Studies on Genotypic x Environmental Interaction on Rice bean [*Vigna umbellata* (Thunb.) Ohwi and Ohashi] Landraces of Nagaland

Thesis

Submitted to

NAGALAND UNIVERSITY

In partial fulfillment for the degree

Of

DOCTOR OF PHILOSOPHY

In

GENETICS AND PLANT BREEDING

By

MARTINA SHITIRI

Admin. No. Ph-179/15; Regn. No. 844/2019

Department of Genetics and Plant Breeding
School of Agricultural Sciences and Rural Development
Nagaland University, Medziphema Campus -797106
Nagaland

2019

AFFECTIONATELY

DEDICATED

TO MY

CHILDREN

DECLARATION

I, **Mrs. Martina Shitiri** hereby declare that the subject matter of this Thesis is the record of work done by me, that the contents of this Thesis did not form the basis of the award of any previous Degree to me or to the best of my knowledge to anybody else, and that the thesis has not been submitted by me for any research degree to any other University/Institute.

This is submitted to SASRD, Nagaland University for the Degree of Doctor of Philosophy in Genetics and Plant Breeding.

Date:

Place: (Martina Shitiri)

Supervisor

NAGALAND UNIVERSITY
MEDZIPHEMA CAMPUS
SCHOOL OF AGRICULTURAL SCIENCES AND RURAL DEVELOPMENT
MEDZIPHEMA- 797106, NAGALAND

CERTIFICATE - I

This is to certify that the Thesis entitled **"Studies on Genotypic x Environmental Interaction on Rice bean [(*Vigna umbellata* Thunb.) Ohwi and Ohashi] Landraces of Nagaland"** submitted to Nagaland University in partial fulfillment of the requirements for the degree of DOCTOR OF PHILOSOPHY in the discipline of Genetics and Plant Breeding, is a record of research work carried out by **Mrs. Martina Shitiri**, Registration No.844/2019 under my personal supervision and guidance.

The results of the investigation reported in the thesis have not been submitted for any other degree or diploma. The assistance of all kinds received by the student has been duly acknowledged

.....

Dated:
Place:

(KIGWE SEYIE)
Supervisor
Professor

NAGALAND UNIVERSITY
MEDZIPHEMA CAMPUS
SCHOOL OF AGRICULTURAL SCIENCES AND RURAL DEVELOPMENT
MEDZIPHEMA-797106, NAGALAND

CERTIFICATE – II
VIVA VOCE ON THESIS OF DOCTOR OF PHILOSOPHY IN GENETICS AND PLANT BREEDING

This is to certify that the Thesis entitled **"Studies on Genotypic x Environmental Interaction on Rice bean [(*Vigna umbellata* Thunb.) Ohwi and Ohashi] Landraces of Nagaland"** submitted by **Mrs. Martina Shitiri**, Admission No. Ph-179/15, Registration No.844/2019 to Nagaland University in partial fulfilment of the requirements for the degree of Doctor of Philosophy (Agriculture) in the discipline of Genetics and Plant Breeding has been examined by the Advisory Board and External examiner on 03/12/2020

The performance of the student has been found **Satisfactory/~~Unsatisfactory.~~**

Members	Signature
1. Dr. Kigwe Seyie (Supervisor)	.....
2. Dr.E.V.Divakara Sastry (External Examiner)	.....
3. Pro-Vice Chancellor Nominee Dean, SASRD	.....
4. Dr.H.P. Chaturvedi	.....
5. Dr. Pankaj Shah	.....
6. Prof. Tongpang Longkumer	.....
7. Dr. Sanjoy Das	..... 3/12/2020

3/12/2020

Head
Department of Genetics and Plant breeding and Plant Breeding

Dean
School of Agricultural Sciences and Rural Development

ACKNOWLEDGEMENTS

I take this wonderful opportunity to express my deep sense of gratitude for all those who have helped me in completion of this thesis successfully.

I thank almighty God for giving me and my family, strength and good health during the course of my investigation and in preparation of this thesis.

My deepest sense of gratitude and appreciation goes to my supervisor Dr.Kigwe Seyie, Associate Professor, Department of Genetics and Plant Breeding for the constant encouragement, valuable suggestions and for his continue endurance shown throughout my research programme and compilation of the thesis, without which the work would not have been completed.

I wish to express my profound thanks to my advisory board members Dr.H.P. Chaturvedi, Assistant Professor, Department of Genetics and Plant Breeding, Dr.Pankaj Shah, Assistant Professor, Department of Genetics and Plant breeding, Dr.Tongpang Longkumer, Professor, Department of Agronomy, and Dr.A.K. Sahu, Assistant Professor, Department of Agricultural Economics for their valuable suggestion and practical approach that has resulted in the work presented. I would also like to convey my sincere thanks to Dr.Malini Sharma, Associate Professor, Department of Genetics and Plant Breeding.

My special thanks to all the technical staffs, Department of Genetic and Plant breeding for their valuable help in every possible way during my Ph.D research work. I would also like to give my sincere thanks to STA, supporting staff, Department of Agronomy for helping me in analyzing crude protein during my course of work.

My heartfelt thanks to my husband, children, parents, brother and sister for their constant prayer, moral support throughout my research work. I owe my success to them.

Place: Medziphema

Date: (Martina Shitiri)

LIST OF ABBREVIATIONS USED

%: Percent

>: More

<: Less

C.V.: Critical variance

cm: Centimetre

M: meter

mm: Millimetre

˚C : Centigrade

et al.: et alli (and others)

Fig. : Figure

g: Gram

viz.: Videlicet (Namely)

Env/E: Environment

df: Degree of freedom

N: number of observation

S.E.: Standard Error

GA: Genetic advance

h^2bs: Heritability

PCV: phenotypic coefficient variation

GCV: Genotypic coefficient variation

RbnG: Rice bean Nagaland genotype

RBD: Randomized block design

Nos: Number

/: per

r: number of replication

Mi: Mean performance

SS: Sum square

MSS: mean sum square

GSS: Genotype sum square

EnSS: environment sum square

ELSS; Environment linear sum square

PDSS: Pool deviation sum square

ESS: Error mean square

C.V. % = Coefficient of variation

SEm± = Standard error of means

S E diff = Standard error of difference of mean

GM = Grand mean

C.D. = Critical difference

bi: regression coefficient

S^2di: deviation mean squares

KSO4: potassium sulphate

CuSO4: Copper sulphate

NaOH: Sodium hydroxide

HCL: Hydrochloric acid

AMMI: Additive Main Effect and Multiplicative Interaction

PC: Principle Components

MV: Mean value

ASV: AMMI Stability values

YSI: Yield Stability Index

CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF PLATES

INTRODUCTION

Legumes, commonly known as pulses, holds significant place in Indian diets because of being a good source of protein and other nutrients which are essential for supplementation of cereal based diets. Legumes occupy second place after cereals as the source of calories and prime source of protein in human diet. India is the major pulse producing country in the world with an aggregate production of 25.23 million tons from an area of 29.99 million hectares (Directorate of pulses development, 2017-18).

Rice bean [*Vigna umbellata* (Thunb.) Ohwi and Ohashi], has been used since long, as pulse and fodder crop (Chandel *et al*., 1988). It is cultivated in the tropical and sub-tropical climatic regions of South East Asia *viz*, India, Nepal, Bangladesh, Thailand, Vietnam and China (Gautam *et al*., 2007). It is considered as underutilize grain legume which is little known with limited research and exploitation. The seeds are highly nutritious, as the protein is high in lysine, high in mineral content and vitamins including thymine, riboflavin, niacin and ascorbic acid (Joshi *et al*., 2006).

Rice bean [*Vigna umbellata* (Thunb.) Ohwi and Ohashi] is also referred as climbing mountain bean, mambi bean, oriental bean and red bean. In India, it is known as rajmoong and satrangi mash. The presumed centre of domestication is Indo-China. Rice bean is a diploid (2n=22) Plant and derived from the wild derivative *V. umbellata* var. gracilis, which is cross-fertile and is distributed from southern China through the north of Vietnam, Laos and Thailand into Myanmar and India (Tomooka *et al*., 1991). In India its distribution is mainly confined to hill tracts of tribal regions of North-Eastern hills, Western and Eastern Ghats in peninsular India (Arora *et al*., 1988). Though little information is available about exact area under this crop

in India, but roughly it is estimated to be grown in around 15,000 ha (Raiger *et al*., 2010). The crop is mainly grown in *Kharif* season and is intercropped with maize. Rice bean plant is a small vine with characteristic hairy appearance bearing bright yellow flowers and later small edible beans (Chandel *et al*., 1978). Bright yellow flowers grow in cluster on the plants and produce large number of slender and slightly curved pods per peduncle. The seed coat colour vary from maroon, green, yellow, brown and light shades of yellow green, speckled and mottled.

In North Eastern Region, Rice bean is considered as traditional crop and grown predominantly under rainfed condition in mixed cropping system, shifting cultivation or in the kitchen garden .In the middle hills of Nepal, ricebean is cultivated along rice bunds and terrace-margins (Khadka *et al*., 2009). Rice bean distribution pattern indicates its adaptivity to diverse environment, ranging from humid tropical, sub-tropical to sub-temperature climate.

The crop plays an important role in improving food security through by increasing the crop diversity and sustainability of cropping system in hilly regions of North East and also harnesses agriculture diversification to broaden food basket. In spite of its multiple benefits, cultivation of this crop has not been potentially exploited. Much research and extension efforts are underway to explore its potentiality as staple food and for its acceptability by people particularly in South East Asia, far East countries and in Tropical Africa.

Protein malnutrition can be achieved by improving this stable crop that are consumed by these people and hence, naturally enriched nutrient requirements of the expanding population of the country can be increase by

reaching each household. Many plant breeding programs have expanded their goals through the combination of yield increase and crop nutritional factor improvement in order to address the challenge of diminishing human malnutrition and the chronic diseases associated to it (Sands *et al*., 2009).

In Nagaland, rice bean is a traditional and indigenous crop, cultivation since time immemorial and is considered as minor legume grown by subsistence farmers of Nagaland. It is grown under diverse conditions with no additional input, which thrives well in rainfed condition and is generally grown as mixed crop in jhum cultivation, inter crop with maize and cultivated along the rice bunds and terrace. Rice bean is known by different local names such as Nkubo-rho (Lotha), Hudron (Yimchunger), Kerhü (Angami), and Azungken (Ao) and is popularly known as *Naga dal*. Area under cultivation is too low compared to other crops and hence low production and productivity. Rice bean is usually used as a dried pulse and vegetable crop at tender stage. It is grown at an altitude of 1000-1200 m and 300-900 m above sea level. There are many types of local land races of rice bean available in Nagaland which is differentiated by seed colour, size, and taste and farmer preferences. Seed colour ranges from ivory to greenish ivory, red, violet and black (Chatterjee & Dana, 1997). The cultivated varieties of rice bean in Nagaland are landraces which are exchanged from one village to another and passed from generation to generation through an informal distribution system, with farmers solely responsible for management of seed.

Genetics variability plays an important role for selecting of genotypes for rapid improvement in yield and yield contributing characters as well as for selecting potential parent for any hybridization programmes. Heritability is an index for determining the relative influence of environment on the

expression of genotypes. Heritability percentage in broad sense is analysis for various characters for seed yield and its components for effective selection. Genetic advance under selection measures the role of genetic progress as the deviation between the mean genotypic values of the selected families and the mean genotypic value of the base population due to selection. The correlation coefficients are estimated to describe the degree of association between independent and dependent variables. A path coefficients analysis measures the direct influence of one variable upon another and allows separation of components into direct and indirect effects.

Genotype x Environment interaction (GxE) is a common phenomenon and this exits when the response of two or more genotypes are not consistence to varying environmental condition. The genotypic values may increase or decrease from one environment to another which might causes the genotypes to rank differently between environments. Environmental factors such as locations, growing seasons, years, rainfall and precipitation in each season, temperature, etc. may either have positive or negative impacts on genotypes. The Genotype x Environment interaction determines if a genotype is widely adapted for an entire range of environmental conditions or selection of separate genotypes for different sub environments. More knowledge about causes of G x E interaction is needed and would be useful for exploration of breeding objectives for optimal cultivar adaptation (Anandan, 2010). Estimation of stability was proved to be a valuable tool for the assessment of varietal adaptability which is an interest of any plant breeder and so it is necessary to study the level of impact of Genotype x Environment interaction for different genotypes to identify the best genotypes possessing better yielding potential across the environments. Although rice bean are grown in diverse environment in Nagaland, there is inadequate information on the stability and response of different genotypes in different environment.

