genotypes in term of stability, the following measure was proposed by Purchase (1997):

*AMMI Stability Value (ASV)*

$$= \sqrt{\left[ \frac{IPCA1SumofSquares}{IPCA2SumofSquares} (IPCA1)score \right]^2 + [IPCA2score]^2}$$

Essentially is the ASV is the good ways from zero out of a two dissipate gram of IPCA1 (Interaction Principal Component Analysis axis 1) score against IPCA2 scores. Since the proportional difference between IPCA1 and IPCA2 scores to make up for relative commitment of IPCA1 and IPCA2 total  $G \times E$  aggregate of square.

### **3.2.14 GGE bi-plot analysis (Genotype + Genotype by Environment)**

It refers to a bi plot that shows the G and GE of a genotype-by-environment data. The key property of a GGE bi plot is that it depends on Tester focused information, whereby the environment fundamental impacts (E) are expelled, and the passage primary impact (G) and the section by interaction (GE) are retained and combined. In this way, a bi plot dependent on tester entered data contains just G+GE, abbreviated as GGE. In GGE-Bi plot analysis, test location evaluation is conducted graphically (Yan 2001). Test areas are assessed by characterizing three parameters: the capacity to segregate between genotypes (separation capacity), the capacity to speak to the objective district (representativeness), and the bi plot good ways from a perfect area (desirability index). The discrimination ability depends on various factors which are either static (or indigenous such as soil type), or dynamic (such as pest pressure). A representative location suggests that varieties selected in that area would have high probability to also perform well in different areas of similar locale. Test areas are at long last evaluated by their "distance" from a perfect, which is intended to be located on the average test-area axis and with the longest vector of all test-areas on the GGE bi plot (Yan 2001). Consequently, the separation capacity of a test area is estimated by the length of its vector on the bi plot; the representativeness is estimated by the cosine of the point between the test location and the "average" area; and the "distance" from an ideal location is the product of the segregation capacity and representativeness (Yan and Holland 2010). The bi-plot technique began with Gabriel (1971), and its utilization hence

extended by Kempton (1984) and Zobel et al., (1988). The broad handiness of GGE bi-plot, where  $G = \text{Genotype} + G \times E = \text{Genotype by environment effect}$ , has as of late been explained (Yan, 2001). GGE bi-plot analysis additionally used to produce diagrams appearing; comparison of situations to perfect condition (Yan and Kang, 2003); “which-won-where” pattern; and environment vectors. The angles between environment vectors were utilized to judge correlations (similarities/dissimilarities) between pairs of environments (Yan and Kang, 2003). These angles make GGE bi-plot a most extensive device in quantitative genetics and varietal stability.

### **3.2.15 Non parametric stability measures**

Nonparametric measures for phenotypic stability dependent on ranks give a helpful option in contrast to parametric measures present utilized which are depend on total information. For a two-way dataset with ‘ $k$ ’ genotypes and ‘ $n$ ’ environments, it was denoted the phenotypic estimation of  $i^{\text{th}}$  genotype in  $j^{\text{th}}$  environment as  $x_{ij}$ , where  $i=1,2,\dots,k$  ,  $j=1,2,\dots,n$  ,  $r_{ij}$  as the rank of the  $i^{\text{th}}$  genotype in the  $j^{\text{th}}$  environment, and  $\overline{r_{ij}}$  as the mean rank over all environments for the  $i^{\text{th}}$  genotype.

#### **3.2.15.1 Huehn’s nonparametric stability statistics**

Huehn (1979) and Nassar and Huehn (1987) proposed six nonparametric methods for assessing GEI and stability analysis. They were depended on ranks of genotypes inside environment. Genotypes with comparable ranking across environments are delegated generally stable. Statistics dependent on yield ranks of genotypes in every environment were communicated as follows:

**(a) Mean of the absolute rank differences ( $S_i^{(1)}$ ) of a genotype**

$$S_i^{(1)} = \frac{2 \sum_{j=1}^{q-1} \sum_{j'=j+1}^q |r_{ij} - r_{ij'}|}{q(q-1)}$$

Where  $\bar{r}_i$  = mean of ranks over environments

$r_{ij}$  = Ranks of genotypes in each environment based on ( $Y_{ij} - \bar{Y}_i + \bar{Y}$ ), rank are assigned from lowest to highest

q = number of environments

**(b) Variance among the ranks over the q environments ( $S_i^{(2)}$ )**

$$S_i^{(2)} = \frac{\sum_{j=1}^q (r_{ij} - \bar{r}_i)^2}{(q-1)}$$

Where,  $\bar{r}_i$  = mean of ranks over environments

$r_{ij}$  = Ranks of genotypes in each environment based on ( $Y_{ij} - \bar{Y}_i + \bar{Y}$ ), ranks are assigned from lowest to highest

q = number of environments

**(c) Mean of the absolute rank differences ( $S_i^{(3)}$ ) of a genotype**

$$S_i^{(3)} = \frac{\sum_{j=1}^q |r_{ij} - \bar{r}_i|}{\bar{r}_i}$$

Where,  $\bar{r}_i$  = mean of ranks over environments



$r_{ij}$  = Ranks of  $i^{th}$  genotypes in  $j^{th}$  environment based on mean yield

Ranks are assigned from lowest to highest

q = number of environments

**(d) Variance among the ranks over the  $q$  environments ( $S_i^{(6)}$ )**

$$S_i^{(6)} = \frac{\sum_{j=1}^q (r_{ij} - \bar{r}_i)^2}{\bar{r}_i}$$

### 3.2.15 Spearman's rank correlation

To measurably think about between the above stability analysis procedures, Spearman's coefficient of rank correlation ( $r_s$ ) was resolved (Steel and Torrie, 1980). Consider, n genotypes are organized in a similar after request to two stability parameters  $X_i$  demonstrates the ranking order (or number) of the  $i^{th}$  genotype for the first parameter,  $Y_i$ , demonstrates the ranking order of the  $i^{th}$  genotype of the second parameter, then  $d_i = X_i - Y_i$  ( $i = 1, 2, 3, \dots, n$ ) and Spearman's rank correlation coefficient ( $r_s$ ) can be portrayed as:

$$r_s = 1 - \frac{6 \sum d_i^2}{n(n^2 - 1)}$$

The importance of  $r_s$  was tried by methods for Student's  $t$  test (Steel and Torrie, 1980) where:

$$t = \frac{r_s \sqrt{n-2}}{\sqrt{1-r_s^2}}$$

With  $n-2$  degrees of freedom. If  $t \geq t_{(0.01;n-2)}$ , the invalid theory is disposed of and  $r_s$  is depicted as highly significant.

## CHAPTER-IV RESULT AND DISCUSSION

The present investigation entitled “Assessment of Parametric and Non Parametric methods for selecting stable and adaptable soybean genotypes in Multi environments” was conducted at four locations for ten genotypes for the year 2017-18.

The Results is presented under the following heads:

### 4.1 Parametric Method

### 4.2 Non Parametric Method

#### 4.1 Parametric Method

##### 4.1.1 Analysis of variance and estimation of change segments

The general performances of genotypes dependent on the mean grain yield environments are presented in Table 4.1 Yield performance are ranked and mean yield were presented in kg/ha.

**Table 4.1: Mean yield (kg/ha) of 10 soybean genotypes over 4 test environments**

| Genotype     | Mean yield (Kg / ha) | Rank |
|--------------|----------------------|------|
| CG Soya-1(c) | 1067.17              | 5    |
| JS 93-05 (c) | 720.08               | 9    |
| JS 97-52 (c) | 848.92               | 7    |
| RSC 10-52    | 1153.92              | 2    |
| RSC 10-71    | 1129.00              | 4    |
| RSC 11-02    | 1483.25              | 1    |
| RSC 11-03    | 1141.83              | 3    |
| RSC 11-04    | 599.92               | 10   |
| RSC 11-05    | 740.33               | 8    |
| RSC 11-06    | 958.17               | 6    |

The first ranked genotypes for mean yield were recorded RSC 11-02 (1483.25) with RSC 10-52 (1153.92) ranked second and RSC 10-71 (1141.83) ranked third. The genotypes with the lowest mean yield was RSC 11-04 (599.92) and JS 93-05(c) (720.08). Means across environments are sufficient indicators of genotypic execution just without G x E. If G x E is present, across environments doesn't tell us how genotypes vary in relative execution over environments.

**Table 4.2 : Joined ANOVA for grain yield and the rate sum of square of the 10 genotypes tested at 4 location environments over a time of year 2017-18**

| Source    | DF | Sum. Sq  | Mean Sq | F value | Significance |
|-----------|----|----------|---------|---------|--------------|
| ENV       | 3  | 1600772  | 533591  | 25.31   | 0.000195     |
| REP (ENV) | 8  | 168612   | 21076   | 3.56    | 0.001577     |
| GEN       | 9  | 75177219 | 835247  | 141.1   | 0.00001      |
| GEN X ENV | 27 | 3715157  | 1375598 | 23.24   | 0.0001       |
| Residuals | 72 | 426154   | 5919    |         |              |

#### **4.1.2: Francis and Kannenberg's coefficient of variability ( $CV_i\%$ )**

On the basis of yield stability a study were made by the mean analysis and assess the performance and stability concurrently. It introduced by simple graphical approach. For all genotype, it measures the performance CV (%) all over the environment conditions in different environment and mean yield against plotted against. All genotype is being characterizes in a group rather than the individual genotype. It was found that the most desirable approach in all is high and small variation group of genotypes. Genotype which is high yield performance and consistent low is most stable one. RSC 11-05, RSC 11-03 and RSC 11-02 are stable genotype fall into the high yield and low variation group.

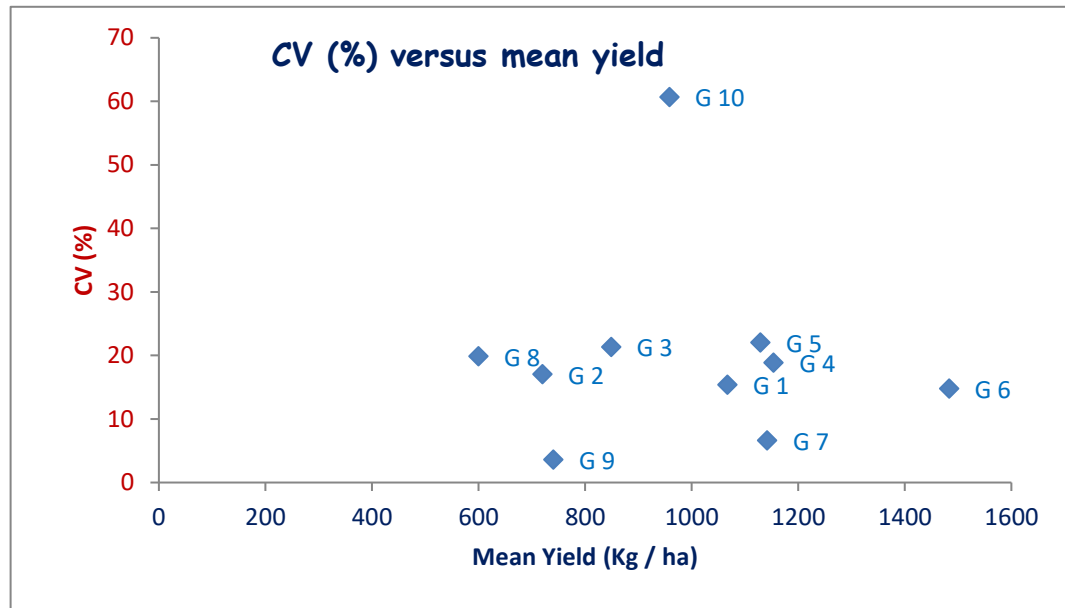
The soybean growing areas of Chhattisgarh and their mean yield ranking and CV of the 10<sup>th</sup> genotype were evaluated at four location represent in Table 4.3 in the year 2017-18.

RSC 11-05 with a CV of 3.58 % followed by RSC 11-03 with a CV of 6.59 and RSC 11-02 with a CV of 14.79 are the genotypes with lowest coefficient of variation across the location.

**Table4.3: Francis and Kannenberg's coefficient of variability  $CV_i(\%)$**

| Code | Genotype     | Mean Yield<br>(Kg / ha) | Rank | $CV_i(\%)$ | Rank |
|------|--------------|-------------------------|------|------------|------|
| G1   | CG Soya-1(c) | 1067.17                 | 5    | 15.38      | 4    |
| G2   | JS 93-05(c)  | 720.08                  | 9    | 17.02      | 5    |
| G3   | JS 97-52(c)  | 848.92                  | 7    | 21.32      | 8    |
| G4   | RSC 10-52    | 1153.92                 | 2    | 18.87      | 6    |
| G5   | RSC 10-71    | 1129                    | 4    | 22.05      | 9    |
| G6   | RSC 11-02    | 1483.25                 | 1    | 14.79      | 3    |
| G7   | RSC 11-03    | 1141.83                 | 3    | 6.59       | 2    |
| G8   | RSC 11-04    | 599.92                  | 10   | 19.85      | 7    |
| G9   | RSC 11-05    | 740.33                  | 8    | 3.58       | 1    |
| G10  | RSC 11-06    | 958.17                  | 6    | 60.65      | 10   |

**Figure 4.1: Mean yield (kg/ha) plotted against CV % from information on 10 genotypes and 4 areas over a time of one year**



#### 4.1.3 Lin &Binn's cultivar performance measure ( $P_i$ )

From this analysis, the most stable genotype ranked first for  $P_i$  was RSC 11-05 (576.7) followed by RSC 11-03 (7411.90) ranked second. Others genotype with low  $P_i$  values and high positioning for mean yield was JS 93-05(c) (13232.10) and RSC 11-04 (15223.10). The positions of the  $P_i$  measure and mean yield are in understanding (Table 4.4) and show that the  $P_i$  measure is more a sign of execution and not really an indication of stability. The most unstable genotype with high  $P_i$  values were RSC 11-06 (105582.4), RSC 10-71 (91820.30), RSC 10-52 (53548.5) and RSC 11-02 (48102.1).

**Table 4.4: Lin & Binn's cultivar performance measure ( $P_i$ ) for soybean yield across the environments**

| Code | Genotype     | $P_i$    | Rank | Mean Yield<br>(Kg / ha) | Rank |
|------|--------------|----------|------|-------------------------|------|
| G1   | CG Soya-1(c) | 34058.7  | 5    | 1067.17                 | 5    |
| G2   | JS 93-05(c)  | 13232.1  | 3    | 720.08                  | 9    |
| G3   | JS 97-52(c)  | 34916.4  | 6    | 848.92                  | 7    |
| G4   | RSC 10-52    | 53548.5  | 8    | 1153.92                 | 2    |
| G5   | RSC 10-71    | 91820.3  | 9    | 1129                    | 4    |
| G6   | RSC 11-02    | 48102.1  | 7    | 1483.25                 | 1    |
| G7   | RSC 11-03    | 7411.9   | 2    | 1141.83                 | 3    |
| G8   | RSC 11-04    | 15223.1  | 4    | 599.92                  | 10   |
| G9   | RSC 11-05    | 576.7    | 1    | 740.33                  | 8    |
| G10  | RSC 11-06    | 105582.4 | 10   | 958.17                  | 6    |

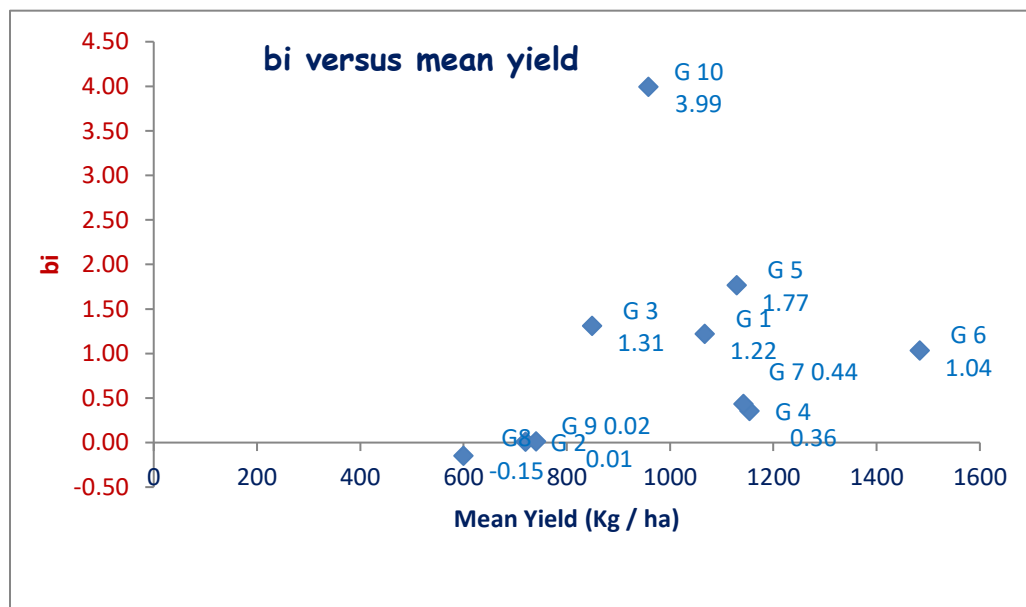
#### 4.1.4 Finlay and Wilkinson's joint regression analysis ( $b_i$ )

As indicated by Finlay and Wilkinson (1963), (Table 4.5) regression coefficients approximating to 1.0 show average stability, yet should consistently be related and deciphered with the genotype mean yield respect decide adaptability. At the point when the regression coefficients are approximating to 1.0 and are related with high yield mean, genotypes are adjusted to all environments. When related with low mean yields, genotypes are ineffectively adjusted to all environments. Regression coefficients above 1.0 demonstrate genotypes with expanding affectability to environmental change, showing below average stability and great specific adaptability to high yielding conditions. Regression coefficients diminishing below 1.0 give a proportion of greater resistance to ecological change, having better than expected dependability however demonstrating more explicit adjusted to low yielding conditions.

**Table 4.5: Finlay and Wilkinson's joint regression analysis ( $b_i$ ) for soybean yield across the environments**

| Code | Genotype     | Mean Yield<br>(Kg / ha) | Rank | $b_i$ | Interpretation                                      |
|------|--------------|-------------------------|------|-------|---|
| G1   | CG Soya-1(c) | 1067.2                  | 5    | 1.22  | Above average stable for, good for rich environment |
| G2   | JS 93-05(c)  | 720.1                   | 9    | 0.01  | Stable good, for environment                        |
| G3   | JS 97-52(c)  | 848.9                   | 7    | 1.31  | Above average stable for, good for rich environment |
| G4   | RSC 10-52    | 1153.9                  | 2    | 0.36  | Stable good, for poor environment                   |
| G5   | RSC 10-71    | 1129.00                 | 4    | 1.77  | Above average stable, good for rich environment     |
| G6   | RSC 11-02    | 1483.3                  | 1    | 1.04  | Above average stable for, good for rich environment |
| G7   | RSC 11-03    | 1141.8                  | 3    | 0.44  | Stable good, for poor environment                   |
| G8   | RSC 11-04    | 599.9                   | 10   | -0.15 | Stable good, for poor environment                   |
| G9   | RSC 11-05    | 740.3                   | 8    | 0.02  | Stable good, for poor environment                   |
| G10  | RSC 11-06    | 958.2                   | 6    | 3.99  | Above average stable for, good for rich environment |

**Figure 4.2 : Regression coefficient ( $b_i$ ) plotted against the mean yield**



#### 4.1.5 Wricke's eco valence analysis

Wricke's eco valence (1962) is an elective technique that is frequently used to determine stability of genotypes dependent on the  $G \times E$  Interaction impacts. It demonstrates the contribution of each genotype to the  $G \times E$  Interaction. The cultivars with the most minimal ecovalence contributed the least to the  $G \times E$  Interaction and along these lines more stable.

The most stable genotype as per the eco valence method of Wricke (1962) was CG Soya-1(c) (3854.93), JS 97-52(c) (11771.36), RSC 11-03(23819.10). These genotypes were not the best positioned for mean yield, being 5<sup>th</sup>, 7<sup>th</sup>, 3<sup>rd</sup> respectively. The most unstable hybrids according the eco valence method, higher  $W_i$  values Wricke's eco valence value for 10 the genotype at 4 environments. Were RSC 10-52 (157658.96), RSC 11-04 (111687.11) and RSC 11-05 (111678.11) these hybrids were positioned 2<sup>nd</sup>, 8<sup>th</sup>, 10<sup>th</sup> for mean yield respectively.

**Table 4.6 :Wricke's ecovalence (  $W_i$  ) analysis for soybean yield across the environments**

| Code | Genotype     | $W_i$     | Rank | Mean yield<br>(Kg / ha) | Rank |
|------|--------------|-----------|------|-------------------------|------|
| G1   | CG Soya-1(c) | 3854.93   | 1    | 1067.2                  | 5    |
| G2   | JS 93-05(c)  | 97326.37  | 7    | 720.1                   | 9    |
| G3   | JS 97-52(c)  | 11771.36  | 2    | 848.9                   | 7    |
| G4   | RSC 10-52    | 157658.96 | 10   | 1153.9                  | 2    |
| G5   | RSC 10-71    | 50898.60  | 4    | 1129.00                 | 4    |
| G6   | RSC 11-02    | 87315.98  | 6    | 1483.3                  | 1    |
| G7   | RSC 11-03    | 23819.10  | 3    | 1141.8                  | 3    |
| G8   | RSC 11-04    | 111687.11 | 8    | 599.9                   | 10   |
| G9   | RSC 11-05    | 111687.11 | 9    | 740.3                   | 8    |
| G10  | RSC 11-06    | 53716.80  | 5    | 958.2                   | 6    |

#### 4.1.6 Eberhart and Russell's joint regression analysis

The pooled analysis of variance for soybean grain yield displayed significant differences among genotypes (G), environments (E) and G x E Interactions (Table 4.7). This showed that genotypes did not differ only genetically but also some of these exhibited differential response to variable environments. The results indicated that the presence of genotypic variability for grain yield and presence of genotype x environment interaction. The stability of genotypes is considered in three parameters i.e. high mean yield, regression coefficient ( $b_i$ ) and deviation from the regression ( $\overline{S_{di}^2}$ ). According to this model a stable variety has a high mean yield,  $b_i = 1$  i.e. non significant deviation from unity and  $\overline{S_{di}^2} = 0$  i.e. non significant deviation from linear regression.