In order to address these problems, this investigation was taken up mainly by generating information on the Variability, G x E interaction and stability parameters by Eberhart and Russel (1966) model and Additive Main Effects and Multiplicative Interactions (AMMI) model, which helps for identification of stable, high yield genotype for cultivation in Nagaland region. Stable genotypes are required to secure sustainable crop production and Genotype × Environment interaction is expected to play an important role in the performance of genotypes under diverse environmental conditions, besides their individual effect. The present investigation is taken up to explain genotype × environment interaction in rice bean of selected landrace genotypes from Nagaland under different sowing dates with 15 days interval and to identify the stable genotypes suitable for cultivation under varying environmental conditions. These available genotypes might provide an immense potential as raw material required for development of improved varieties. Hence, it is needed to evaluate crop genotypes at different environment for their performance on the following objectives:

1. To assess the magnitude of Genetic Variability in Rice bean genotypes of Nagaland.
2. To determine the direct and indirect effects of yield components on the yield
3. To determine the stability of Rice bean genotypes over different environments.

REVIEW OF LITERATURE

2.1. Genetic Variability

Total variability is a metric trait which is divided into genotypic variability and phenotypic variability. The assessment of genetic variability for yield and its components is a pre-requisite for improvement of the crop to the desired level. Genetic variability is of prime momentous for the improvement of many crops including *Vigna sp*. Genetic improvement of any crop depends upon the existence, nature and range of genetic diversity available for manipulation. Fisher (1918) partitioned the total phenotypic variance into genotypic and environmental variances. He further divided the genotypic variance into additive, dominance and epistatic effects. He stated that only the genetic variation which is heritable. Selection is effective when genetic variation is significant among the individual in the population. Hence, genetic variability is of paramount importance to plant breeder for starting a breeding programme in any crop.

Thomas *et al.* (1983) made 170 collections of ricebean from Nepal, Sikkim and Himalaya and observed good range of variability with regard to seed yield and its components.

Satyan *et al.* (1988) observed variability in the three generations for seed yield and its components in amphidiploids progenies from an inter specific hybrids between mung bean and rice been.

Ahmad and Rabbani (1992) reported highly significant differences among twenty accessions of rice bean (*Vigna umbellata*) for days to maturity, pods/branch, pod length, seeds/pod, 100-seed weight and grain yield per plant indicating considerable range of variation.

Zahoor Ahmad and Ashiq Rabbani (1992) reported highly significant differences among twenty accessions of rice bean (*Vigna umbellata*) for days to maturity, pods per branch, pod length, seeds per pod, 100-seed weight and grain yield per plant indicating considerable range of variation.

Chaudhari (1997) observed 60 rice bean genotypes for genetic variability and reported a wide range and variation for most of the yield components except for pod length, branches per plant, 100 grain weight and grain protein content.

Sunayana *et al*. (2018) in their studies on genotype × environment interaction for stability of yield potentiality in Asiatic cotton on three different date of sowings (10-04-2015, 15-05-2015, 5-06-2015, 26-04-2016, 5-05-2016 and 2-06-2016) during *Kharif* seasons of 2015 and 2016 observed significant differences among the genotypes and environments for seed cotton yield per plant, lint yield per plant, seed index, lint index, ginning outturn, seeds per boll, boll weight, bolls per plant, monopods per plant, plant height, days to boll bursting and days to first flower indicated presence of variability among genotypes and environments.

2.1.1. Genotypic and Phenotypic Coefficient of variation

Burton and De Vane (1953) suggested that genetic coefficient of variation together with heritability estimates would give potential information for improvement from selection and importance of expected genetic gain which is needed by a breeder.

Gadekar and Dhumale (1990) studies twenty two genotypes of *Vigna umbellata* for grain yield, number of branches per plant, number of seeds per pod and other five characters and recorded high PCV and GCV for Grain yield, number of branches per plant and number of seeds per pod and

number of pods per plant with high PCV but moderate GCV, indicating more influence of environment.

Singh and Dhiman (1991) reported high genotypic and phenotypic co-efficient for 100-seed weight, branches per plant, plant height, leaves per plant in rice bean and also reported high heritability estimates for 100-seed weight, days to flowering and days to maturity and high genetic advance for 100-seed weight, leaves per plant, branches per plant and plant height in rice bean.

Mishra *et al.* (1995) studied genetic variability in 10 germplasm lines of rice bean and observed high genotypic coefficients of variation for all the traits except grain per pod. Moderate to high heritability and high genetic gain were reported for seed yield, days to 50 % flowering, plant height, 1000 seed volume and test weight.

Jadhav (1996) studied genetic variability in 50 genotypes of rice bean and reported that GCV and PCV were higher for all traits except days to 50 % flowering, days to maturity and pod length for which it was least.

Lokesh *et al*. (2003) recorded high PCV and GCV for pods per plant, clusters per plant, plant height, seed yield per plant, days to flowering and pods per cluster.

Dodake and Dahat (2011) studied 50 genotypes of rice bean for 12 different characters including growth and yield attributes and observed high values of genotypic and phenotypic coefficients of variation for harvest index, number of root nodules per plant, seed yield per plant, number of pods

per plant and number of branches per plant. The lowest genotypic and phenotypic coefficients of variation were recorded for days to maturity.

Nwofia *et al.* (2012) observed that the phenotypic coefficient of variation (PCV) was higher than the corresponding genotypic coefficient of variation (GCV) for all the traits in cowpea an indication that all the attributes interacted with the environment.

2.1.2. Heritability and genetic advance

Heritability in broad sense refers to the ratio of genotypic variance to the total phenotypic variance. The estimates of heritability help the plant breeders in selection of elite genotypes from diverse genetic population and also are good index of the transmission of characters from parents to their off springs. Genetic advance refers to the realized gain in the genetic value of the selected single plant over the base population. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection from heritability estimate alone. Johnson *et al*, (1955) reported that the efficient selection in improving a plant character depends largely on the existence of transmissibility of the character. The presence of high magnitude of variability in the germplasm of breeding material may indicate the greater possibility of improvement through selection but existence of high transmissibility is an important prerequisite for realization of such possibility. Johnson *et al*, (1955) reported heritability coupled with genetic advance and genetic gain (%) increases the utility of these estimates for the purpose of selection of parents for hybridization

Das (1979) reported high heritability for number of seeds per plant (89.2 %) and seed size (99.8 %). Das and Dana (1985) reported narrow sense

heritability estimates of 12.4, 30.4, 95.8 and 85.6 per cent for plant height, number of branches, days to flower and number of pods respectively which indicates that the inheritance and days to flower and number of pods are determined by additive gene effects, suggesting that the conventional breeding procedures involving crosses between high yielding parents having different values for these two characters followed by selection in segregating generations would lead to the development of early variety with higher number of pods per plant.

Das and Dana (1985) recorded high degree of heritability for number of seeds per pod, number of pods per plant and seed size in rice bean.

Gadekar and Dhumale (1990) recorded high heritability for days to flowering, number of branches per plant and number of seeds per pod. Moderate heritability for 100 seed weight, length of pod, grain yield/plant was recorded. They also observed highest genetic advance for branches per plant followed by number of seeds per pod, grain yield/plant and seed weight in Ricebean. Moderate genetic advance were observed for number of pods per plant, plant height and days to 50% flowering.

Gadekar and Dhumale (1990) observed very high estimates of heritability for days to flowering, number of branches per plant and number of seeds per pod and moderate heritability for 100 seed weight, length of pod and grain yield per plant.

Sarma *et al*. (1991) studied 19 cultivars of rice bean and reported high heritability for 100 seed weight, days to maturity and pod length. Kumar *et al*. (1997) observed heritability and genetic advance for thirty selected rice bean mutant lines. High heritability together with genetic advance was

observed for plant height, indicating the predominance of additive gene effect for these traits.

Chaudhari (1997) revealed that heritability in broad sense was the highest for grain protein contents followed by grain yield per plant and plant height. High heritability with high genetic advance were observed for grain protein content, plant height, grain yield per plant, 100 grain weight, days to maturity and days to 50 % flowering.

Singh *et al*. (1997) studied 32 rice bean cultivars and recorded high heritability for days to maturity, 100-seed weight, plant height, pods per plant and length of pod. They also recorded highest genetic advance for 100 seed weight, pods per plant, seed yield per plant and plant height.

Lokesh *et al*. (2003) observed high heritability followed by high genetic advance as per cent of mean for pods per plant, plant height, seed yield per plant and clusters per plant in 79 genotypes of ricebean.

Mehta *et al*. (2007) observed twenty eight strains of soybean for fodder potential and for their desirable traits. High genetic advance with high heritability were recorded for leaf area while, high heritability with low genetic advance could be recorded for stem girth and crude protein per plant.

Sarkar and Mukerjee (2007) observed heritability in eleven quantitative characters for eighteen genotypes of ricebean. The broad sense heritability in percentage for plant height (94.9%), days to 50% flowering (95.70%), pod per plant (98.60%) and days to maturity (93.70%) were high. Considering the heritability were moderate to high for almost all characters except branches per plant, seed per pod and 100 seed weight.

2.1.3. Correlation

Robinson (1951) observed that the correlation values are of potential importance since selection is usually concerned with changing two or more traits simultaneously. Dewey and Lu (1959) used correlation coefficients first time in plant for path analysis by following Wright (1921).

Gadekar *et al.* (1990) reported pods per plant and seeds per pod as chief contributors to seed yield per plant and strongly correlated with these traits with seeds per pod and days to 50 % flowering at the genotypic level.

Singh *et al.* (1992) reported that grain yield showed significant positive correlations with number of pods per plant and number of seeds per pod. Baisakh (1992) studied inter-relationship between yield and it's attributes in 12 genotypes of rice bean and observed high genotypic correlations and observed significant positive correlation with yield for characters, pods per plant, plant height and clusters per plant at genotypic level. These characters also had significant positive association among themselves, indicating that selection for these characters may improve the grain yield simultaneously.

Sharma and Hore (1994) observed that yield components had significant and positive correlations between days to flower and days to maturity, between pod length and seeds per pod, plant height with branches per plant and between pod per plant and 100 seed weight. The plant height showed significant negative correlation with days to flower and days to maturity.

Mishra *et al.* (1995) studied inter-relationships between yield and it's components in 10 germplasm lines of rice bean and observed that seed yield was significant positively associated with pods per plant.

Singh *et al*. (1998) observed that grain yield is correlated with number of pods per plant and number of seeds per pod, total biomass, and the number and dry weight of nodules per plant and also reported that plant height appears to have negative correlation between days to maturity and yield suggesting possibility of developing early maturing types without yield reductions.

Thaware *et al.* (2000) observed that plant height, days to initiation of flowering, days to 50 % flowering, peduncles per plant, pods per plant and grains per plant showed consistently positive and significant correlation with grain, indicating that these characters are the major yield attributes for consideration of selection indices in rice bean.

Chaudhari *et al.* (2000) observed that genotypic correlation coefficient was high in magnitude indicating inherent relationship between the characters. In their studies all different traits showed positive correlation with grain yield per plant except grain protein content which showed significant negative correlation (r = - 0.32) with grain yield per plant. The character plant height (r = 0.38), number of branches per plant (r =0.27) and pod length (r = 0.36) showed significant positive association with grain yield. However, the highest value of correlation coefficient between grain yield and pods per cluster (r =0.75) and pods per plant (r = 0.93) indicated the close association with yield and suggested that plant height, number of branches per plant, Clusters per plant, pods per cluster, and pods per plant and pod length might bring an improvement in grain yield.

Pol *et al*. (2001) reported correlation between the morpho physiological and yield component of ricebean and observed that plant height, number of branches per plant, number of leaves, leaf area, leaf dry matter per plant, total dry matter per plant, 100 grain weight, harvest index, absolute growth rate was significantly and positively correlated with the yield.

Borah *et al*. (2001) in their studies observed that grain yield is correlated with number of pods per plant and number of seeds per pod, total biomass, and the number and dry weight of nodules per plant and also with number of branches, clusters, pod length and 100-seed weight.

De *et al*. (2007) observed correlation coefficients between length of side leaflet, breadth of side leaflet, length of top leaflet, breadth of top leaflet, area of side leaflet, area of top leaflet and total area were found highly significant and positive. Singh and Singh (1994) reported significant and positive association of days to flowering, plant height, pods per plant, seeds per pod and pod length with seed yield.

2.1.4. Path coefficient

The concept of path coefficient analysis was originally developed by Wright (1921), but the technique was first used in plant breeding by Dewey and Lu (1959). They found that it permits a critical examination of specific forces acting to produce a particular correlation. This technique was utilized in the analysis of components of seed production in crested wheat grass (*Agropyron cristatum*). The total correlation coefficient was partitioned into their direct and indirect effects and assigned the value of path coefficients

contributing to yield which gives rather much clearer picture of the complex association which is of value in selection programmes.