Eberhart and Russell considered  $b_i$  as a measure of responsiveness and accordingly a genotype having the regression coefficient unity (i.e.  $b_i = 1$ ) is average responsive. A regression coefficient with less than unity means that the genotype is less responsive to environment. On the other hand, the regression coefficient is greater than unity for a genotype indicates high responsive of the genotype towards environmental factors. Similarly, deviation from linear regression, a stable genotype is one which has got  $\overline{S_{di}^2} = 0$  and genotype is less stable which has got  $\overline{S_{di}^2} \neq 0$ .

There are only four varieties namely G1 (CG Soya-1 (c)), G3 (JS 97-52 (c)), G7 (RSC 11-03), G9 (RSC 11-06) how's for deviation from regression is non significant, hence they are the only varieties to be considered for their stability and responsiveness.

The other varieties namely G2 (JS 93-05 (c)), G4 (RSC 10-52), G5 (RSC 11-71), G6 (RSC 11-02), G8 (RSC 11-04), G10 (RSC 11-06) are unstable varieties, as for as concern



varieties G1 (CG Soya-1(c)), and G3 (JS 97-52 (c)) are significant from  $b=0$  but non significant differently from  $b=1$ .

Hence this two varieties are stable varieties average responsive and suitable from all environments.

The varieties G7 (RSC 11-03) and G9 (RSC 11-05) have responses not significant different from  $b=0$ . Out of this G9 (RSC 11-05) is significant from  $b=1$  in the lower tell, hence G9 (RSC 11-05) may be said be low responsive suitable for unfavourable environments and the varieties G7 (RSC 11-03) is stable but with very poor environments.

**Table 4.7 : Analysis of Variance of Eberhart and Russell model for soybean yield across the environments**

| Source of variation | DF | Sum Sq     | Mean Sq   | F Value | Significance |
|---------------------|----|------------|-----------|---------|--------------|
| Genotype            | 9  | 2505739.80 | 278415.53 | 6.07    | 0.001        |
| Environment         | 3  | 533590.70  | 177863.57 | 3.87    | 0.05         |
| G X E               | 27 | 1238385.83 | 45866.14  | 7.74    | 0.001        |
| Env + G X E         | 30 | 1771976.53 | 59065.88  | -       | -            |
| Env (Linear)        | 1  | 533590.70  | 533590.70 | 21.01   | 0.001        |
| Env X Gen (Linear   | 9  | 730536.65  | 81170.74  | 3.20    | 0.005        |
| Pooled deviation    | 20 | 507849.18  | 25392.46  | 12.87   | 0.001        |
| G1                  | 2  | 1222.46    | 611.23    | 0.31    | 0.620        |
| G2                  | 2  | 45088.79   | 22544.40  | 11.43   | 0.001        |
| G3                  | 2  | 6622.54    | 3311.27   | 1.68    | 0.320        |
| G4                  | 2  | 135561.14  | 67780.57  | 34.36   | 0.001        |
| G5                  | 2  | 19611.63   | 9805.81   | 4.97    | 0.001        |
| G6                  | 2  | 87245.50   | 43622.75  | 22.11   | 0.001        |
| G7                  | 2  | 6849.98    | 3424.99   | 1.74    | 0.220        |
| G8                  | 2  | 41375.30   | 20687.65  | 10.49   | 0.001        |
| G9                  | 2  | 2099.11    | 1049.56   | 0.53    | 0.750        |
| G10                 | 2  | 162172.73  | 81086.36  | 41.10   | 0.001        |
| Pooler Error        | 72 | 426154.00  | 1972.93   |         |              |
| Total               | 39 | 4277716.33 |           |         |              |

**Table 4.8 :Eberhart and Russell's regression coefficient ( $b_i$ ) and deviation from regression ( $\bar{S}_{di}^2$ ) of soybean at across locations**

| Code | Genotype     | Mean yield (Kg/ha) | $\bar{S}_{di}^2$ | ( $b_i$ ) | SE ( $b_i$ ) | t Value<br>H0: b=0 | t Value<br>H0: b=1 |
|------|--------------|--------------------|------------------|-----------|--------------|--------------------|--------------------|
| G1   | CG Soya-1(c) | 1067.2             | 361.7NS          | 1.222NS   | 0.107        | 11.419**           | 2.075NS            |
| G2   | JS 93-05(c)  | 720.1              | 20571.4**        | 0.011NS   | 0.650        | 0.016NS            | ---                |
| G3   | JS 97-52(c)  | 848.9              | 1338.3NS         | 1.311NS   | 0.249        | 5.261**            | 1.247NS            |
| G4   | RSC 10-52    | 1153.9             | 65807.6**        | 0.356NS   | 1.127        | 0.316NS            | ---                |
| G5   | RSC 10-71    | 1129.0             | 7832.8**         | 1.766NS   | 0.429        | 4.119NS            | ---                |
| G6   | RSC 11-02    | 1483.3             | 41649.8**        | 1.036NS   | 0.904        | 1.146NS            | ---                |
| G7   | RSC 11-03    | 1141.8             | 1452.05NS        | 0.436NS   | 0.253        | 1.721NS            | ---                |
| G8   | RSC 11-04    | 599.9              | 18714.7**        | -0.148NS  | 0.623        | -0.238NS           | ---                |
| G9   | RSC 11-05    | 740.3              | 823.37NS         | 0.016**   | 0.140        | 0.117NS            | -7.013*            |
| G10  | RSC 11-06    | 958.2              | 79113.4**        | 3.994NS   | 1.233        | 3.240**            | ---                |

*Note : \*\* significance at 1 % level of significance*

#### **4.1.7 Perkins and Jinks' stability model (1968)**

Perkins and Jinks' in an attempt to improve the stability model of Eberhart and Russell opined that genotype-environment interaction is more important from stability point of view. As such they proposed to regress genotype x environmental interaction on environmental indices rather than the mean performances of genotypes over the environment ( $Y_{ij}$ ).

**Table 4.9: Analysis of Variance by Perkins and Jinks' Model for soybean**

| Source                               | DF  | Sum Sq     | Mean Sq  | F Value   | Sig.  |
|--------------------------------------|-----|------------|----------|-----------|-------|
| Lines (difference between genotypes) | 9   | 2505739.80 | 278415.5 | 2093350.0 | 0.001 |
| Environment (joint regression)       | 3   | 533590.6   | 177863.5 | 1337320.0 | 0.001 |
| Lines X Environment                  | 27  | 1238385.8  | 45866.14 | 344858.2  | 0.001 |
| Heterogeneity between regression     | 9   | 730536.6   | 81170.7  | 610306.0  | 0.001 |
| Remainder                            | 18  | 507849.1   | 28213.8  | 212133.0  | 0.001 |
| Error                                | 300 | 40.023     | 0.133    |           |       |

Perkins and Jinks shown results (Table 4.10) varieties of soybean RSC 11-04 (-1.14) and JS 95-05(c) (-0.98) getting 1<sup>st</sup> and 2<sup>nd</sup> rank for stable situations. Soybean varieties getting rank for lowest adaptability are RSC 10-71 (0.77) and RSC 11-06 (2.99) are 9<sup>th</sup> and 10<sup>th</sup> respectively.

**Table 4.10: Perkins and Jinks regression coefficient ( $b_i$ ) of soybean at across areas**

| Code | Varieties    | Mean yield (Kg/ha) | Rank | ( $b_i$ ) | Rank |
|------|--------------|--------------------|------|-----------|------|
| G1   | CG Soya-1(c) | 1067.2             | 5    | 0.22      | 7    |
| G2   | JS 93-05(c)  | 720.1              | 9    | -0.98     | 2    |
| G3   | JS 97-52(c)  | 848.9              | 7    | 0.31      | 8    |
| G4   | RSC 10-52    | 1153.9             | 2    | -0.64     | 4    |
| G5   | RSC 10-71    | 1129.0             | 4    | 0.77      | 9    |
| G6   | RSC 11-02    | 1483.3             | 1    | 0.036     | 6    |
| G7   | RSC 11-03    | 1141.8             | 3    | -0.56     | 5    |
| G8   | RSC 11-04    | 599.9              | 10   | -1.14     | 1    |
| G9   | RSC 11-05    | 740.3              | 8    | -0.97     | 3    |
| G10  | RSC 11-06    | 958.2              | 6    | 2.99      | 10   |

#### 4.1.8 The AMMI stability value (ASV)

The ASV is comparable with the methods of Shukla's and Wricke's which was described by (Purchase) 1997. In Chhattisgarh soybean genotypes is also suitable for study by this method.

Table 4.11 depict 10 genotypes which indicated its ASV with its ranking and the AMMI model IPCA 1 and IPCA 2 scores for each genotype.

Genotypes JS 97-52(c) (5.598484), CG Soya-1(c) (6.156094), RSC 11-03 (12.501843), RSC 11-02 (16.419619) and JS 97-05 (c) (18.147965), are the most stable genotypes analysed by the ASV ranking. RSC 11-06 (119.753488), RSC 10-52 (49.792962), RSC 11-04 (45.690164), and RSC 11-02 (16.419619) are the most unstable genotypes.

**Table 4.11: AMMI stability value (ASV) and ranking with the IPCA 1 & 2 scores for the 10 varieties**

| SN | Varieties    | Mean    | Rank | IPCA Score 1 | IPCA Score 2 | ASV        | Rank |
|----|--------------|---------|------|--------------|--------------|------------|------|
| 1  | CG Soya-1(c) | 1067.17 | 5    | -166.22      | 24.397       | 6.156094   | 2    |
| 2  | JS 93-05(c)  | 720.08  | 9    | 564.13       | -16.488      | 18.147965  | 5    |
| 3  | JS 97-52(c)  | 848.92  | 7    | 252.89       | 46.331       | 5.598484   | 1    |
| 4  | RSC 10-52    | 1153.92 | 2    | -329.24      | -363.40      | 49.792962  | 9    |
| 5  | RSC 10-71    | 1129.00 | 4    | -298.63      | 197.76       | 33.530375  | 7    |
| 6  | RSC 11-02    | 1483.25 | 1    | -1017.16     | -200.01      | 16.419619  | 4    |
| 7  | RSC 11-03    | 1141.83 | 3    | -286.89      | -98.515      | 12.501843  | 3    |
| 8  | RSC 11-04    | 599.92  | 10   | 799.91       | -227.37      | 45.690164  | 8    |
| 9  | RSC 11-05    | 740.33  | 8    | 514.15       | -160.47      | 31.980703  | 6    |
| 10 | RSC 11-06    | 958.17  | 6    | -32.929      | 797.78       | 119.753488 | 10   |

#### 4.1.9 Combined analysis of variance according to the best AMMI model

According to AMMI model, combined analysis of variance is presented for 10 genotypes in one year at 4 different location. AMMI model best fit for the data set that was analysed by the significant result in ANOVA analysis. The ANOVA demonstrated highly significant difference ( $P < 0.01$ ) for environments, genotypes and significantly genotype x environment interaction (GEI). IPCA 1 and IPCA2 axes were additionally exceptionally significant ( $P < 0.01$ ).