A path coefficient is simply standardized partial-regression coefficient and as such measures the direct influence of one variable upon another and permits the separation of the correlation coefficients into components of direct and indirect effects. The path analysis reveals that association of independent traits with dependent traits is due to their direct effect on it or is a consequence of their indirect effect via some other traits.

Gadekar and Dhumale (1990) observed pods per plant and length of pod showed high direct effects on grain yield and also reported that number of seeds per pod with significant correlation with indirect effect via length of pod.

Singh *et al.* (1992) observed that pods per plant, days to maturity and seeds per pod have high direct positive effects on grain yield.

Sonene *et al.* (1999) observed positive direct contribution through cluster per plant, days to maturity, days to flowering on grain yield per plant while it is also reported that days to 50% flowering, clusters per plant and pods per plant showed positive indirect effect towards grain yield via most of the characters in *Vigna umbellata*. They suggested that selection based on clusters per plant, days to maturity and days to 50% flowering would be advantageous in improvement of seed yield in ricebean

Lokesh *et al*. (2003) observed high direct and positive effect were recorded for cluster per plant, days to flowering, pods per cluster, 1000 grain

weight and pod length. The indirect effect of various characters via other character was also recorded.

Rahim *et al*. (2010) observed that number of pods per plant and number of seeds per pod are the important characters for increasing seed yield with positive direct effects.

Machikowa and Laosuwan (2011) reported high positive direct effect on seed yield and branches per plant while indirect effects for most characters were high through pods per plant. They suggested that genotypic correlations and path analyses will have efficiency in selection for seed yield in early maturing soybean through the selection of pods per plant.

Mahto *et al*. (2016) observed that the characters seed yield per plant, number of pods per plant, number of branches per plant and plant height had high positive direct effects towards seed yield in fababean.

2.2. Crude protein

Singh *et al*. (1980) reported that rice bean protein content of seeds of rice bean varied from 17.81 to 25.18 per cent. A similar result was reported by Singh *et al.* (1985). Whereas, Rodriguez and Mendoza (1991) compared three varieties of rice bean and reported that rice bean had 17.26 to 21.42 per cent crude protein content.

Igbedioh *et al*. (1995) noticed the effect of processing on biochemical constituents of pigeon pea and climbing bean (rice bean) and reported that the crude protein content in rice bean was 18.50 per cent. Saikia *et al*. (1999)

found variation in the protein content in different rice bean genotypes and present between 16.9 to 18.0 per cent.

Jilani *et al.* (2001) studied the quality characteristics of five forage crops viz. rice bean, cow pea, lablab bean, sesbania and sorghum and reported that the crude protein in rice bean and cow pea seeds were 20.00 and 21.00 per cent, respectively. Srivastava *et al.* (2001) compared the nutritional quality of seventeen rice bean genotypes and reported that the crude protein content varied from 20.34 to 22.97 per cent. According to Kaur and Kawatra (2002), the raw seeds of rice bean contained 260.3 g/kg crude protein content.

Khabiruddin *et al.* (2002) observed variations in crude protein content in dry mature seeds of the rice bean genotypes from 15.8 to 19.0 per cent.

Saharan *et al*. (2002) observed that rice bean had 18.2 g per 100g crude protein content. Sadana *et al.* (2006) investigated fourteen genotypes of rice bean and reported the protein content to range from 17.3 to 19.9 per cent. Whereas, Raiger *et al*. (2010) that the values of crude protein content in rice bean genotypes varied between 17.5 to 21.0 per cent.

Awasthi *et al*. (2011) reported that crude protein content in rice bean varied between 17.9 to 19.4 per cent. Katoch (2011) also observed that crude protein content in rice bean as 22.75 per cent.

2.3. Genotype and Environment interaction

Comstock and Moll (1963) categorized the environment as micro and macro while Allard and Bradshaw (1964) divided the environmental

variation into two factors *i.e.* predictable (soil type, planting date and agronomic practices) and unpredictable (seasonal fluctuation in weather and other factors). Baker (1988) reported that the interaction of cultivar with environmental factors is an important consideration for plant breeders. Genotype x environment interaction (GEI) has been defined as failure of genotypes to achieve the same relative performance in different environments.

Genotype and Environment interaction should be investigated so that the breeder can decide to restructure the programme to minimize the interaction effect or exploit it to produce varieties with specific adaption to particular environment (Eisemann *et al*. 1990). Genotype and environment interaction of an individual is determined by both genotype and the environment; these two effects are not always additive which indicates that GEI are present. The interaction indicates that genotypes react in different ways to variables environmental condition. Beck *et al.* (1991) reported that when genotypes are grown under a wide range of environments and outside their usual adaptation zone, the occurrence of large GEI is expected. Key concept of GEI analysis is genotype stability and by definition, genotypes exhibiting a high degree of GEI are unstable across sites (Berger *et al*. 2007). Large GEI makes it difficult for the identification of better performing genotypes. The GEI is of practical significance when the ranking of genotypes varies among environments; this is known as crossover interactions (Crossa and Cornelius, 1997, Masindeni, 2013). Understanding the cause of GEI is important as it helps in selecting varieties with the best adaptation and that can give stable yields. Varieties that show low GEI have high stable performance which are desirable for crop breeders and farmers, because that indicates that the environment has less effect on them and their good performance is largely due to their genetic composition.

Dobhal & Gautam (1994) observed that ricebean lines showed differential response when grown in different environment. Genotype x Environment interaction was significant for all the traits indicating that the genotypes were markedly interacting with environments for all the traits.

Singh *et al*. (1998) observed fifteen genotypes of rice bean over six environments and revealed that the mean square due to genotypes wee significant for all the traits, indicating the presence of variation among the genotypes.

Thaware *et al.* (1998, 2000) evaluated sixty genotype of ricebean and observed highly significant variation among the genotypes with high significant interaction between G x E interaction also reported that the major was attributed by G x E (linear) component.

Moldovan *et al*. (2000) indicated that genotype-environment interaction are of major importance because they provide information about the effects of different environment on genotype performance and play a key role for the assessment of performance stability of the breeding material germplasm. GxE analysis is used to provide unbiased estimates of yield and other agronomic characteristic and to determine yield stability or the ability to withstand both predictable and unpredictable environmental variation (Kamdi, 2001).

A set of eight elite lines of ricebean was tested in multilocational trial during Kharif 2000 at three diverse environments in randomized block design with three replications. Genotype x Environment interactions leading to stability were worked out which indicated that variance due to environments and deviations to be significant. Sinha *et al.* (2000) reported

that the genotype x environment interactions were significant in case of number of branches per plant, days to first picking, number of pods per plant, number of pods per cluster, pod length, pod diameter, pod weight, pod yield per plant. The linear component of G x E interaction was found to be significant for all the characters except number of pods per plant, number of pods per cluster and pod length. The G x E interactions (linear) was also significant when tested against pooled error. The variance showed a rational uniformity for the characters studied Shukla *et al*. (2003).

Hossain *et al*. (2003) in there studied on Genotype x Environment interaction across five environments with different sowing dates on different traits observed significant difference in genotype, genotype-environment interaction. Days to maturity, number of branches per plant and 100 seed weight was found stable.

Twenty six cowpea (*Vigna unguiculata* L.) genotypes were evaluated for the estimation of genotype x environment interaction and stability of cowpea genotypes under five different environmental conditions by Ali *et al*. (2004). They reported that some genotypes showed excellent and trustworthy stable performance over different environment based on three parameters (high mean seed yield, non-significant regression coefficient and deviation from regression).

The variety Konkan rice bean-1 (RB-10), a fodder type cultivar, was developed by single plant selection through multi-environment testing and found to be superior over the control Rb-6. Thaware *et al*. (2005).

Singh *et al*. (2009) in their investigation on stability of mungbean genotype in three locations revealed significance of environment (linear)

component for all the characters in pooled analysis indicated existence of substantial differences among the three environment in respect to their influence on expression of six characters in eighty genotypes.

Akhtar *et al*. (2010) studied in fifteen Mungbean genotypes under five locations for genotype x environment interaction to study stability parameters that is high mean seed yield, regression coefficient and deviation from regression.

Fifteen genotype of mungbean were evaluated over five locations and observed that the genotypes x environment and both variance due to genotype and environment were found to be significant, Lal *et al*. (2010).

Arslanoglu *et al*. (2011) also reported significant G×E interaction in the protein content of eight soybean cultivars, but they did not estimate the adaptability and stability parameters.

Chaudhari *et al.* (2013), based on their study on 36 genotypes of cowpea under four seasons observed that magnitude of genotype x environment linear and pooled deviation from linearity was high for protein content.

Firas and AL-Aysh (2013) observed that GEI was found to be highly significant ($P \leq 0.01$) for all the characteristics studied; the number of podded branches per plant, the number of seeds per pod, 10-green pod weight (g) and seed yield per plant (g) which was investigated using parameters of coefficient regression (b_i) and deviation from regression line (S^2di).

Tony *et al*. (2013) in there studied on Genotype and Environment interaction on yield and related traits on soyabean in different planting dates revealed the effect of genotype (G), environment (E) and G × E interactions on pod number per plant; plant height, first pod height, number of branches per plant, leaf area, number of days to 50% flowering and seed yield were found significant.

Gupta *et al. (*2014) observed that significant mean squares due to G x E interaction indicated that the genotypes interacted considerably with environmental conditions that existed over different years. The environment (linear) and environmental interaction [G x E (linear)] components were highly significant for all of these 6 traits. Significant pooled deviation (non-linear) was observed for grain yield per plant and pod yield per plant. Significant pooled deviation suggested that the performance of different varieties fluctuated considerably in respect to their stability for these characters.

Danillo *et al*. (2016) evaluated forty-four inbred lines and cultivars under seven different environmental conditions, either rain-fed or irrigated crop management, in seven sites the Brazilian semi-arid region. Statistically significant differences in the genotype as well as in the genotype environment interaction were observed in all the assays. The inbred lines presenting the highest protein contents showed the lowest grain yields, and it indicated the prominent “phenotypic cost” of protein in overall cowpea seed production. However, the breakage between the herein assessed associations was observed in inbred lines subgroups such as ‘C3Q’, ‘C3M’, ‘C2S’, and ‘CIJ’. These lines showed yield close to or above 1050 kg per ha and mean protein content of 27%, as well as good adaptability and stability in different environments.

2.4. Stability studies (Eberhart and Russel model)

Generally, the term stability refers to the ability of the genotypes to be consistent, both high or low yields levels in various environments. The yield Stability of performance is one of the most desirable properties of a genotype to be released as a variety for cultivation. Stability is a complex product of genetic yield potential to stress conditions. As a result, several methods of measuring and describing genotypic response across environments have been developed and utilized. For this purpose, multilocational trials, over a number of years are conducted. Sometimes unilocational trials can also serve the purpose provided different environments are created by planting experimental materials at different dates of sowing, using various spacing, doses of fertilizers and irrigational levels, etc (Luthra eta al. 1974 and Tehlan,1973.). The stability of varieties was defined by high mean yield and regression co-efficient close to unity and deviation from regression as small as possible. The stability of seed yield in different crop has statistically evaluated through analysis of GEI in cultivar adaption traits conducted over several environments (Crossa, 1990, Piepho, 1998). Phenotypic stability has two concepts, static and dynamic (Becker & Leon, 1988). The static phenotypic stability exists when a genotype maintains its performance independently of variations in the environmental conditions. This type is called biological stability. A genotype has dynamic stability if its performance varies with environmental changes but in a predictable way. This kind of stability is called agronomic stability.

The phenotypic stability can be defined as the ability of genotype to produce a narrow range of phenotypes in different environments. Phenotypically stable varieties are desired for commercial production of crop plants. In breeding programmes, it is also important to screen and identify

phenotypically stable genotype which could perform more or less uniformly under different environmental conditions. However, a better way of ascertaining phenotypic stability was given by Finlay and Wilkinson (1963). They considered linear regression slope as a measure of stability. Eberhart and Russell (1966) emphasized on the need of considering both the linear (b_i) and non-linear (S^2di) component of genotype-environment interaction in judging the stability of genotypes. Perkins and Jinks (1968) used regression coefficient and the deviation from regression, as the parameters of stability, but regression of genotype x environment interaction obtained on environmental index. Genotypes x environment interactions which commonly occur in plant material are of considerable importance in developing improved varieties. Hence in recent years much emphasis has been laid on nature of G x E interactions. Later Paroda and Hayes (1971) advocated that linear regression could simply be regarded as a measure of response of a particular genotype, whereas, the deviation around the regression line is considered as a measure of stability, genotype with the lowest deviations being the most stable.