**Table 4.12: Combined analysis of variance (ANOVA) according to the AMMI 2 model for year 2017-18**

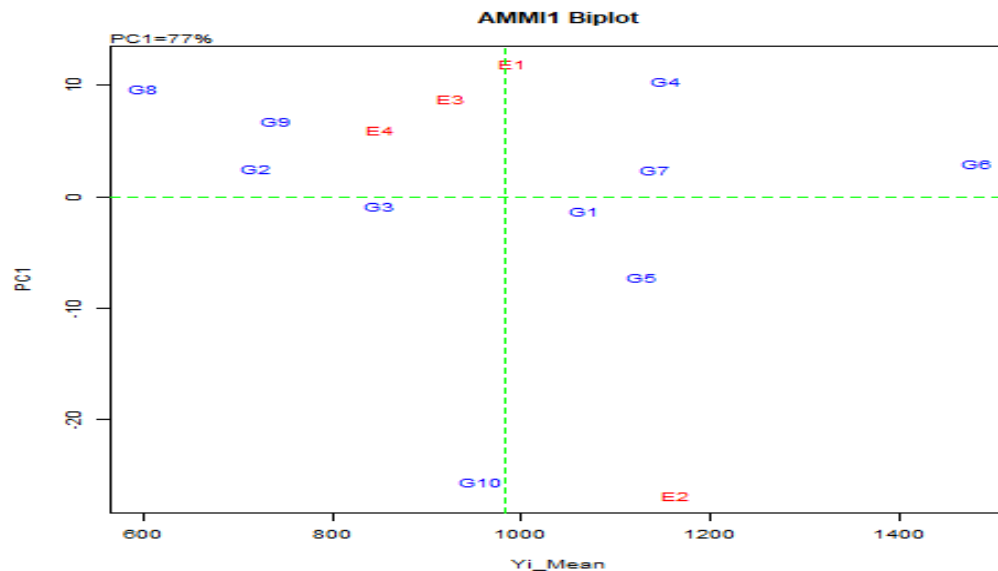
| Source          | DF | Sum Sq    | Mean Sq   | F value  | Pr(>F) |
|-----------------|----|-----------|-----------|----------|--------|
| Location        | 3  | 1600772   | 533591    | 25.3169  | 0.0001 |
| Rep within Env. | 8  | 168612    | 21076     | 3.5609   | 0.001  |
| Genotype        | 9  | 7517219   | 835247    | 141.1174 | 0.0002 |
| Genotype x Env. | 27 | 3715157   | 137598    | 23.2477  | 0.0002 |
| Residual        | 72 | 426154    | 5919      |          |        |
| IPCA 1          | 11 | 2861029.2 | 260093.56 | 45.22    | 0.0001 |
| IPCA 2          | 9  | 610773.4  | 67863.71  | 11.80    | 0.0001 |
| IPCA 3          | 7  | 243354.9  | 34764.99  | 6.04     | 0.0001 |

#### 4.1.10 The AMMI model

By plotting both the genotype and the environments on a similar diagram, the relationship between the genotype and the environments can be seen obviously. The IPCA scores of a genotype in the AMMI analysis are a sign of the stability of a genotype over conditions. The more prominent the IPCA scores, either positive or negative, as it is a relative value, the more explicitly adjusted a genotype is to sure conditions. The more IPCA scores evaluated to zero, the more stable the genotype to overall environments sampled. From the biplot, conditions are dispersed from lower yielding situations in quadrants I (upper left) and IV (base left) to the high yielding environments in quadrants II (upper right) and III (base right) (Fig.4.3). The high yielding conditions ordered by the AMMI 1 model are E1, and E2. The lower yielding environments were E3 and E4. Therefore, Adet was commonly arranged under high yielding wheat environment as compared to the three relatively classified under low yielding environments (Holeta, Kulumsa and Sinana). The genotypes grouped under favourable environments with above-average means were G1 (CG Soya-1(c)), G4 (RSC10-52), G5 (RSC 10-71), G6 (RSC 11-02), and G7 (RSC 11-03) among them G6 (RSC 11-02) and G7(RSC 11-03) is seen as more stable. Genotypes gathered under low yielding conditions are appeared at the lower left quadrant of the biplot which are G2(JS 93-05(c)), G3(JS 97-52(c)),G8(RSC 11-04),G9

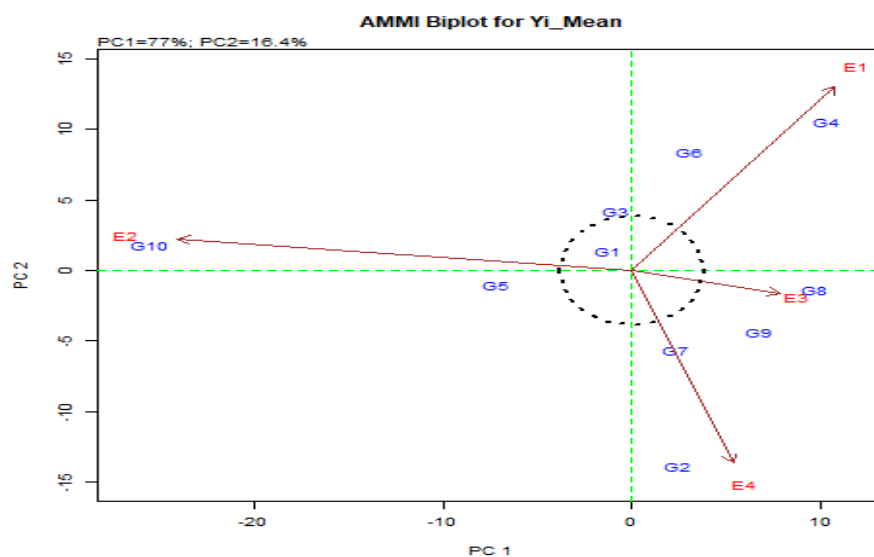
(RSC 11-05), and G10 (RSC 11-06) is the most unstable genotypes recognized by the AMMI model.

**Fig 4.3:AMMI model 2 bi plot for 10 soybean genotypes and 4 environments evaluated during 2017-18 Chhattisgarh**



**Fig 4.4: Plotted IPCA1 and IPCA2 score of soybean genotypes evaluated during 2017-18 in Chhattisgarh.**

In Figure 4.4 Genotype G2, G4, G8 and G10 are now an outlier (unstable) but to a lesser extent. G1 ,G3, G8 and G9 are demonstrating to be more stable, when plotting the IPCA 1 and IPCA 2 scores.



**Table 4.13: The IPCA 1 and IPCA 2 scores for the 10 genotypes, sorted on environmental mean yield, used in the study**

|    | <b>Genotype</b> | <b>Mean Yield<br/>(Kg / ha)</b> | <b>Rank</b> | <b>IPCA Score1</b> | <b>IPCAScore2</b> |
|----|-----------------|---------------------------------|-------------|--------------------|-------------------|
| 1  | CG Soya-1(c)    | 1067.17                         | 5           | -166.22            | 24.397            |
| 2  | JS 93-05(c)     | 720.08                          | 9           | 564.13             | -16.488           |
| 3  | JS 97-52(c)     | 848.92                          | 7           | 252.89             | 46.331            |
| 4  | RSC 10-52       | 1153.92                         | 2           | -329.24            | -363.40           |
| 5  | RSC 10-71       | 1129.00                         | 4           | -298.63            | 197.76            |
| 6  | RSC 11-02       | 1483.25                         | 1           | -1017.16           | -200.01           |
| 7  | RSC 11-03       | 1141.83                         | 3           | -286.89            | -98.515           |
| 8  | RSC 11-04       | 599.92                          | 10          | 799.91             | -227.37           |
| 9  | RSC 11-05       | 740.33                          | 8           | 514.15             | -160.47           |
| 10 | RSC 11-06       | 958.17                          | 6           | -32.929            | 797.78            |

**Table 4.14: IPCA 1 and IPCA 2 scores for the sorted on environmental mean yield and evaluated at 4 areas for year 2017-18**

| <b>Location</b> | <b>Code</b> | <b>Env. Mean</b> | <b>IPCA 1</b> | <b>IPCA 2</b> |
|-----------------|-------------|------------------|---------------|---------------|
| Bemetara        | E1          | 991.83           | -0.60         | -0.47         |
| Jagdapur        | E2          | 1165.2           | -0.59         | 0.80          |
| Kawardha        | E3          | 927.36           | -0.35         | -0.29         |
| Raipur          | E4          | 852.63           | -0.40         | -0.21         |



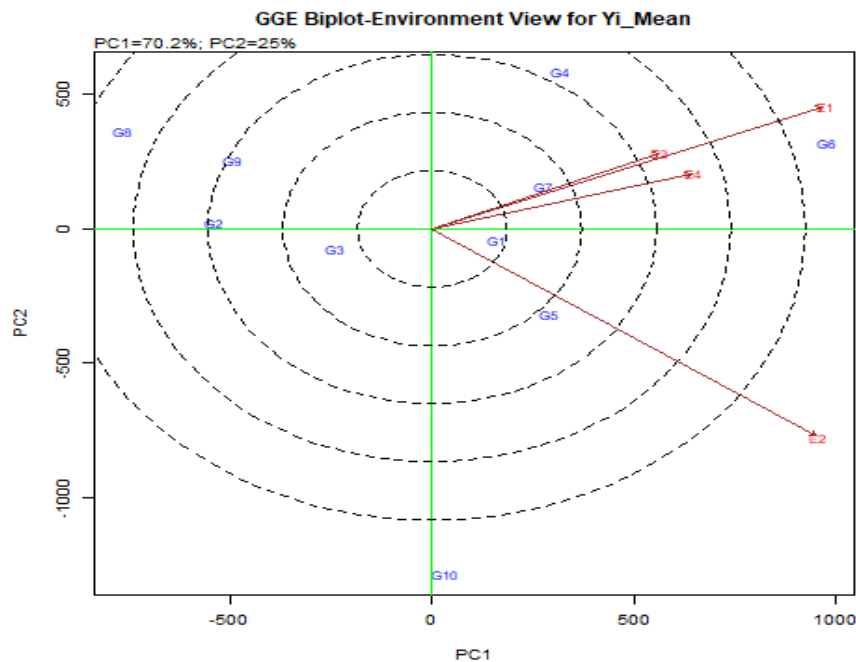
#### 4.1.11 Environment evaluation based on GGE bi-plot for soybean

##### 4.1.11 .1 Relationships among test environments

The smallest angle somewhere in the range of E3 and E4 environment suggests that the highest associations between them. The large angle somewhere in the range of E1 and E2 shows the poor association between these areas.

GGE bi-plot, which was depended on condition cantered scaling, was draw to evaluate the model of situations (Fig. 4.5). The vector perspective on the GGE bi-plot provided a summary of the between connections among the areas. The lines that associate the test environments to the bi-plot starting point called environment vectors. The cosine of the angle between the vectors of two conditions approximates the correlation between them. The separation between two environments measures their dissimilarity in discriminating the genotypes.

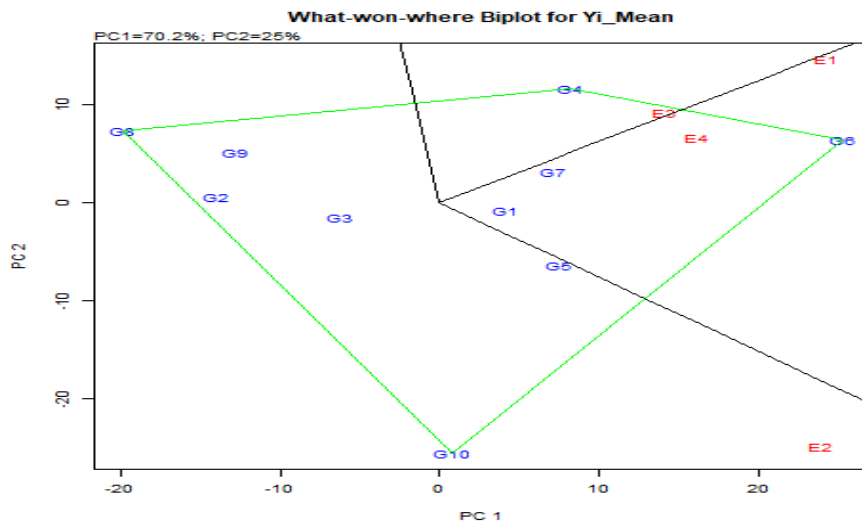
**Fig 4.5: GGE bi-plot relationship among environments of soybean genotypes.**



#### 4.1.11.2 Which Won Where GGE bi plot

The perpendicular lines were balance lines between adjacent genotypes on the polygon, which encourage visual comparison of them. Fig (4.6) Lines 1 are G3 (JS 97-52(c))-G4 (RSC 10-52) and lines 2 are perpendicular to side G4 (RSC 10-52) – G6 (RSC 11-02); line 3 is perpendicular to the side G6 (RSC 11-02)- G10 (RSC 11-06); line 4 is perpendicular to side G10 (RSC 11-06) – G8 (RSC 11-04). These 4 lines separate the bi-plot into 4 sectors, and the environment fall into 2 of them (Fig 4.6).

**Fig 4.6: Polygon view of the GGE bi plot based on symmetrical scaling for which won where for 10 genotypes and 4 areas**



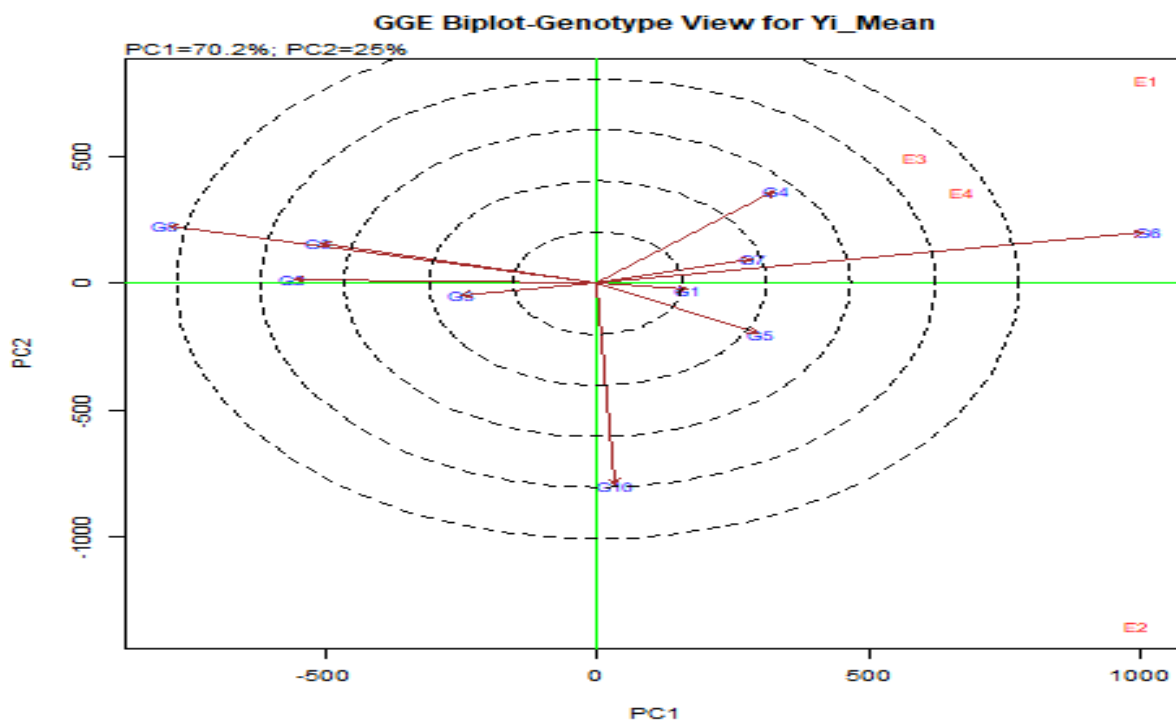
This bi-plot exceptionally and entirely utilized for mega-environment analysis based genetic correlation between environment and what-won-where pattern; utilized condition assessment dependent on their discriminating ability and representativeness; and genotype estimation dependent on their mean execution and stability across a mega-environment. The polygon made by including the markers of the genotypes that was further away from the bi-plot source with the end goal that every single other genotype confined in the polygon. Genotypes

situated on the vertices of the polygon performed either the best or the poorest in one or more conditions since they had the long distance from the source of bi-plot.

#### 4.1.11.3: Positioning of genotypes dependent on yield and stability

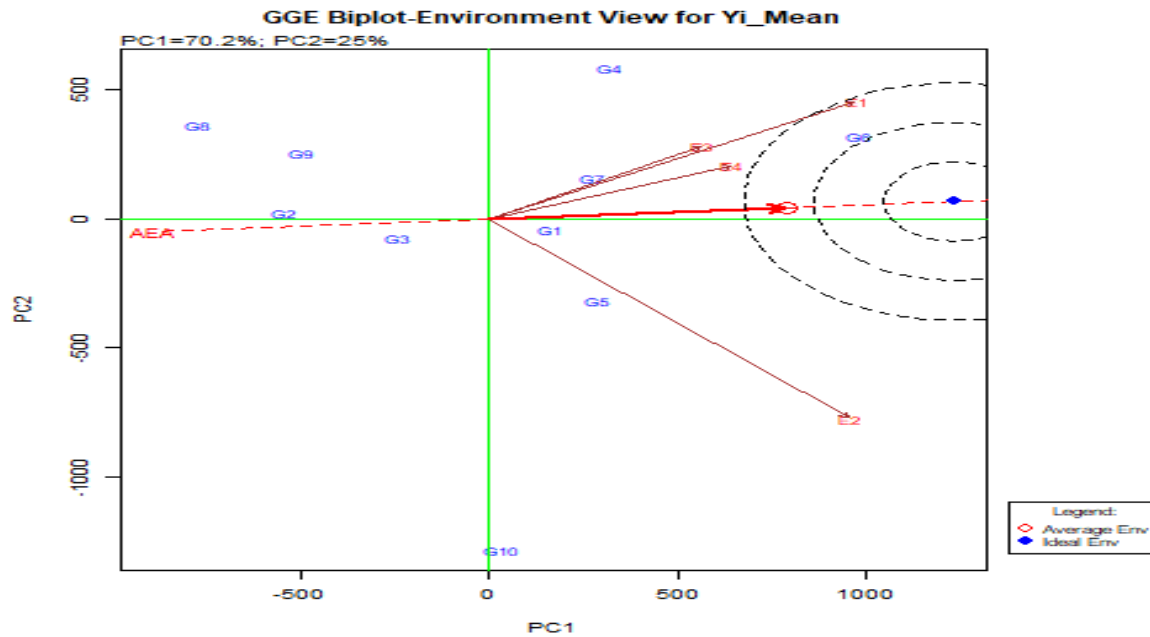
The positioning of genotypes dependent on their mean grain yield and yield stability for conditions showed in Figures (4.7), Figures (4.8) and Figures (4.9). It detailed that when PC1 in a GGE bi-plot approximates the G (mean execution), PC2 must approximate the  $G \times E$  related with every genotype, which is a measure of instability. The line going through the bi-plot started point and the environmental average demonstrated by circles and known as the average environment coordinate (AEC) axis, which was characterized by the normal PC1 and PC2 scores for all situations.

**Fig 4.7: GGE biplot on genotype cantered scaling for soybean**



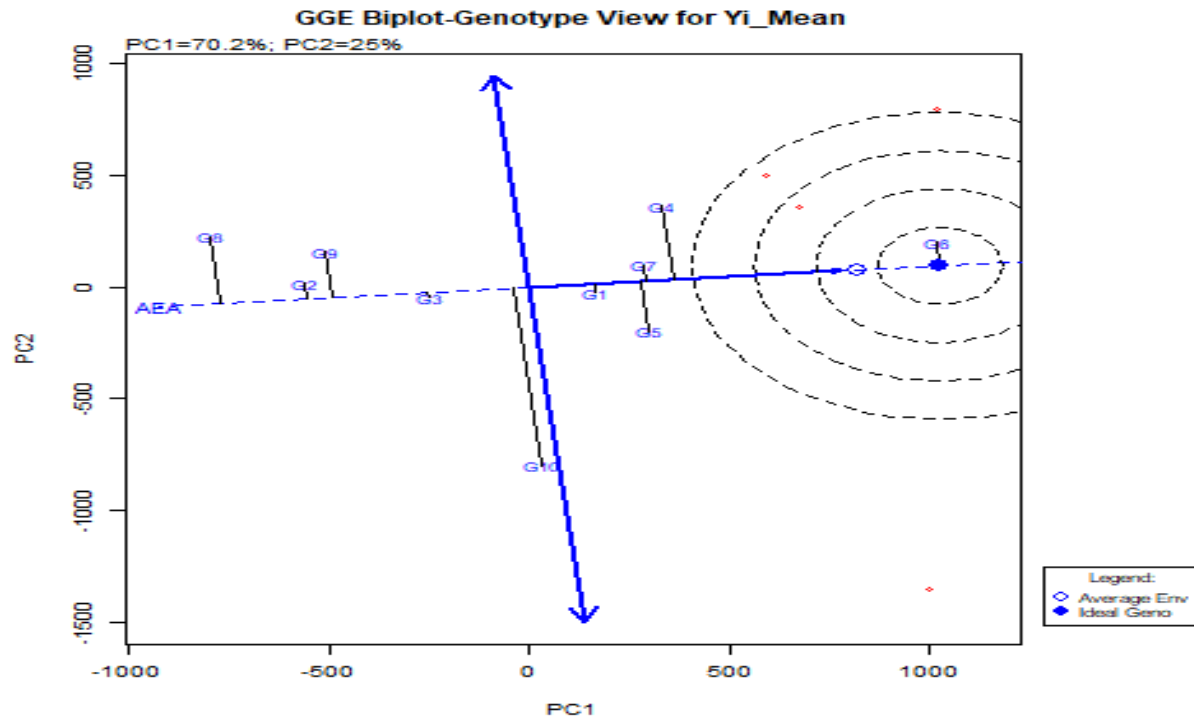
Projection of genotype markers into this axis should be approximates the mean yield of the genotypes. Accordingly, genotypes RSC11-02(G6), RSC11-04(G8) and RSC11-06(G10), discovered higher grain yield, followed by genotypes RSC10-52(G4), RSC10-71(G5) and JS93-05(G2) from yield dataset. The line which goes through the origin but perpendicular to the AEC with double arrows represents the status of the genotypes stability. A situation in either course away from the bi-plot beginning, on the axis, shows greater GXE interaction and reduced stability. Genotype CG Soya (G1), RSC11-03(G7), and RSC10-52(G4) discovered more stable than the others. (Figure 4.7)