Eberhart and Russell (1966) model consists of three parameters, (a) mean yield over locations or seasons, (b) regression coefficient and (c) deviation from regression. According to this model a stable variety is one with a regression coefficient of unity (b=1) and a minimum deviation from the regression line (S^2 d=0). Using their definition a breeder would usually desire to develop a variety with high mean yield and satisfying the above requirements for stability (Phundan and Narayanan, 2004). Eberhart and Russell (1966) method was preferred because of its explicit nature. Perkin and Jinks (1968) described a regression coefficient similar to that of Finlay and Wilkinson except that the observed values are adjusted for location effects before the regression. Grausgruber *et al*, (2000) and Rharrabti *et al*,

(2003) suggested yield stability has been the prime objective of plant breeders, recently, emphasis is being laid on stability of its quality components as well.

Joshi (1972 and 1969) evaluated the stability of six Mungbean varieties for the seed yield and reported the presence of G × E interaction for all the genotypes studied.

Reddy *et al*. (1990) studied stability analysis of yield for eleven genotypes of green gram in different seasons showed that genotype PIMS 88-4 was stable for plant height and RGG-88-4 reported above average response for plant height. Pusa-115 and ML-267 were most stable genotypes for cluster per plant while UPM-89-3-4 suitable in poor environment. For pods per plant PDM-54 genotype was stable. All genotypes were found unstable for seed yield. However, Pusa 54 and UPM-79-1-12 were suitable for seed yield/plant.

Gupta *et al.* (1991) carried out stability analysis of 30 genotypes of mungbean in 6 environments for seven characters viz, days to maturity, plant height, number of branches per plant, number of pods per plant, seeds per pod, 100 seed weight and seed yield per plant. The analysis of variance for stability revealed significant difference among genotypes, environment and GEI for all the characters studied.

Naidu and Satyanarayana (1991) evaluated stability for 20 genotype of mungbean in 6 environments for 6 characters. They noted that both linear and non-linear components of GEI were significant for all the characters.

Mishra (1994) on 11 genotypes of rice bean revealed that the genotype SRBS 74 had high mean for grain yield with regression value close to unity and less deviation from regression hence it is stable for different environmental condition. However the genotypes SRBS 23, SRBS 50 and SRBS 60 showed unstable in performance as they had high deviation from regression.

Singh and Sohu (1995) determined the stability of two groundnut multiline along with their four respective component lines with two checks over 12 unilocational environments. Each multiline was constructed from a different cross (multiline 1 from M 145 x NCA 1107 and Multilines 2 from M 37 x NCA 1107) in Fs by compositing equal proportions of seed from four phenotypically similar sib lines. The G x E interaction was highly significant for pod yield. Multilines were stable across environments but some component lines (pure lines) were superior in pod yield and were also as stable as the multiline themselves.

Singh *et al*. (1998) while evaluating fifteen genotypes of rice bean, under six environments reported that the genotypes RCRB1-301 and EC 18585 were stable with regression coefficient near unity and minimum deviation from regression for days to 50% flowering. The genotype RCRB1-301 was stable for days to maturity and least responsive to environment variations.

Wilmar *et al. (*2000) in their studies on stability on different sowing dates Sept 27, Oct 20, Nov 17, and Dec 17 in 1993/94 and Sept 20, Oct 20, Nov 17, and Dec 14 in 1994/95 reported that procedures of regression analysis and minimum variance among planting date means were efficient for selecting stable lines during the four sowing seasons. High yielding

genotypes with lower values for the variance among sowing date means (VM) and for the residual variance (RV) were found to be ideal and genotypes with small VM values are more stable across the different sowing dates.

Minimol *et al.* (2000) studied 10 genotypes of groundnut in six environments in two seasons, i.e. *Kharif* and summer, for six quantitative traits viz., seed weight per plant, shelling per cent, Pod yield per plot, oil content and worked out stability. G x E interactions were observed to be significant for all traits. Non-linear components of G x E interactions were important for shelling percentage, pod yield per plot and oil content. For seed weight per plant and 100-pod weight, however, linear as well as non-linear components were observed to be important.

Muhammad *et al*. (2003) evaluated stability of grain yield for twenty-five genotypes of chickpea under 12 diverse environments within Pakistan found that G X E interaction was highly significant and both linear as well as non-linear components were equally important for determining the yield stability. The genotypes; 96051, 90280, C44, 91A039, NCS95004, NCS950010, NCS950180, 99101, A-16, 91A001, NCS950012 and 93009 produced above average yield. The genotypes 96051 and 98280 gave highest grain yield but their high deviation from regression showed fluctuation in the performance under different environments. The genotypes C44, NCS950183 and 93009 had also above average yield but their low deviation from regression revealed more stable performance compared to others.

Shukla *et al*. (2003) evaluated eight elite lines of rice bean. Genotypes (G) x Environment (E) interactions leading to stability were worked out for

green forage and dry matter yield and plant height. Results indicated variance due to environments and deviations to be significant.

Alghamdi (2004) evaluated Five soybean genotypes (Giza 35, Crawford, Giza 82, Clark and Giza 111) were evaluated in six sowing dates (Feb. 25, Mar. 25, Apr. 25, May 25, June 25 and July 25) during the two consecutive growing summer seasons of 2000 and 2001 to explore the genotypes x environment effects and stability in performance of soybean genotypes for seed yield.

Rao *et al.* (2004) evaluated ten Mungbean genotypes at five locations to study their stability. The genotype MGG-347 was considered as the most stable among all the genotypes and its performance could be predicted over the environments.

Javed *et al*. (2006) observed six maize genotype across six environments and reported that pooled analysis of variance for grain yield was significantly different for genotypes across the environments.

Singh *et al*. (2006) observed highly significant pooled deviation for all the characters except days to flowering, pods per cluster, pod length, seeds per pod and seed weight and also suggested that the performance of the various genotypes under study fluctuated significantly from their respective linear path of response to environments.

Gyanendra *et al*. (2007) in their studies on fifteen genotypes of rice bean under six environments for three consecutive years observed stable genotypes for different traits, pods per plant, pod length, number of seeds per pod, 100 seed weight and seed yield.

Kavitha *et al*. (2009) in their study on stability performance of 20 malt barley genotypes involving commercial cultivars and elite lines were compared by using regression on environmental means for grain yield and its components such as days to flowering, plant height, tillers per plant, grains per spike, grain weight per spike and 1000- grain weight in eight unilocational environments revealed significant among the genotypes for all the traits studied in all the eight individual environments.

Sarvamangala *et al.* (2010) studied twenty genotypes of cowpea were evaluated over three seasons to study the stability parameters viz., regression coefficient (b_i) and mean square deviations (S^2di) from linear regression along with per se performance for five yield related traits. Variances due to genotype, environment, genotype x environment, environment + (genotype x environment), environment (linear) were significant for pod per plant and seed yield per plant.

Gupta *et al*. (2014) in their studies on fifty two rice bean genotypes during Kharif seasons for three consecutive years observed suitable genotypes for cultivation in NER region and identify suitable parents for hybridization programmes. Two lines, IC-187911 and RCRB 1-3 with high grain yield per plant, average stability and predictable performance over three years, were identified as suitable for cultivation in the region.

Gabriel *et al* (2015) evaluated twenty nine cowpea genotypes, including four Ugandan genotypes, for grain yield, protein stability and adaptability under diverse environments in a randomized complete block design with three replications. The analysis showed that cowpea grain yield and protein content were significantly ($P < 0.01$) affected by genotypes (G), environments (E), and interaction (G x E).

Santos *et al.* (2015) evaluated twenty cowpea genotypes and observed that, the genotypes MNC03-737F-5-1 BRS-Tumucumaque, BRS- Guariba, MNC02-684F- 5-6, MNC03-725F-3, MNC02-682F-2-6, BRS-Cauamé, BRS-Itaim and MNC03- 737F- 5-11 showed adaptability and stability sufficient for recommendation for the region by using Eberhart and Russell method.

Sunayana *et al*. (2018) in their studies on genotype × environment interaction for stability of yield potentiality in Asiatic cotton on three different date of sowings (10-04-2015, 15-05-2015, 5-06-2015, 26-04-2016, 5-05-2016 and 2-06-2016) during *Kharif* seasons of 2015 and 2016 observed that mean square due to genotypes x environment (linear) were significant for all the characters indicating the preponderance of linear component of G x E interaction than non linear component. The cotton varieties HD 123 and HD 432 were recorded high mean with regression coefficient (b_i) near unity and non significant deviation from regression (S_2d_i) for seed cotton yield per plant, lint yield per plant and monopods per plant indicated that these genotypes had average response and high stability over the environments. The estimation of environmental additive effect (I_j) estimates revealed that environment 4 was best for seed cotton yield and lint yield.

2.5. Additive Main Effects and the Multiplicative Interaction Analysis (AMMI) model.

Among multivariate methods, the additive main effects and the multiplicative interaction analysis (AMMI) model is widely used in GEI studies for different crops (Singh *et al.* 2000 and Crossa *et al.* 1990) to separate the additive portion from interaction by way of an analysis of

variance. AMMI model has been revealed to be more efficient because it captures a large portion of the GxE interaction sum of squares and separates main and interaction effects that present agricultural researchers with different opportunities. (Ebdon and Gauch, 2002; Bose *et al*., 2014). AMMI biplot analysis is considered to be an effective tool to detect the GxE interaction patterns graphically. The AMMI model describes the GxE interaction in more than one dimension and it offers better opportunities for interpreting GE interaction than analysis of variance (ANOVA) and regression of the mean (Vargas *et al.* 2001). AMMI (additive main effects and multiplicative interaction) models were used to represent an additive component, and the effect of interaction (Gauch, 1992). Furthermore, statistical model results from AMMI analysis are plotted in a graph showing the main and interaction effects for both genotypes and environments on the same scatter plot, with the noise rich residual discarded and the data separated into a pattern rich model to gain accuracy (Gauch and Zobel, 1996). Purchase (1997) developed the AMMI Stability Value based on the AMMI model's principal components axis 1 and 2 respectively scores for each cultivar. In general, the ranking of genotypes changes from one environment to another and this is also an indication for the existence of G x E interaction due to variation among the testing environments. The ASV parameter has been used as an auxiliary criterion to define more stable genotypes in other crops such as wheat Farshadfar *et al*, (2011) and rice Das *et al*, (2010).The YSI method incorporates both yield and stability into a single index, reducing the problem of using only yield stability as the sole criterion to select varieties, taking into account that the most stable genotypes do not always have the best yield performance Oliveira and Godoy, (2006). The YSI parameter associated with genotype classification is based on the ASV parameter (which accounts for IPCA1 and IPCA2). This

method has been successfully used in other crops, such as wheat Farshadfar, (2008).

Samonte *et al*. (2005) compared the performance of six cultivars of rice across three main cropping seasons at four locations using AMMI analysis and reported highest yielding cultivars at different environments as well as ideal cultivars and test locations.

Nimbalkar *et al*. (2006) evaluated eleven French bean genotypes including four checks during Kharif 2002 at five different agro climatic zones and analysed by using AMMI model. It was reported that the ANOVA exhibited significant for genotypes main effect, environmental additive effect and G X E interaction.

Mohammed (2009) conducted experiment involving eight wheat lines with four checks across five environments during 1992-96.AMMI model of analysis was employed to assess the phenotypic stability of these genotypes and observed significant differences among genotypes, environments and GxE.

Chaudhary and Wu (2011), evaluated fifteen varieties of soybean for stability of grain yield (ton/ha), protein content (%), and oil content (%) at six different locations of Eastern South Dakota. Mixed linear model and Additive main effects and multiplicative interactions (AMMI) were applied to detect genotype-by-environment (GE) interactions and stability of each variety regarding these three traits. Variance components for genotypic and GE interaction effects were significant for all these three traits, indicating that the tested genotypes ranked differently at these locations. Based on AMMI analysis, genotypes HEFTY H15Y12 and HEFTY H19Y12 for grain

yield, genotypes HEFTY H12Y12, SD 2172, NORTHSTAR 1325R2, and NORTHSTAR 1726NR2 for protein content, and genotypes HEFTY H12Y12 and NUTECH 6145 for oil content had general adaptability under the conditions of Eastern South Dakota.

Thangavel *et al.* (2011), in their studied on additive main effects and multiplicative interaction (AMMI) model on the yield and yield component traits data of 58 mungbean genotypes grown in six moisture stress location-year environments observed that Main effects due to environments (E), genotypes (G) and G × E interaction were found significant for plant height, number of branches per plant, number of clusters per plant, number of pods per plant, 100 seed weight and grain yield per plant. Interaction Principal Component Axis 1 (IPCA 1) and IPCA 2, statistically significant ($P < 0.01$) for all the traits studied. The IPCA 1 of traits studied was accounted more than 62% of the G × E sum of squares.