**Fig 4.8: GGE biplot dependent on condition centered scaling for soybean**



Another interesting observation from the vector perspective of the bi-plot is that the length of the environment vectors approximates the standard deviation inside every environment, which was a proportion of its separating capacity. In this manner, E1 (Bemetara) and E2 (Jagdalpur) are discovered the most discriminative environments (Fig 4.8)

**Fig 4.9: Comparison of 10 soybean genotypes against ideal genotype for grain yield and stability across four locations**



Yield execution and stability of genotype were utilized by an average environment coordination (AEC) technique (Yan, 2001, 2002, and Yan and Hunt, 2002). Within a single mega-environment, genotypes should be assessed on both mean execution and stability across environments. Fig 4.9 indicates the average environment coordination (AEC) perspective on the GGE bi-plot. The single-headed line is the AEC abscissa, it highlights higher mean yield across environments. In this way, RSC11-02 (G6), CG Soya-1(c)(G1), RSC10-52(G4) and RSC10-71(G5) found the elevated mean yield. The double-headed line is the AEC ordinate; it points to greater variability (poorer stability) in either direction. In this way, RSC11-04 (G8), RSC11-05 (G9) and RSC11-06(G10) discovered most unstable whereas RSC11-02 (G6) and CG Soya-1(c)(G1) were found most stable, followed by JS 93-05(c)(G2), JS 97-52(c)(G3) (Fig 4.9)

## 4.2 Non parametric analysis

Huehn (1979) and Nassar and Huehn (1987) proposed four non-parametric measures of phenotypic stability

### 4.2.1 Mean of the absolute rank differences $S_i^{(1)}$ of a genotype and change among the positions $S_i^{(2)}$ over the environments

Non-parametric techniques are depending on the positions of the genotypes across areas. They give equivalent load to every area or condition. Genotype with less change in position expected to be more stable. The mean absolute rank differences  $S_i^{(1)}$  appraises all possible pair wise rank difference across areas for every genotype. The  $S_i^{(2)}$  evaluations are basically the change of positions for every genotype over situations. For the fluctuation of ranks  $S_i^{(2)}$ , smaller estimates may show relative stability. Frequently  $S_i^{(2)}$  has less force for distinguishing stability than  $S_i^{(1)}$ .

**Table 4.15: Mean absolute rank difference and change of ranks for mean yield of 10 soybean genotypes**

| Genotypes    | Mean yield<br>(Kg/ha) | Rank | $S_i^{(1)}$ | Rank | $S_i^{(2)}$ | Rank |
|--------------|-----------------------|------|-------------|------|-------------|------|
| CG Soya-1(c) | 1067.17               | 5    | 0.42        | 1    | 2.92        | 1    |
| JS 93-05(c)  | 720.08                | 9    | 0.79        | 7    | 11.58       | 7    |
| JS 97-52(c)  | 848.92                | 7    | 0.50        | 2    | 4.00        | 2    |
| RSC 10-52    | 1153.92               | 2    | 1.25        | 10   | 18.92       | 9    |
| RSC 10-71    | 1129.00               | 4    | 0.67        | 6    | 8.00        | 5    |
| RSC 11-02    | 1483.25               | 1    | 0.63        | 5    | 8.25        | 6    |
| RSC 11-03    | 1141.83               | 3    | 0.58        | 3    | 5.67        | 4    |
| RSC 11-04    | 599.92                | 10   | 0.92        | 8    | 15.00       | 8    |
| RSC 11-05    | 740.33                | 8    | 0.59        | 4    | 5.58        | 3    |
| RSC 11-06    | 958.17                | 6    | 1.13        | 9    | 20.25       | 10   |

The consequences of  $S_i^{(1)}$  and  $S_i^{(2)}$  showed that the genotypes CG Soya-1(c) and JS 97-52(c) ranked 1<sup>st</sup>, 2<sup>nd</sup> separately as indicated by RSC 10-52 and RSC 10-06 they involved the genotypes RSC 10-52 and RSC 11-06 ranked is 10<sup>th</sup>, 9<sup>th</sup> and 9<sup>th</sup>, 10<sup>th</sup> position in mean yield as well therefore these genotypes were found to be most unstable and adjusted to all condition.

#### **4.2.2 Mean of the absolute rank differences $S_i^{(3)}$ of a genotype and variance among the positions $S_i^{(6)}$ over the environments.**

The  $Y_{ij}$  values must not be remedied for the genotypic impacts before positioning since data about characteristic level would be lost. Huehn (1979) proposed two non-parametric statistics for the simultaneous estimation of execution and stability which are  $S_i^{(3)}$  and  $S_i^{(6)}$ . This statistic measure stability in units of the mean position of the  $i^{th}$  genotype utilizing  $S_i^{(3)}$ , the distinction among rank and mean position are weighted with themselves avoiding the possibility that a lot of smaller rank differences may lead to the same  $S_i^{(3)}$  values as a few larger differences. These  $S_i^{(3)}$  and  $S_i^{(6)}$  non-parametric measures were worked out by utilizing the ranks which were assigned to genotype on the based on unique mean information inside condition and introduced in Table 4.16

**Table 4.16 : Mean of the absolute rank differences  $S_i^{(3)}$  of a genotypes and variance among the positions  $S_i^{(6)}$  over the environments**

| Genotypes    | Mean yield<br>(Kg / ha) | Rank | $S_i^{(3)}$ | Rank | $S_i^{(6)}$ | Rank |
|--------------|-------------------------|------|-------------|------|-------------|------|
| CG Soya-1(c) | 1067.17                 | 5    | 0.44        | 3    | 0.22        | 1    |
| JS 93-05(c)  | 720.08                  | 9    | 0.71        | 5    | 1.29        | 7    |
| JS 97-52(c)  | 848.92                  | 7    | 0.57        | 4    | 0.86        | 6    |
| RSC 10-52    | 1153.92                 | 2    | 1.71        | 10   | 3.14        | 9    |
| RSC 10-71    | 1129.00                 | 4    | 0.80        | 6    | 0.73        | 5    |
| RSC 11-02    | 1483.25                 | 1    | 1.20        | 8    | 0.60        | 4    |
| RSC 11-03    | 1141.83                 | 3    | 1.08        | 7    | 1.46        | 8    |
| RSC 11-04    | 599.92                  | 10   | 0.32        | 1    | 0.30        | 2    |
| RSC 11-05    | 740.33                  | 8    | 0.40        | 2    | 0.40        | 3    |
| RSC 11-06    | 958.17                  | 6    | 1.69        | 9    | 6.31        | 10   |

The  $Y_{ij}$  values must not be revised for the genotypic impacts before positioning since data about characteristic level would be lost. Huehn (1979) proposed two non-parametric statistics for the concurrent estimation of execution and stability which are  $S_i^{(3)}$  and  $S_i^{(6)}$ . These insights measure stability in units of the mean position of the  $i^{th}$  genotype utilizing  $S_i^{(3)}$ , the distinction among rank and mean position are weighted with themselves avoiding the possibility that a lot of smaller rank difference may lead to the same  $S_i^{(3)}$  value as a few large differences.

Thenrasu  $S_i^{(3)}$  and  $S_i^{(6)}$  non-parametric measures were worked out by utilizing the positions which were appointed to genotypes on the based on unique mean information inside condition and introduced in Table 4.16. The consequences of  $S_i^{(3)}$  and  $S_i^{(6)}$  showed that the genotypes RSC 11-04 and RSC 11-05 ranked 1<sup>st</sup>, 2<sup>nd</sup> and 2<sup>nd</sup>, 3<sup>rd</sup> separately as indicated by and they involved genotypes RSC 10-52 and RSC 11-06 ranked 10<sup>th</sup>, 9<sup>th</sup> and 9<sup>th</sup>, 10<sup>th</sup> situation in



mean yield also accordingly these genotypes were seen as generally unstable and adjusted to all conditions.

#### 4.2.3 Comparisons of the different stability procedures

Rank assessments of the genotypes dependent on 07 different parametric and 04 different non-parametric estimations with mean yield are introduced in Table 4.17. Demonstrated the rank order for stability of the 10 genotypes of soybean crop, as indicated by the different parametric and non-parametric stability measures.

Spearman's rank correlation was resolved for each pair of mean yield and stability statistics (Table 4.17). Mean yield demonstrated highly significant ( $p < 0.01$ ) positive rank correlation with  $S_i^{(3)}$  (0.45), and significant ( $P < 0.05$ ) rank correlation with  $S_{(i)}^{(6)}$  (0.27),  $\bar{S}_{di}^2$  (0.25) and P & J ( $b_i$ ) (0.42). But highly negatively ( $P < 0.05$ ) corresponded with Lin & Bin (Pi, -0.43) compared with different estimations.

Non parametric measure  $S_{(i)}^{(1)}$  was highly significantly positively correlated with  $S_i^{(2)}$  (0.96), CV (0.45),  $W_i$  (0.72),  $\bar{S}_{di}^2$  (0.83), and ASV (0.92).  $S_{(i)}^{(1)}$  was significant ( $P < 0.05$ ) positively correlation with  $S_{(i)}^{(3)}$  (0.44),  $S_{(i)}^{(6)}$  (0.43), CV (0.43), and Lin & Bin (0.44). In any case, exceptionally adversely ( $P < 0.05$ ) correlated with P & J (bi, -0.23) compared with different estimations.

$S_i^{(2)}$  demonstrated highly significant ( $p < 0.01$ ) positive rank correlation with  $S_i^{(1)}$  (0.96),  $S_i^{(6)}$  (0.56),  $W_i$  (0.61),  $\bar{S}_{di}^2$  (0.93) and ASV (0.85). Significant ( $P < 0.05$ ) rank correlation with  $S_{(i)}^{(3)}$  (0.53), CV (0.44), Lin & Bin (Pi, 0.44).

$S_i^{(3)}$  demonstrated highly significant ( $p < 0.01$ ) positive correlation with  $S_i^{(6)}$  (0.79), Lin & Bin (Pi, 0.62), and  $\bar{S}_{di}^2$  (0.33) and ASV (0.85).  $S_i^{(3)}$  exhibited significant ( $P < 0.05$ ) correlation with  $S_{(i)}^{(1)}$  (0.45),  $S_{(i)}^{(2)}$  (0.43), CV (0.21), P & J (bi, 0.42) and ASV (0.33).

$S_i^{(6)}$  non parametric procedures exhibited significant positive correlation with most of the stability measures except  $W_i$  (0.13).

CV parametric procedures exhibited significant positive correlation with most of the stability measures except  $W_i$  (-0.15). Pi parametric procedures exhibited significant positive correlation with most of the stability measures, namely;  $S_i^{(1)}$ ,  $S_i^{(2)}$ ,  $S_i^{(3)}$ ,  $S_i^{(6)}$ , CV (%),  $\bar{S}_{di}^2$ , P & J (bi), ASV and mean yield. Pi parametric procedures exhibited negative correlation with  $W_i$  (-0.12).

Wrick eco valence ( $W_i$ ) parametric procedures exhibited significant positive correlation with most of the stability measures, namely;  $S_i^{(1)}$  (0.72),  $S_i^{(2)}$  (0.61), and  $W_i$  exhibited significant ( $P < 0.05$ ) correlation with  $\bar{S}_{di}^2$  (0.44), and ASV (0.43).  $W_i$  procedures exhibited negative correlation with CV (%) (-0.15), Pi (-0.12) and P & J (bi, 0.65).

Eberhart and Russell deviation from regression ( $\bar{S}_{di}^2$ ) parametric procedures exhibited significant ( $p > 0.01$ ) positive correlation with most of the stability measures, namely;  $S_i^{(1)}$  (0.55),  $S_i^{(2)}$  (0.44),  $S_i^{(3)}$  (0.73),  $W_i$  (0.72), ASV (0.64) and mean yield (0.65).  $\bar{S}_{di}^2$  parametric procedures exhibited negative correlation with  $S_i^{(6)}$  (-0.33) and P & J (-0.44).

P & J (bi) parametric procedures exhibited positive correlation with the stability measures, namely;  $S_i^{(3)}$  (0.42),  $S_i^{(6)}$  (0.27), CV (0.52), Pi (0.71) and mean yield (0.42). P & J (bi)

parametric procedures exhibited negative correlation with  $S_i^{(1)}$  (-0.20),  $S_i^{(2)}$  (-0.14), Wi (-0.65),  $(\bar{S}_{di}^2)$  (-0.01) and ASV (-0.08).

ASV parametric procedures exhibited significant ( $p > 0.01$ ) positive correlation with most of the stability measures, namely;  $S_i^{(1)}$  (0.92),  $S_i^{(2)}$  (0.85), and Wi (0.65). ASV parametric procedures exhibited significant ( $p > 0.05$ ) positive correlation with  $S_i^{(3)}$  (0.33),  $S_i^{(6)}$ , CV (0.43), and Pi (0.43). ASV parametric procedures exhibited negative correlation only with P & J (bi, \*-0.08)

**Table 4.17: Spearman rank correlation between mean yield and stability measures for 10 genotypes across 4 environments**

|                 | $S_i^{(1)}$ | $S_i^{(2)}$ | $S_i^{(3)}$ | $S_i^{(6)}$ | CV (%) | $P_i$  | $W_i$   | $ER$    | P & J<br>( $b_i$ ) | ASV  | Mean<br>Yield |
|-----------------|-------------|-------------|-------------|-------------|--------|--------|---------|---------|--------------------|------|---------------|
| $S_i^{(1)}$     | 1.00        |             |             |             |        |        |         |         |                    |      |               |
| $S_i^{(2)}$     | 0.96**      | 1.00        |             |             |        |        |         |         |                    |      |               |
| $S_i^{(3)}$     | 0.44*       | 0.53*       | 1.00        |             |        |        |         |         |                    |      |               |
| $S_i^{(6)}$     | 0.43*       | 0.56**      | 0.79**      | 1.00        |        |        |         |         |                    |      |               |
| CV (%)          | 0.43*       | 0.44*       | 0.21*       | 0.35*       | 1.00   |        |         |         |                    |      |               |
| $P_i$           | 0.44*       | 0.44*       | 0.62**      | 0.38*       | 0.77** | 1.00   |         |         |                    |      |               |
| $W_i$           | 0.72**      | 0.61**      | 0.09        | 0.13        | -0.15* | -0.12  | 1.00    |         |                    |      |               |
| $ER$            | 0.55**      | 0.44**      | -0.33*      | -0.12       | 0.13   | -0.13  | 0.72**  | 1.00    |                    |      |               |
| P & J ( $b_i$ ) | -0.20*      | -0.14       | 0.42*       | 0.27*       | 0.52** | 0.71** | -0.65** | -0.44** | 1.00               |      |               |
| ASV             | 0.92**      | 0.85**      | 0.33*       | 0.37*       | 0.43*  | 0.43*  | 0.67**  | 0.64**  | -0.08              | 1.00 |               |
| Mean Yield      | 0.24        | 0.21        | 0.45**      | 0.27*       | 0.16   | -0.43* | 0.15    | 0.65**  | 0.42*              | 0.08 | 1.00          |

Note: \* and \*\* at 0.05 and 0.01 level of probability respectively

Comparison of the different stability parameters methods viz., Statistical techniques such as conventional analysis of variance (ANOVA), stability parameters, ranking method and multivariate methods were recognized for analysis of multi-area genotype versatility preliminaries. ANOVA method tends to the part of normal creation over years and areas for flexibility of genotypes. This method depicts the principle impacts of genotypes and area, effectively. Stability method tends to the part of inconstancy of creation. Different stability measures think about various part of changeability. The principal component analysis describes the pattern in G x E Interaction and feature the wide adaptability and specific adaptability of genotypes. The study has clearly indicated that the AMMI model can sum up patterns and relationships of genotypes and environments successfully, just as give a significant expectation evaluation that multivariate techniques are too complex to even think about providing a straightforward proportion of yield stability, which permits a ranking of genotypes. It is clearly indicating the variation of genotypes to environments and can be utilized to distinguish the predominant genotypes in connection with the environments and years. The time periods for the different genotypes are equivalent to those figured from AMMI bi-plot. The G x E effect was hybrid sort as uncovered by differential yield ranking of the genotypes over the environment. GGE bi-plots are successful enough for dissecting and imagining the patterns of G x E of the soybean multi-environment information regarding environment and genotype assessments.

As per Hühn (1990a), non-parametric stability examination methodology have the accompanying focal points: they diminish the inclination brought about by anomalies, no suppositions are required about the conveyance of watches esteems, they are anything but difficult to utilize and decipher and increases or cancellations of one or a couple of genotypes

don't cause a lot of variety of results. Accordingly, numerous scientists applied distinctive non-parametric statistics to evaluate stability. Huehn (1990 a, b) recommended for a cultivar with most extreme stability,  $Si(1) = Si(2) = Si(3)$ .  $Si(1)$  and  $Si(2)$  depend on positions of the genotypes across situations and they put equivalent load from every condition.  $Si(1)$  Estimates depend on all conceivable pair-wise positions contrasts thereon situations stand for every genotype, while  $Si(2)$  depends on the fluctuation positions for every genotype across conditions. In this test, characterization of genotypes dependent on these parameters was comparative. As indicated by Hühn (1990b)  $Si(1)$  and  $Si(2)$  are works just of the dependability estimations while numeral estimations of  $Si(3)$  and  $Si(6)$  consolidate yield and strength dependent on yield positions of genotypes in every condition. The aftereffects of this examination indicated that these parameters were fundamentally ( $P < 0.05$ ) and decidedly corresponded with one another. Flores et al. (1998) likewise announced critical and positive relationship between  $Si(1)$  and  $Si(2)$ . Scapim et al. (2000) likewise discovered high critical relationship in  $Si(1)$ ,  $Si(2)$  and  $Si(3)$ . It recommends one of the three measurements could be utilized at evaluated strength. These measurements were adversely related with grain yield. Nassar and Hühn (1987) showed its  $Si(1)$  and  $Si(2)$  are related with the static natural idea by dependability, as they characterize stability in the feeling of homeostasis. Sabaghnia et al. (2006) additionally announced its  $Si(1)$  and  $Si(2)$  speak to static idea of steadiness. Therefore,  $Si(1)$  and  $Si(2)$  could be utilized as a trade off technique that select genotypes with moderate yield and yield stability. Unmistakable grouping of  $Si(1)$  and  $Si(2)$  additionally affirms that they two non-parametric insights be characterize stability as far as static or natural idea and consequently would have little importance in choosing genotypes that can react to changing ecological situations.  $Si(3)$  and  $Si(6)$  were unequivocally related to Thennarasu's non-parametric measurements.

These propose that Thennarasu's non-parametric strength gauges didn't add significant data to those measurements acquired by Nassar and Hühn (1987). Along these lines, the utilization of Hühn (1990b) stability parameters could be a strategy for decision as there is a factual system accessible to test the significance of  $Si$  (1) and  $Si$  (2). In any case, Thennarasu's (1995) non-parametric stability assessments would be significant options in contrast to parametric models.

The outcome shows that both the parametric and nonparametric methods gave a moderately comparative outcome. Nonparametric stability measurements are hence helpful options in contrast to parametric estimations (Yue et al. 1997).

## CONCLUSION AND RECOMMENDATION

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The AMMI model gives a helpful method in diagnosing genotype  $\times$  environment interaction patterns. It enables clustering of genotypes dependent on likeness of reaction qualities and recognizing expected patterns across conditions. The number of PCA axes retained for most applications is generally  $s \leq 3$ , which is intended to reduce the dimension of the system and provide a more parsimonious description of the underlying interaction structure. The AMMI model gives effectively interpretable data just as the relationship between a genotype and environment.

The following major findings emerged for the multi-environment yield trial data set analyzed here.

- The results from the study concluded that a significant variation existed between 10 soybean genotypes in four areas for yield in soybean crop. The presence of genotype  $\times$  environment interaction finishes up high yielding genotypes which are stable in various areas.
- The Genotypes RSC 11-05, RSC 11-02, CG Soya-1(c), and JS 97-52(c) were found to be the high yielding and most stable genotypes in different location of Chhattisgarh state. The genotypes RSC 11-06, RSC 11-04, JS 97-05(c), and RSC 10-52 were found to be unstable with low yielding according to the parametric methods.
- According to Nassar and Huehn nonparametric methodology  $Si^{(1)}$  and  $Si^{(2)}$  there were significant differences in rank stability for grain yield among 10 soybean genotypes grown in 4 areas during 2017-18.