Tolessa *et al*. (2013) evaluated fourteen field pea genotypes at sixteen environments during 2007 and 2008 and observed that pooled analysis of variance for grain yield showed significant differences among the genotypes, environment and GXE interaction effects. The application of AMMI analysis biplots facilitated the visual comparison and identification of superior genotypes that support decisions on variety selection and recommendation in different environments.

Bose *et al.* (2014) reported that nine genotypes possessing cold tolerance at seedling stage over four environments was analysed to identify stable high yielding genotypes suitable for boro environments for genotypes x environments interaction using AMMI, AMMI stability values(ASV), and Yield stability index(YSI).The combined analysis of variance shows that genotype, environments and GxE interaction are highly significant which

indicates possibility of selection of stable genotypes across the environments. The results of AMMI analysis indicate that the first two components were highly significant. The study revealed that genotypes GEN6 were found to be more stable based on all stability analysis. The above mention stability analysis could be useful for identification of stable high yielding genotypes and facilitates visual comparisons of high yielding genotype across the multi-environments.

Oliveira *et al*. (2014) reported high yield stability and adaptability in yellow passion fruit using AMMI analysis. Twelve varieties were evaluated in eight environments and observed that analysis of variance for genotype, environments and GxE interaction showed attributable effects. The first two multiplicative components of the interaction accounted for 68% of the total sum of squares. The scores of the principal components showed high variability for the environments relative to variety effects. High varietal phenotypic stability was observed in three environments, which can be used in yellow passion fruits breeding programs for initial selection. A biplot-AMMI analysis and yield stability index incorporating the AMMI stability value and yield capacity in a single non-parametric index were useful for discriminating genotypes with superior and stable fruit yield

Jogendra *et al*. (2018) evaluated twenty-one genotype of pigeon pea for consecutive three years under rainfed condition based upon different characters using AMMI model and reported significant differences among the years and measured more than 50% of the treatment sum of squares. It was also reported that PCA1 of the interaction captured more than 60% of the interaction sum of squares for almost all the traits. Nine stable and high yielding genotypes *viz.,* PUSA 2003-1; CORG-2001-5; WREG- 28; PANT-A-286; H-94-6; GT 101; ICPL-99004; ICPL-85010 and UPAS-120 exhibited

stable performance under the rainfed environmental conditions for more than one traits studied and also under more than one year.

Mohanlal *et al.* (2020) evaluated twenty-one black gram genotypes for three seasons from Rabi 2017 to Rabi 2018 to assess the genotype x environmental interactions. Analysis of variance for the pooled data over seasons showed significant difference between genotypes, seasons and the interaction between genotypes and seasons for seed yield per plant. Genotypes recorded high yield during Rabi seasons as compared to that of Kharif season which showed that winter season was more favourable for black gram cultivation. According to AMMI biplot 2, KGB-28 was comparatively non-sensitive to environmental interactive forces with significant high seed yield per plant. Hence this genotype (KGB-28) can be selected for seed yield per plant. Based on the present study, the genotype KGB-28 can be recommended as a stable genotype for black gram cultivation.

MATERIALS AND METHODS

The present investigation entitled "**Studies on Genotypic x Environmental Interaction on Rice bean [(*Vigna umbellata* Thunb.) Ohwi and Ohashi] Landraces of Nagaland"** was carried out during *Kharif and post Kharif* season for six sowing dates with fifteen days interval during 2016-2017 and 2017-2018, at School of Agriculture and Rural Development (SASRD), Medziphema Campus, Nagaland, experimental farm (Genetics and Plant Breeding).The techniques followed and materials used during the course of investigations are presented under following sub headings**:**

3.1. Experimental design and site

The experiments included thirteen landraces of rice bean genotypes. Field experiments were conducted at the experimental farm, SASRD, Medziphema, Nagaland. All the experimental material was grown in six environments which comprised of two years, 2016-2017 and 2017-2018 growing season with different dates of sowing. Thus the following six environments were created by the following growing season, Environment one (Env-1): 1st June, 2016-2017, Environment two (Env-2): 15th June, 2016-2017, Environment three (Env-3): 1st Aug, 2016-2017, Environment four (Env-4): 1st June, 2017-2018, Environment five (Env-5): 15th June, 2017-2018, Environment six (Env-6): 1st July, 2017-2018. In each of the six environments each genotypes of individual experiment was conducted in Randomized block design (RBD) with three replication in each of the individual environments at an interval of fifteen days. The details of Environment are as follows (Table 1).

Table 1. Details of different environment and notation

Environment	Sowing dates (with fifteen days interval)
Env 1	Kharif (1st fortnight)-1st July, 2016-17
Env 2	post Kharif (2nd fortnight)-15th July, 2016-17
Env 3	post Kharif (1st fortnight)-1st August, 2016-17
Env 4	Kharif (1st fortnight)-1st June, 2017-18
Env 5	Kharif (2nd fortnight) -15th June, 2017-18
Env 6	Kharif (1st fortnight) -1st July, 2017-2018

Sometimes the unilocational trials can also serve the purpose provided different environments are created by planting experimental material at different sowing dates on the same location (Luthra *et al*. 1947 and Tehlan, 1973). Mather and Jinks (1982), Mukai (1988), and Wu and O'Malley (1998) reported on two types of environmental variations: (1) micro environmental, which cannot easily be identified or predicted (e.g., year-to-year variation in rainfall, drought conditions, extent of the insect damage) and (2) macro-environmental variances which can be identified or predicted (e.g., soil type, management Practices, controlled temperatures).

3.1.1. Climatic condition

The sites of the experimental areas fall under sub-tropical climate with high humidity and moderate temperature with medium to high rainfall. The

Table 2. Metrological data during the period of crop investigation (June 2016-December 2016)

Month	Temperature (c)		Relative humidity (%)		Total Rainfall (mm)
	Max(c)	Min(c)	Max	Min	
June	31.52	24.90	89.00	68.50	47.72
July	32.32	25.56	91.75	72.25	63.75
August	33.80	24.36	92.40	69.00	82.40
September	32.55	23.95	94.00	73.00	69.40
October	31.56	21.74	93.80	69.20	7.16
November	27.55	15.22	94.85	63.67	32.67
December	26.55	11.02	94.50	53.50	1.45

Source: ICAR Regional centre, Jharnapani, Nagaland

Table 3. Metrological data during the period of crop investigation (June 2017-December 2017)

Month	Temperature (c)		Relative humidity (%)		Total Rainfall (mm)
	Max(c)	Min(c)	Max	Min	
June	31.60	23.80	93	72	278.7
July	31.40	24.40	94	75	485.6
August	32	24.70	93	72	492.5
September	31.60	24.70	95	74	235.9
October	30.68	23.50	95	72	33.90
November	28.1	16.3	96	63	16.4
December	25.5	12.3	96	66	31.8

Source: ICAR Regional centre, Jharnapani, Nagaland

temperature ranges from 12° C during winter to 32° C during summer. The average annual rainfall varies from 2000 to 2500 mm. The meteorological data's taken during the periods of investigation (2016 and 2017) are presented in Table 1 and Table 2, respectively.

3.1.2. Soil condition

The soil is acidic in nature with pH varying from 4.5 - 6.2. The organic matter content is low which varied from 1.2 - 2.9 %.

3.1.3. Field preparation

The experimental areas were prepared as follows during the two seasons; the land was ploughed by tractor in the month of March, which was followed by two harrowing with the help of tractor drawn disc harrow. After thorough preparation of soil, plots were kept for solarization. For adequate nutrient supply for its optimum production, farm yard manure was applied in plots during field preparation.

3.1.4. Aftercare and Intercultural operations

With a view to minimize the interference of weeds with crops, attention was given to weed control, The first weeding was done after 25-30 days of transplanting by simply scrapping the soil and hand weeding with very light earthing up. The second intercultural operation was done similarly after 40-50 days. In the subsequent months very few weeding was done accompanied by light hoeing. Monsoon rain was the only source of irrigation throughout the experimental period.

3.2. Experimental details

3.2.1. Source of planting material

The experimental materials were collected from farmers cultivating ricebean focusing from three district of Nagaland, viz, Tuensang, Wokha and Medziphema. The experimental material used in present study comprised of thirteen genotypes (Details given below) of Rice bean.

Sl. No.	Genotypes	Place of collection	Source
1	RbnG1	Wokha	Farmers
2	RbnG2	Wokha	Farmers
3	RbnG3	Socünoma village	Farmers
4	RbnG4	Wokha	Farmers
5	RbnG5	Medziphema	Farmers
6	RbnG6	Medziphema	Farmers
7	RbnG7	Tuensang	Farmers
8	RbnG8	Wokha	Farmers
9	RbnG9	Tuensang	Farmers
10	RbnG10	Wokha	Farmers
11	RbnG11	Tuensang	Farmers
12	RbnG12	Tuensang	Farmers
13	RbnG13	Wokha	Farmers

Analysis of GEI and stability has not received much attention in North-east India as evidenced by low availability of widely adapted Ricebean cultivars in the region. Therefore, this study was undertaken only on fixed/selected genotypes which are commonly used by farmers of these

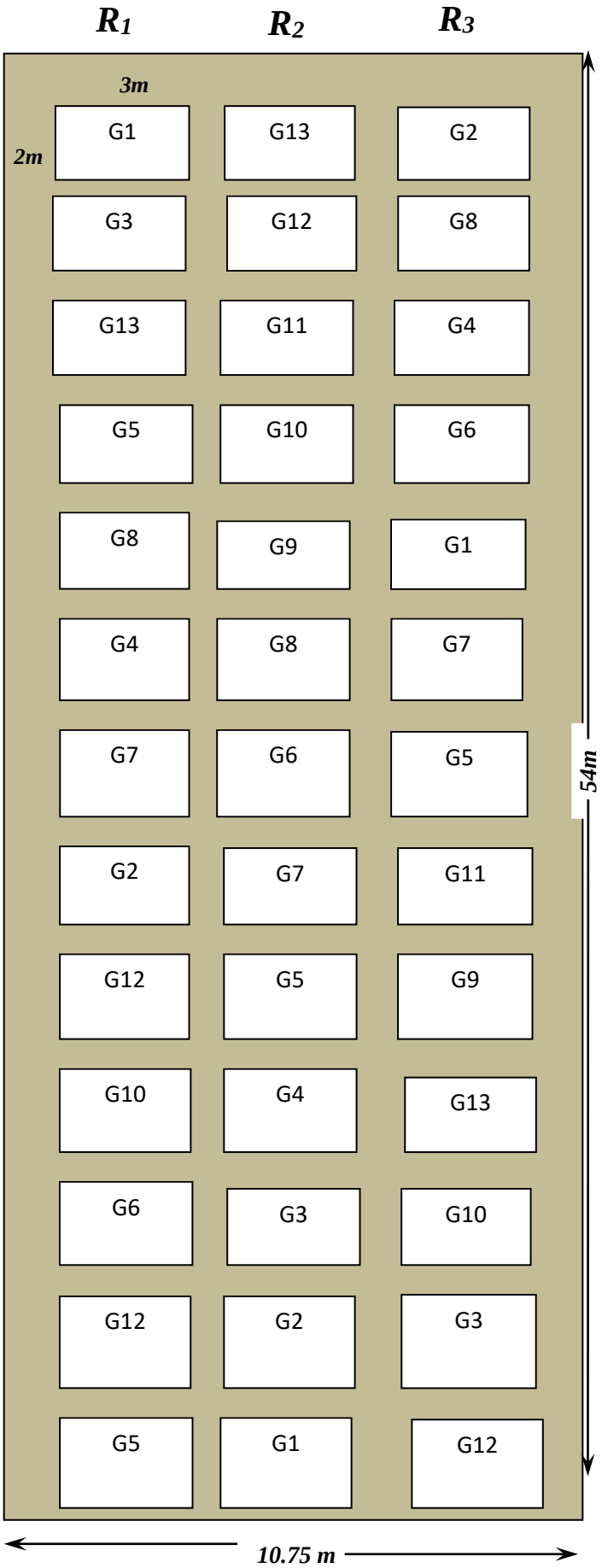
Plate.no. 1. Seeds of different Landraces of Rice bean

respective districts. In order to identify and recommend high yield and stable genotypes for wide and specific production as well as to identify informative and representative test environments in the state.

3.2.2. Details of layout

The experiment was laid out in Randomized Block Design (RBD) with three replications for different Individual environments. Each replication consists of thirteen genotypes and genotypes are randomly allocated to the plots in each individual environment. The Layout plan is given in Fig. 1 and other details are given as below:-

Crop	: Rice bean
Season	: Kharif and post Kharif
Design	: Randomized Block Design
Replication	: Three
Genotypes	: Thirteen
Total number of plots	: 78
Plot size	: 3.0 x 2.0 sq. m
Row to row distance	: 1m
Plant to plant distance	: 50 cm
Number of rows in each plot	: 3
Number of plants per row	: 7
Total number of plants per plot	: 21
Number of plants for observation per plot	: 5



Landraces

RbnG1 - Wokha

RbnG2 - Wokha

RbnG3 - Socünoma village

RbnG4 - Wokha

RbnG5 - Medziphema

RbnG6 - Medziphema

RbnG7 -Tuensang

RbnG8 - Wokha

RbnG9 - Tuensang

RbnG10 - Wokha

RbnG11 - Tuensang

RbnG12 - Tuensang

RbnG13 - Wokha

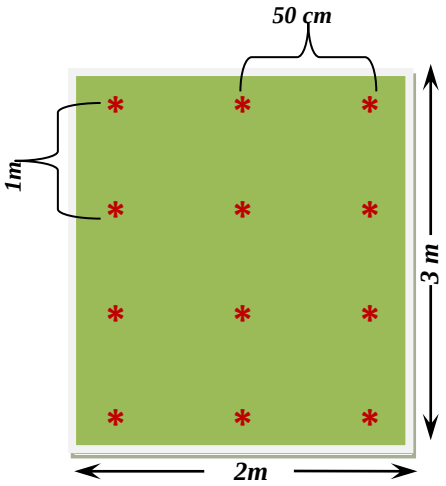


Fig. 1: Layout of the Experiment in Randomized Block Design (RBD) for individual environment. In each replication genotypes were allocated randomly.

3.3. Observations recorded

For collections of datas, five randomly plants were selected from each plot and replication for eleven characters to be studied *viz*, primary branches, number of pods per cluster, number of pods per plant, pod length (cm), number of seeds per plant, plant height, 100 seed weight (g), protein content (%) and seed yield per plant (g). For days to 50% flowering and days to 80% maturity data were recorded based on visual observation.

3.3.1. Days to 50 % flowering

Total numbers of days were observed from sowing till the date when 50 % plants in each plot were flowered and the average number of days for 50% flowering was calculated.

3.3.2. Primary branches

Numbers of branches on five randomly selected plants were counted and average was worked out.

3.3.3. Number of pods per cluster

Total numbers of pods per cluster were counted at maturity and average was taken.

3.3.4. Number of pods per plant

Total number of pods per plant was recorded at maturity and average was calculated.

3.3.5. Length of Pod (cm)

The length of five randomly selected pods was measured in centimetre in each of the five observational plants and average was calculated.

3.3.6. Number of seeds per pod

Total number of seeds per pod counted at maturity and average was calculated.

3.3.7. Plant height (cm)

Plant height was measured at maturity, from ground level to the top of main shoot and average was worked out.

3.3.8. Days to 80% Maturity

The total number of days from sowing to the date when 80% maturity of the plants in a plot were dry and matured was observed and average was calculated.

3.3.9. 100 seed weight (g)

The weight of 100 seeds of five randomly selected plants was weighed for each genotype and average was recorded.

3.3.10. Seed yield per plant (g)

The seeds obtained from five randomly selected plants were weighed, and average yield per plant was calculated.

3.3.11. Crude protein (%)

The seeds of selected genotypes from each plot and replication were collected after harvest and seeds were dried in the sun for few days. After

drying of the seeds 5 gram of sample seeds was grinded for crude protein analysis.

3.4. Statistical analysis

3.4.1. Analysis of variance

The data based on the mean of individual environment and pooled over environments statistically analyzed described by Panse and Sukhatme (1967) to find out overall total variability present in the material under study for each character and for all the populations. The first and foremost step is to carry out analysis of variance to test the significance of differences among the genotypes tested. Analysis of variances for individual environment and pooled analysis of variance were presented as follows.

ANOVA for each individual environment would be:

Source of variation	**d.f.**	**MSS**	**Expected value of MSS**	**Cal F.**
Replication	(r-1)	M1	-	M2/M3
Genotypes	(g-1) (r-1)	M2	σ2e + rσ2g	
Error	(g-1)	M3	σ2e	
Total	(rg-1)			

Where,

r = number of replications

Partitioning of pooled ANOVA would be:

Source of Variation	**d.f.**	**MSS**	**Expected MSS**
Env	e-1	MSe	-
Rep/env	e(r-1)	MSr	-
Genotypes	g-1	MSg	σ2e+σ2ge+eσ2g
Genotypes x environment	(g-1)(e-1)	MSeg	σ2e+σ2ge
Error	m*	MSe	σ2e

Where,

e: Number of environments

r: Number of replications

g: Number of genotypes under study

MSr: Sum of square for replications

MSg: Sum of square for genotypes

MSe: Sum of square for error

M* Degrees of freedom pooled over environments

MSe: Mean square due to error

A significant value of F test indicates that the test entries differ significantly among themselves, which require the computing of C.D.

$$S.Ed\pm. = \sqrt{2MSe/r}$$

Where,

S.Ed± = Standard error of the difference between two treatment means

MSe = Error mean square

r = number of replications

3.4.2. The mean of different characters were calculated as:-

Mean=Σxi/N

Where,

Σxi = Sum of all the observation for ith character.

n = Number of observations.

Range was recorded by observing the lowest and the highest mean Values for each character.

3.4.3. Estimation of genotypic and phenotypic variance

The component of variance was calculated as follows:-

Genotypic variance ($\sigma^2 g$) = Msg-Mse/r

Where,

MSg = Mean square due to genotype

MSe = Mean square due to error

r = Number of replication

Phenotypic variance (σ^2p) = $\sigma^2p = \sigma^2g + \sigma^2e$

Where,

σ^2g = Genotypic variance

σ^2e = Environmental variance

3.4.4. Estimation of phenotypic and genotypic coefficients of variation

The phenotypic and genotypic coefficients of variation in percent were estimated, given by Burton and De Vane (1952).

$$PCV\ \% = \frac{\sqrt{\text{Phenotypic variance } (\sigma 2p)}}{\text{Mean of the character}} x100$$

$$GCV\ \% = \frac{\sqrt{\text{Genotypic variance } (\sigma 2g)}}{\text{Mean of the character}} x100$$

Where,

PCV = Phenotypic coefficient of variation

GCV = Genotypic coefficient of variation

The estimates of PCV and GCV were classified according to Sivasubramanian and Madhavamenon (1973).

< 10 percent = low

10-20 percent = moderate

> 20 percent = high

3.4.5. Heritability

It is the ratio of genotypic variance to the total phenotypic variance. Heritability for the present study was calculated in broad sense by following the formula as suggested by Hanson *et al*. (1956).

$$\text{Heritability } (h^2_b\ \%) = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where, h2 ($_b$) = Heritability in broad sense

σ^2 g = Genotypic variance

σ^2p = Phenotypic variance

Heritability percent in broad sense was classified into three groups (Allard, 1960),

High = More than 70%

Medium = 50% to 70%

Low = Less than 50%

3.4.6. Genetic advance

Improvement in the mean genotypic value of selected plants over the parental population is known as genetic advance. Expected genetic advance was calculated by the method suggested by Johnson *et al*. (1955).

$$G\ A = Kx \sqrt{\sigma^2 p x \sigma^2 g} / \sigma^2 p$$

Where, GA = Genetic Advance

K = Constant (Standard selection differential) having the value of 2.06 at 5 per cent level of selection intensity

$\sigma^2 p$ = Phenotypic variance

$\sigma^2 g$=Genotypic variance

The genetic advance as percent of mean is classified as,

< 10 per cent = low

10-20 per cent = moderate

> 20 per cent = high

Genetic advance as percentage of mean was calculated by the following formula:

$$GA\ (\%\ of\ mean) = \frac{\text{Genectic advance}}{\text{mean of character}} X100$$

GA was categorized as

< 10 percent = low

10-20 percent = moderate

> 20 percent = high

3.4.7. Correlation studies

The correlation coefficient at genotypic and phenotypic levels was determined according to the formula given by Al-Jibouri *et al.* (1958) as follows:

3.4.7.1. Genotypic correlation coefficient between character x and y

$$rg_{xy} = \frac{\text{Cov.xy (g)}}{\sqrt{\text{var.x(g) X var.y(g)}}}$$

3.4.7.2. Phenotypic correlation coefficient between character x and y

$$rp_{xy} = \frac{\text{Cov.xy (p)}}{\sqrt{\text{var.x(p) X var.y(p)}}}$$

Where,

Cov.xy (g) and Cov.xy (p) denotes genotypic and phenotypic co-variance for the characters x and y respectively.

Var. x (g) and Var. x (p) denotes genotypic and phenotypic variance for the character x.

Var. y (g) and Var. y (p) denotes genotypic and phenotypic variance for the character y.

The calculated genotypic and phenotypic correlation coefficients were tested for‘t’.ss

$$t = \frac{r\sqrt{n-2}}{\sqrt{1-r^2}}$$ at (n-2) degree of freedom

The calculated t value was compared with t-value at 5 % or at 1 % probability level with (n-2) degree of freedom for its significance.

3.4.8. Path coefficient analysis

It is a simple standardized partial coefficient method to detect the direct and indirect effects of the independent variable on dependent variable. It permits separation of correlation into components of direct and indirect effects. The method of path coefficient was developed by Wright (1921) and modified by Dewey and Lu (1959). The following set of simultaneous equations were formed and used for estimation of direct and indirect effects on yield components.

$r_1y = p_1y + r_{12}p_2y + r_{13}p_3y + \ldots\ldots\ldots\ldots + r_1yp_1y$

$r_2y = r_2ypiy + p_2y + r_{23}p_3y + \ldots\ldots\ldots\ldots + r_{21}yp_1y$

$r_ky = rki + rkip_2y + r_{13}p_3y + \ldots\ldots\ldots\ldots + r_2iypiy$

$rx_ky = rxkipiy + rzk_2\ p_2y + rxk_3\ p_3y + \ldots\ldots\ldots\ldots + p_ky$

r_xky = Coefficient of correlation between the independent character.

p_iy to p_ky = Direct effects of character 1 to k on dependent character y.

r_{12} to rk-1, = Coefficient of correlation among causal factors. The above equations were written in a matrix form as under-

A C

r_1Y 1 r_{12} r_{13}…….r_1i P_1Y

r_2Y r_{21} 1 r_{23}…….r_2i P_2Y

. . .

. . .

r_kY rk_1 rk_2 rk_3……1 P_kY

Than $B = [C]^{-1} A$

Where,

C_{11} C_{12} C_{13}…….C_1i

C_{21} C_{22} C_{23}..... C_2i

[C]-1 =

.

.

Ci_1 Ci_2 Ci_3 Cii

Then the direct effects were calculated as follows –

$P_1Y=\sum_{i=1}^{k}$ C1i riy

$P_2Y \sum_{i=1}^{k}$ C2i riy

$P_kY \sum_{i=1}^{k}$ Cki rky

Residual effect was obtained as per for formula given below –

R = Σ 1-Piyriy

Where,

R = Residual effect

P = Path coefficient

r = Genotypic correlation

i = Individual trait

y = yield

Path coefficients were rated based on the scales given below.

> 1.0 = Very High

0.30 – 0.99 = High

0.2 – 0.29 = Moderate

0.1 – 0.19 = Low

3.5. Crude protein (AOAC 2000)

For protein analysis seeds from each individual environment were collected after harvest and tested. The nitrogen content of the Rice bean

Plate no.2. Crude protein analysis by KEL PLUS

Plate no 3.Overview of different growing environment at vegetative stage

genotypes was determined by the Kjeldahl method using a KEL PLUS distillation Unit which involves the following three steps;-

1. Digestion

- Digestion mixture of 1gm of grinded seed sample is prepared in digestion tube ,25ml of Concentrated Sulphuric acid, 5gm of catalyst mixture KSO4 +CuSO4 (5:1).
- The digestion mixture tube was kept in the KELPLUS machine for digestion
- Continue the digestion till the mixture turn into bluish green or greyish white
- Allow the tube to cool

2. Distillation

- Distillations involve the separation and isolation of nitrogen from the digestion tube.
- The volume was made upto the mark with distilled water and mixed. Measured aliquot (10 ml) was taken in a distillation flask and add 40% NaOH into the digestion tube through alkali loading tube
- On heating,the ammonia is distilled out and collected in 4 % boric acid(25ml) containing mixed indicator(4 drops of bromoceresolgreen and methyl red) as trapping medium
- Start distillation, light pink colour of seed sample change into sky blue colour

3. Titration

- The determination of amount of nitrogen in the condensation flask is done by titrating with 0.1N HCL. A blank sample was also run along with the sample.
- Sky bluish colour turn in to pink colour again which indicates completion of titration.

Nitrogen (%) = $\frac{Titre\ value\ x\ 0.00014x\ volume\ made}{Aliquot\ taken(ml)x\ weight\ of\ sample(g)}$x 100

Crude protein (%) = Nitrogen (%) x 6.25

3.6. Stability Analysis Eberhart and Russell's model (1966)

Following the methodology of Eberhart and Russell's model (1966), three parameters namely (i) overall mean of each genotype over a range of environments, (ii) the regression of each genotype on the environmental index and (iii) a function of the squared deviation from the regression were estimated. Eberhart and Russell (1966) used to study the stability of genotypes under different environments,

$$Y_{ij} = \mu_i + b_i I_j + \delta_{ij}$$

Where, Y_{ij} = mean of ith genotype in jth environment.

μ_i = mean of ith genotype over all the environments

b_i = regression coefficient of the i^{th} genotype on the environmental index which measures the response of this genotype to varying environments.

I_j = environmental index which is defined as the deviation of the mean of all the genotypes at a given location from overall mean with $\Sigma_j - I_j = 0$ and

δ_{ij} = the deviation from regression of the i^{th} genotype at j^{th} environment

3.6.1. Analysis of variance for stability

In this method, the total variance is first divided into two components i.e., genotype and environment plus interaction [E+ (GxE)]. The second component is further subdivided into three components, environment linear, genotype x environment (linear and pooled deviation. The variance due to pooled deviations is further divided into variance due to individual genotype.

The analysis of variance proposed by Eberhart and Russell (1966) is given below.

ANOVA to estimate stability parameters (Eberhart and Russell, 1966)

Source	d. f	S. S	MSS
Total	ge -1	$\sum_i \sum_j Y_{ij}^2$ - CF	
genotype	(g-1)	$1/e\sum_j Y_i^2$-C.F	M1
E+(GxE)	(n-1) + (g-1) (n-1) = g (n-1)	$\sum_i\sum_j Y_{ij}^2$-$\sum Y_i 2/e$	
Environment(linear)	1	$1/g(\sum_j Y_j I_j)^2/\sum_j I_j^2$	
G x E (linear)	(g-1)	$\sum_i[\sum_j Y_{ij} I_j)^2/\sum_j I_j^2]$-Env.(linear)S.S	M2
Pooled deviation	G (n-2)	$\sum_i\sum_j \delta_{ij}^2$	M3
Pooled error	n(r-1)(g-1)M	Pooled replication X genotypes SS over environment	

Where,

g= number of genotypes

e=number of environments

r=replications

According to this model, a stable genotype is the one which has regression coefficient (b) equal to unity (b-1) and deviation from regression is small ($S^2di=0$). A genotype with significant b value (b>1) is said to be highly responsive-suitable for favourable environments and with significant b value (b<1) is said to be low responsive-suitable for unfavourable environments. When deviations are not significant, the conclusion may be drawn by the joint consideration of mean yield and regression Values given (Eberhart and Russell, 1966).

3.6.2. Estimation of stability parameters

Computation of regression coefficient (bi) for each genotype

$b_i = \sum_j Y_{ij} I_j / \sum_j I^2 j$

Where,

b_i = regression coefficient of ith genotype

$\sum_j I^2 j$ = Sum of squares of environmental indices (I_j) which are common to each value of b_i.

$\sum_j Y_{ij} I_j$= Sum of products of environmental index (I_j) and the corresponding means (X) of that genotypes at each environment (Y_{ij}).

These values may be obtained as follow-

$(X)\ (I_j) = \Sigma_j\ Y_{ij}\ I_j = (S)$

(I_j) = Vector for environmental index, and

(S) = Vector for sum of products i.e., $\Sigma\ Y_{ij}\ I_j$

Computation of mean square deviation (S_2di) from linear regression is,

$S^2\ di = (\sum d^2_{ij}/n\text{-}2)\text{-}(S_e^2/r)$

Where, $\sum d^2_{ij} = \sum y_{ij}^2 - \frac{Y_i^2}{t} - \frac{(\sum Y_{ij} I_i)^2}{\Sigma I_j^2}$

S_e^2 = pooled error mean square

r = Number of replications

e = Number of environments

3.6.3. Computation of environmental index (Ij)

$I_j = \sum i\ Y_{ij}\ /g - \sum_i \sum_j Y_{ij\ /}\ ge,$

With $\sum_j I_j = 0$

Test of Significance

The mean sum of squares due to genotypes and environments were tested against pooled deviation. Whereas, mean sum of squares due to G x E interaction was tested against pooled error.

Environment (linear) and G x E (linear) were tested against pooled deviation, if pooled deviation is non-significant both these linear components were tested against pooled error. Mean sum of squares due to pooled deviations were tested against pooled error.

The following tests of significance were carried out:

1. To test the significance of the difference among genotype means namely

Ho = $\mu_1 = \mu_2 = \mu_3 = \ldots. \mu_n$

F =Mean sum of square due to genotype/ M.S. due to pooled deviation

= $MS_{1/} MS_3$

2. To test that the genotypes did not differ for their regression on environmental index

i.e. Ho = b1 = b2 = b3……. Bn, the 'F' test used was

F =M.S. due to G x E (linear)/ M.S. due to pooled deviation

= MS2/ MS3

3. Individual deviation from linear regression was tested as follows:

F= $[\sum_J S^2$ ij/n-2] / M. S. pooled error

Against F table value at (e-2) (g-2), at 5% or 1% probability level

3.7. Additive Main Effects and Multiplicative Interaction Model (AMMI)

The additive main effects and multiplicative interaction (AMMI) model (Gauch, 1992) one of the most widely used statistical methods. It can be used to understand and structure interactions between genotypes and environments. AMMI is a combination of ANOVA for the main effects of the genotypes and the environment together with principal components analysis of the genotype-environment interaction (Zobel *et al*., 1998 and Gauch, 1988).

The Additive Main effect and Multiplicative interaction (AMMI) is a statistical tool which leads to identification of stable genotypes with their adaptation behaviour .In this method main effects are initially accounted for regular analysis of variance and then the interaction is analysed through principal component analysis. The additive main effect and multiplicative interaction (AMMI) method proposed by Gauch (1992) was a significant advance in the analysis and interpretation of G×E interaction.

The AMMI model equation is:

$$y_{ij} = \mu + g_i + e_j + \sum_{n=1}^{n} \lambda_k \alpha_{ik} y_{ij} + r_{ij} + \varepsilon_{ij}$$

Where,

- Y_{ij} is the observed mean yield of the ith genotype in jth environment
- μ is the grand mean
- G_i is the deviation of the ith genotype from the grand mean and E_j is the deviation of the jth environment from the grand mean.

- λ_k is the singular value for PC axis k.
- α_{ik} and δ_{jk} are the Principal Components scores for axis k of the ith genotype and jth environment, respectively.
- R_{ij} is the residual and ε is the error (Gauch, 1992).

Pooled Analysis of variance for Stability-AMMI Model

Source	DF	Mean square	Expected MS
Total	(ger-1)		
Treatment	(ge-1)		
Genotype	(g-1)	MS1	MS1/MS3
Environment	(e-1)	MS2	MS2/MS3
Interaction IPCA 1 IPCA 2 Residual	(g-1)(e-1) (g+e-1-2n) (g+e-1-2n)	MS3 MS4	MS3/MSe MS4/MSe
Error	(r-1)(ge-1)	MSe	

3.7.1. Interpretation of AMMI biplots

The biplot display of PCA scores plotted against each other provides visual inspection and interpretation of G x E interaction components. The abscissa of the biplots represents the main effects, while its ordinates represent the IPC1 scores showing GE of the genotypes and environments. Displacements from the X-axis indicate the differences in the main effects,

while displacement from the Y-axis indicates differences in interaction effects. An important interpretation of the biplots is that the main effect for genotypes reflects breeding advances, while the main effect for environments reflects the overall comparison of environments. From the biplots the genotypes are classified into four distinct classes-

- Genotypes with high mean and positive IPCAI
- Genotypes with high mean and negative IPCAI
- Genotypes with low mean and positive IPCAI
- Genotypes with low mean and negative IPCAI

Genotypes with high mean performance and stability must fulfil two criteria *viz.*, least deviation from the horizontal line (IPCAI score=0) and high mean performance (right –hand side from the vertical line), while the genotypes having most deviating IPCA scores are regarded as least stable genotypes. To graphically explain the GEI and adaptation of genotypes to environments, the AMMI biplot between the IPCA1 scores and IPCA2 scores was used. The more IPCA scores approximate to zero, the more stable the genotype over all environments. Genotypes that are close to each other tend to have similar performance and those that are close to environment indicates their specific adaptation. The greater the IPCA scores, either positive or negative, as it is a relative value, the more specifically adapted a genotype is to certain environments, Purchasse, (1997).

Interaction biplot between IPCAI and IPCAII in AMMI 2, the environmental scores are joined to the origin by side-lines. The genotypes occurring close together on the plot will tend to have similar yields in all the environments, while genotypes far apart may either differ in mean yield or show different pattern of response over the environments. Hence the

genotypes near the origin are not sensitive to environmental interaction and those distant from the origin are sensitive and have large interaction. Genotypes and environments that fall in same sectors interact positively and if they fall in opposite sectors interact negatively. If they fall into adjacent sectors interaction is somewhat complex.

3.7.2. AMMI stability value (ASV)

ASV as described by Purchase (2000) was calculated as follows:

$$\text{ASV}=\sqrt{\left[\frac{IPCA1\ sum\ of\ square}{IPCA2\ sum\ of\ square}(IPCA1score\right]^2+(IPCA2score)^2}$$

Where, SS_{IPCA1} is sum of squares of interaction principal component analysis 1, SSIPCA2 is sum of squares of interaction principal component analysis 2, IPCA 1 is interaction principal component analysis 1 and IPCA 2 is interaction principal component analysis 2.

3.7.3. Yield stability index

The yield stability index (YSI) was calculated as:

$$YSI = RASV + RY$$

Where: RASV is the rank of the AMMI stability value and RY is the rank of the mean grain yield of genotypes (RY) across environments.

Plate no 4.Vegetative stage of 13 genotypes of Rice bean


R1 T7


R1 T9


R1 T10


R1 T11


R1 T12

Plate no 5. Flowering stage of different genotypes

RESULTS AND DISCUSSIONS

The result obtained through the statistical and biometrical analysis of data of the present investigation is presented in this chapter. The experimental result of the present investigation is presented under following headings:

4.1. Environment-wise analysis of variance

Analysis of variance (Table 4) of each character was carried out in each environment to highlight the differences among the genotypes in each environment. Environment wise analysis of variance revealed that mean sum of square due to genotypes were highly significant for all the traits under study for days to 50% flowering, primary branches, pods per clusters, number of pods per plant, pod length, number of seeds per pods, plant height and days to 80% maturity, 100 seed weight, protein content and seed yield per plant However, primary branches in Env3 (1st Aug-post Kharif sowing) was found to be non-significant. The significant differences among the genotypes indicated that the genotypic different exhibited were real and expressed in the environment under investigation.

4.2. Mean performance

The mean performance of all the thirteen genotype of ricebean and range of variation for yield and yield related traits are presented in Table 5.

Days to 50% flowering

Significant variations among the genotypes were observed with regard to days to 50% flowering. The genotype RbnG8 produced first flowering earliest in 83.61 days. On the other hand the maximum number of

Table 4. Environment wise analysis of variance for various yield attributing traits of Ricebean

Source of variation	Df	Mean sum of square					
		E_1	E2	E3	E4	E5	E6
		1st June,2016	15th June,2016	1st July,2016	1st June,2017	15th June,2017	1st july,2017
Days to 50% flowering							
Rep	2	69.72	6.33	4.33	3.41	1.72	4.33
Gen	12	101.65**	168.85**	52.09**	92.34**	103.25**	93.90**
Error	24	5.52	1.53	1.78	0.77	2.08	3.25
Primary branches							
Rep	2	0.11	0.25	0.03	0.01	0.03	0.00
Gen	12	0.298**	0.25**	0.08	0.48**	0.52**	0.42**
Error	24	0.05	0.04	0.07	0.01	0.01	0.02
Pods per cluster							
Rep	2	0.11	0.13	0.04	0.07	0.01	0.00
Gen	12	0.22**	0.39**	0.54**	0.71**	0.80**	0.38**
Error	24	0.10	0.06	0.04	0.04	0.01	0.02
No.of pods per plant							
Rep	2	38.25	2.26	54.72	4.00	12.43	8.75
Gen	12	355.85**	619.43**	431.97**	222.75**	281.87**	311.78**
Error	24	7.72	10.86	28.94	7.17	9.13	5.78
Pod length							
Rep	2	0.00	0.05	0.04	0.12	0.28	0.13
Gen	12	1.9**	2.41**	1.78**	2.43**	1.00**	1.33**
error	24	0.11	0.05	0.08	0.09	0.06	0.15
No.of seeds per pod							
Rep	2	0.10	0.07	0.03	0.11	0.01	0.01
Gen	12	5.57**	4.94**	3.29**	5.09**	4.02**	5.93**
Error	24	0.08	0.07	0.07	0.06	0.08	0.07

*, ** significant at 5% and 1% probability levels respectively

Source of variation	Df	Mean sum of square					
		E_1	**E2**	**E3**	**E4**	**E5**	**E6**
		1st June,2016	15th June,2016	1st July,2016	1st June,2017	15th June,2017	1st july,2017
Plant height(cm)							
Rep	2	63.61	109.44	23.79	0.14	23.52	14.00
Gen	12	3578.44**	746.68**	2197.82**	4633.52**	2820.70**	1609.92**
Error	24	11.96	29.72	21.95	9.61	69.68	23.82
Days to 80% maturity							
Rep	2	34.18	8.31	0.03	57.41	4.95	4.85
Gen	12	170.26**	123.45**	83.53**	96.75**	118.59**	154.31**
Error	24	7.10	0.36	1.75	4.22	1.98	2.01
100 seed weight(g)							
Rep	2	0.20	0.79	0.51	0.03	1.62	0.67
Gen	12	159.13**	143.08**	156.85**	140.08**	184.55**	172.91**
Error	24	0.65	0.96	0.59	0.15	0.47	0.42
Seed yield per plant(g)							
Rep	2	8.19	17.78	0.20	0.64	0.31	3.99
Gen	12	40.99**	114.33**	97.51**	201.06**	42.33**	85.10**
Error	24	2.49	9.30	3.86	1.08	1.41	2.29

*, ** significant at 5% and 1% probability levels respectively

days 100.5 to produce first flowering was taken by genotype RbnG3.The general mean observed was 94.47 days. Comparison of environments means revealed that Env 4 took the longest day for 50% flowering and Env 3 took minimum days to flowering.

Primary branches

Differences in primary branches were observed among the genotypes. The maximum number of primary branches was recorded in genotype RbnG4 (2.86) and minimum was observed in RbnG2 (2.30). The general mean recorded was 2.64. Comparison of environments means revealed that Env 2 and Env 3 recorded minimum number of branches and Env 6 recorded maximum number of branches.

Pods per cluster

Significant difference was observed for pods per cluster. The maximum number of was recorded in genotype RbnG2 (4.24) and minimum was observed in RbnG3 (2.42). The general mean recorded was 3.06. Comparison of environments means revealed that Env 3 recorded minimum number of pods per cluster and Env 4 recorded maximum number of pods per cluster.

Number of pods per plant

The character exhibited significant difference, among the genotypes the highest number of pods per plant was recorded in RbnG1 (61.63) and the lowest was observed in RbnG11 (36.63). The general mean recorded was 51.24. Comparison of environments means revealed that Env 2 and Env 3 recorded minimum number of pods per plant and Env 6 recorded maximum number of pods per plant.

Table 5. Mean performance of genotype on thirteen genotype of rice bean for different traits over six environments

Genotype	Days to 50% flowering	Primary branches	Pods per cluster	No. of pods per plant	Pod length (cm)	No. of seeds per pod	plant height (cm)	Days to 80% maturity	Protein content (%)	100 seeds weight (g)	seed yield per plant (g)
RbnG1	96.89	2.82	3.02	61.63	7.52	6.45	138.18	133.22	20.33	3.93	26.62
RbnG2	93.33	2.3	2.56	39.98	8.46	3.82	98.07	128.72	18.13	21.50	27.02
RbnG3	100.5	2.58	2.96	52.4	8.27	5.77	121.96	133.33	21.24	10.06	29.66
RbnG4	94.06	2.86	3.22	57.16	7.79	6.93	140.33	132.28	12.23	3.97	28.03
RbnG5	90.78	2.5	2.78	54.81	9.48	5.96	148.18	125.61	16.59	18.01	31.37
RbnG6	91.77	2.73	2.5	49.41	7.78	6.18	138.12	124.55	19.79	12.73	27.77
RbnG7	97.89	2.61	2.36	52.64	7.4	5.73	100.28	127.89	13.76	11.88	26.84
RbnG8	83.61	2.66	3	59.86	7.57	6.43	154.77	121.06	20.30	11.83	37.82
RbnG9	93.61	2.28	2.77	40.14	8.57	3.76	116.22	131.28	14.18	21.19	29.93
RbnG10	95.67	2.84	3.18	58.93	8.29	6.29	167.59	132.61	13.80	4.40	28.12
RbnG11	96.33	2.63	2.33	36.63	8.95	3.63	108.09	131.78	13.15	21.03	28.13
RbnG12	96.78	2.68	2.46	45.18	8.09	4.59	122.96	132.72	14.23	19.03	31.61
RbnG13	96.89	2.83	2.98	57.33	7.78	6.18	135.33	135.83	17.35	3.36	26.01
Grand mean	94.47	2.64	2.78	51.24	8.15	5.52	130.01	130.07	15.96	12.53	29.15
CV (%)	1.67	6.94	14.42	6.63	3.64	4.92	4.06	1.34	8.53	5.85	6.36
SEM±	0.37	0.04	0.09	0.80	0.07	0.06	1.24	0.41	0.56	0.17	0.44
CD 5%	1.19	0.14	0.30	2.56	0.22	0.20	3.98	1.32	1.42	0.55	1.40

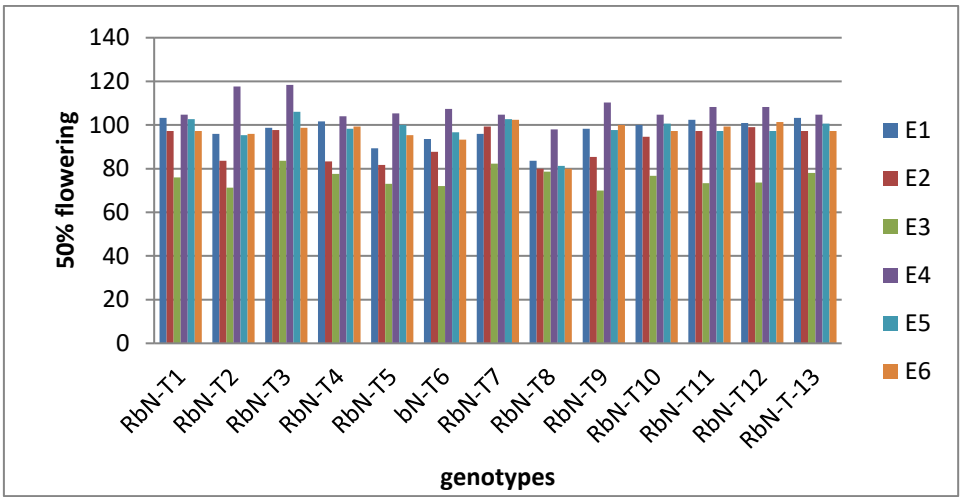


Fig. 2. Mean performance of 50% flowering at across six environments

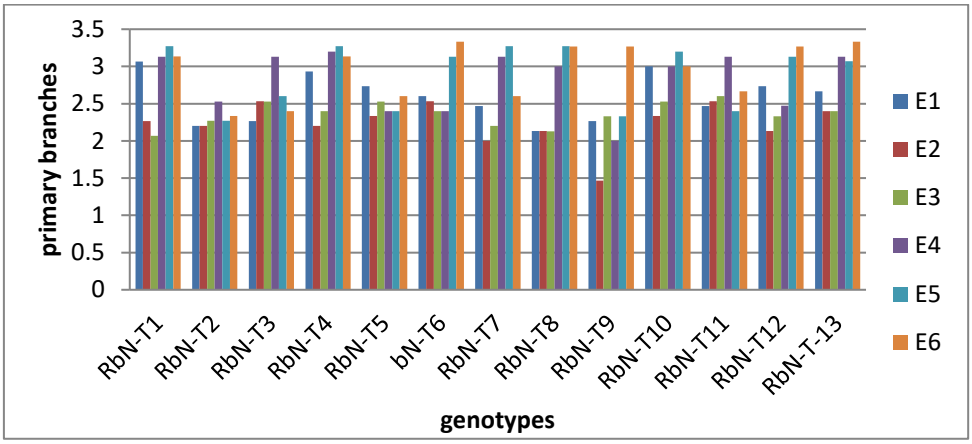


Fig. 3. Mean performance of primary branches across six environments

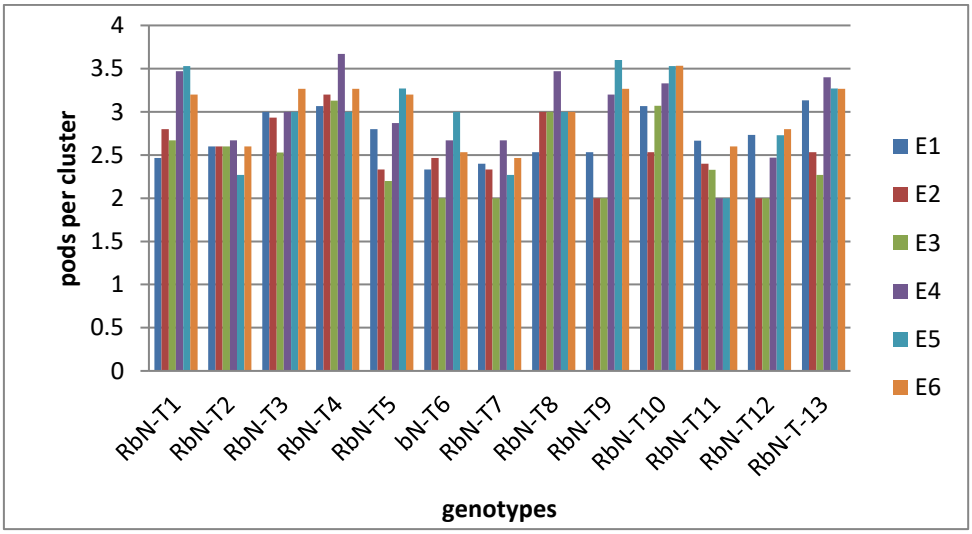


Fig.4. Mean performance of pods per cluster across six environments

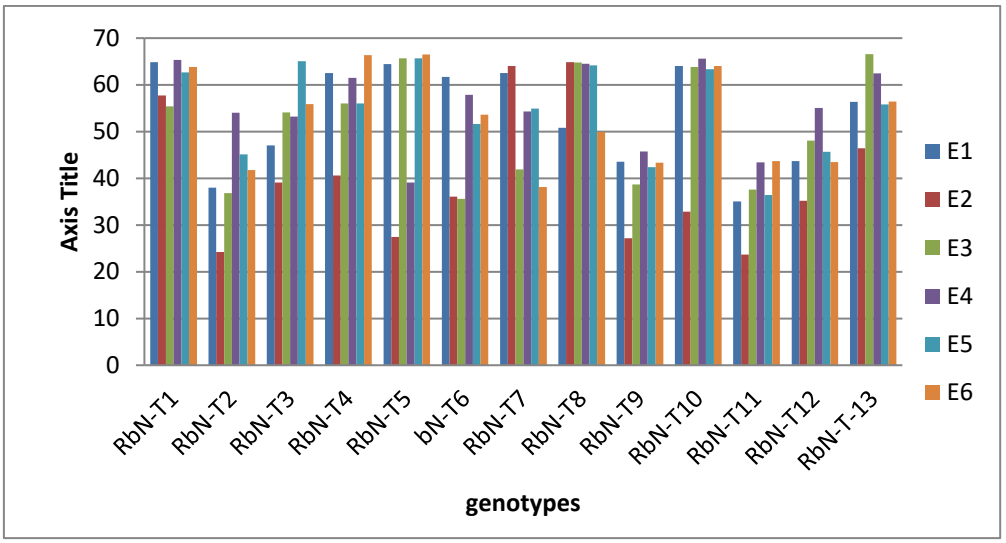


Fig .5. Mean performance of Number of pods per plant across six environments