- The genotypes CG Soya-1(c), RSC 11-02 and JS 97-52(c). were found to be the high yielding and most stable genotypes in four location of Chhattisgarh. While RSC 10-52, RSC 11-06, RSC 11-03 genotypes were very low yield and least stability in non-parametric measures.
- The parametric way to deal with study stability think about just the individual aspect of stability however doesn't give on overall picture of response. The fundamental explanation is that the genotype reactions to condition are multivariate. Principal coordinate analysis facilitates low dimensional plot of a lot of information from data about similarities and dissimilarities between pair of perception.
- The different stability measurements (parametric and non-parametric) utilized in this study showed affiliation and separation (no relationship) among them in positioning of the genotypes dependent on stability.
- Using the AMMI model, the current investigation uncovered that the most of the all out change of yield part characteristics was clarified by E. The G x E Interaction results indicated that the situations at the examination areas effectively affected genotype execution. The environment at the E1 (Bemetara) and E2 (Jagdalpur) was ideal for most of characteristics under investigation. The genotypes G1 (CG Soya-1 (c)), G4 (RSC 10-52), G5 (RSC 10-71), G6 (RSC 11-02) and G7 (RSC 11-03) among them G6 (RSC 11-02) and G7 (RSC 11-03) indicated the best execution and stability in yield quality attributes. Consequently, these genotypes can be suggested for more extensive development or for the Chhattisgarh locales with similar agro-atmospheres.
- In the GGE-biplot analysis, the genotypes found in the primary concentric circle are considered as perfect genotypes. Desirable genotypes are ones lying near to the perfect

genotype. In the current study, genotype G1 (CG Soya-1(c)) was close to the ideal genotype and located on the first concentric circle followed by G3 (JS 97-52(c)) and G7 (RSC 11-03) located in the second circle. G2 (JS 93-05(c)), G5 (RSC 10-71) and G9(RSC 11-05) were undesirable genotypes and were discovered removed from the principal concentric circle.

- From the outcome it was reasoned that nonparametric stability measurements was helpful alternatives to parametric measurements.

## **RECOMMENDATION**

- The comparison of results of stability analysis suggests that description of stability of a genotype vary with the method employed to test the stability.
- This study recommends genotype RSC 11-05,CG Soya-1(c),RSC 11-04 and JS 97-05(c) are superior genotypes in favourable environment conditions.
- From this study we recommend use of Monte-Carlo method or a bootstrap method can be useful in efficiency studies.

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# APPENDIX-A

| Location  | Replication | Genotypes    | Yi   |
|-----------|-------------|--------------|------|
| Raipur    | 1           | CG Soya-1(c) | 900  |
| Raipur    | 1           | JS 93-05(c)  | 800  |
| Raipur    | 1           | JS 97-52(c)  | 600  |
| Raipur    | 1           | RSC 10-52    | 900  |
| Raipur    | 1           | RSC 10-71    | 1000 |
| Raipur    | 1           | RSC 11-02    | 1300 |
| Raipur    | 1           | RSC 11-03    | 1100 |
| Raipur    | 1           | RSC 11-04    | 500  |
| Raipur    | 1           | RSC 11-05    | 700  |
| Raipur    | 1           | RSC 11-06    | 600  |
| Raipur    | 2           | CG Soya-1(c) | 970  |
| Raipur    | 2           | JS 93-05(c)  | 800  |
| Raipur    | 2           | JS 97-52(c)  | 650  |
| Raipur    | 2           | RSC 10-52    | 900  |
| Raipur    | 2           | RSC 10-71    | 900  |
| Raipur    | 2           | RSC 11-02    | 1400 |
| Raipur    | 2           | RSC 11-03    | 1200 |
| Raipur    | 2           | RSC 11-04    | 500  |
| Raipur    | 2           | RSC 11-05    | 710  |
| Raipur    | 2           | RSC 11-06    | 700  |
| Raipur    | 3           | CG Soya-1(c) | 800  |
| Raipur    | 3           | JS 93-05(c)  | 930  |
| Raipur    | 3           | JS 97-52(c)  | 620  |
| Raipur    | 3           | RSC 10-52    | 910  |
| Raipur    | 3           | RSC 10-71    | 980  |
| Raipur    | 3           | RSC 11-02    | 1317 |
| Raipur    | 3           | RSC 11-03    | 1115 |
| Raipur    | 3           | RSC 11-04    | 462  |
| Raipur    | 3           | RSC 11-05    | 715  |
| Raipur    | 3           | RSC 11-06    | 600  |
| Jagdarpur | 1           | CG Soya-1(c) | 1290 |
| Jagdarpur | 1           | JS 93-05(c)  | 818  |
| Jagdarpur | 1           | JS 97-52(c)  | 973  |
| Jagdarpur | 1           | RSC 10-52    | 1026 |
| Jagdarpur | 1           | RSC 10-71    | 1364 |
| Jagdarpur | 1           | RSC 11-02    | 1634 |
| Jagdarpur | 1           | RSC 11-03    | 1282 |
| Jagdarpur | 1           | RSC 11-04    | 504  |
| Jagdarpur | 1           | RSC 11-05    | 858  |
| Jagdarpur | 1           | RSC 11-06    | 1865 |
| Jagdarpur | 2           | CG Soya-1(c) | 1270 |
| Jagdarpur | 2           | JS 93-05(c)  | 756  |

|            |   |              |      |
|------------|---|--------------|------|
| Jagdalspur | 2 | JS 97-52(c)  | 1148 |
| Jagdalspur | 2 | RSC 10-52    | 996  |
| Jagdalspur | 2 | RSC 10-71    | 1508 |
| Jagdalspur | 2 | RSC 11-02    | 1698 |
| Jagdalspur | 2 | RSC 11-03    | 1294 |
| Jagdalspur | 2 | RSC 11-04    | 489  |
| Jagdalspur | 2 | RSC 11-05    | 708  |
| Jagdalspur | 2 | RSC 11-06    | 1719 |
| Jagdalspur | 3 | CG Soya-1(c) | 1298 |
| Jagdalspur | 3 | JS 93-05(c)  | 824  |
| Jagdalspur | 3 | JS 97-52(c)  | 1064 |
| Jagdalspur | 3 | RSC 10-52    | 1226 |
| Jagdalspur | 3 | RSC 10-71    | 1626 |
| Jagdalspur | 3 | RSC 11-02    | 1480 |
| Jagdalspur | 3 | RSC 11-03    | 1158 |
| Jagdalspur | 3 | RSC 11-04    | 556  |
| Jagdalspur | 3 | RSC 11-05    | 621  |
| Jagdalspur | 3 | RSC 11-06    | 1903 |
| Bemetara   | 1 | CG Soya-1(c) | 1125 |
| Bemetara   | 1 | JS 93-05(c)  | 602  |
| Bemetara   | 1 | JS 97-52(c)  | 921  |
| Bemetara   | 1 | RSC 10-52    | 1474 |
| Bemetara   | 1 | RSC 10-71    | 1031 |
| Bemetara   | 1 | RSC 11-02    | 1574 |
| Bemetara   | 1 | RSC 11-03    | 995  |
| Bemetara   | 1 | RSC 11-04    | 684  |
| Bemetara   | 1 | RSC 11-05    | 723  |
| Bemetara   | 1 | RSC 11-06    | 651  |
| Bemetara   | 2 | CG Soya-1(c) | 995  |
| Bemetara   | 2 | JS 93-05(c)  | 506  |
| Bemetara   | 2 | JS 97-52(c)  | 806  |
| Bemetara   | 2 | RSC 10-52    | 1279 |
| Bemetara   | 2 | RSC 10-71    | 973  |
| Bemetara   | 2 | RSC 11-02    | 1610 |
| Bemetara   | 2 | RSC 11-03    | 1072 |
| Bemetara   | 2 | RSC 11-04    | 541  |
| Bemetara   | 2 | RSC 11-05    | 768  |
| Bemetara   | 2 | RSC 11-06    | 586  |
| Bemetara   | 3 | CG Soya-1(c) | 1078 |
| Bemetara   | 3 | JS 93-05(c)  | 630  |
| Bemetara   | 3 | JS 97-52(c)  | 935  |
| Bemetara   | 3 | RSC 10-52    | 1511 |
| Bemetara   | 3 | RSC 10-71    | 1081 |
| Bemetara   | 3 | RSC 11-02    | 2001 |
| Bemetara   | 3 | RSC 11-03    | 1291 |
| Bemetara   | 3 | RSC 11-04    | 741  |

|          |   |              |      |
|----------|---|--------------|------|
| Bemetara | 3 | RSC 11-05    | 785  |
| Bemetara | 3 | RSC 11-06    | 786  |
| Kawardha | 1 | CG Soya-1(c) | 1075 |
| Kawardha | 1 | JS 93-05(c)  | 700  |
| Kawardha | 1 | JS 97-52(c)  | 820  |
| Kawardha | 1 | RSC 10-52    | 1175 |
| Kawardha | 1 | RSC 10-71    | 1031 |
| Kawardha | 1 | RSC 11-02    | 1250 |
| Kawardha | 1 | RSC 11-03    | 995  |
| Kawardha | 1 | RSC 11-04    | 781  |
| Kawardha | 1 | RSC 11-05    | 735  |
| Kawardha | 1 | RSC 11-06    | 725  |
| Kawardha | 2 | CG Soya-1(c) | 1005 |
| Kawardha | 2 | JS 93-05(c)  | 600  |
| Kawardha | 2 | JS 97-52(c)  | 825  |
| Kawardha | 2 | RSC 10-52    | 1250 |
| Kawardha | 2 | RSC 10-71    | 973  |
| Kawardha | 2 | RSC 11-02    | 1160 |
| Kawardha | 2 | RSC 11-03    | 1000 |
| Kawardha | 2 | RSC 11-04    | 641  |
| Kawardha | 2 | RSC 11-05    | 876  |
| Kawardha | 2 | RSC 11-06    | 685  |
| Kawardha | 3 | CG Soya-1(c) | 1000 |
| Kawardha | 3 | JS 93-05(c)  | 675  |
| Kawardha | 3 | JS 97-52(c)  | 825  |
| Kawardha | 3 | RSC 10-52    | 1200 |
| Kawardha | 3 | RSC 10-71    | 1081 |
| Kawardha | 3 | RSC 11-02    | 1375 |
| Kawardha | 3 | RSC 11-03    | 1200 |
| Kawardha | 3 | RSC 11-04    | 800  |
| Kawardha | 3 | RSC 11-05    | 685  |
| Kawardha | 3 | RSC 11-06    | 678  |

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## RESUME

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|                 |   |
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| Degree              | Year   | University/Institute |
|---------------------|--|----------------------|
| 1. Higher Secondary | 2010   | CGBSE, Raipur        |
| 2. Bsc. (Ag)        | 2016   | IGKV, Raipur         |
| 3. M.Sc .(Ag)       | Course work complete,<br>Thesis is being submitted<br>For the partial fulfilment<br>of the degree. | IGKV, Raipur         |

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Professional Experience : Rural Agriculture Work Experience (RAWE)

Publications : Nil

Signature

DATE:

PLACE: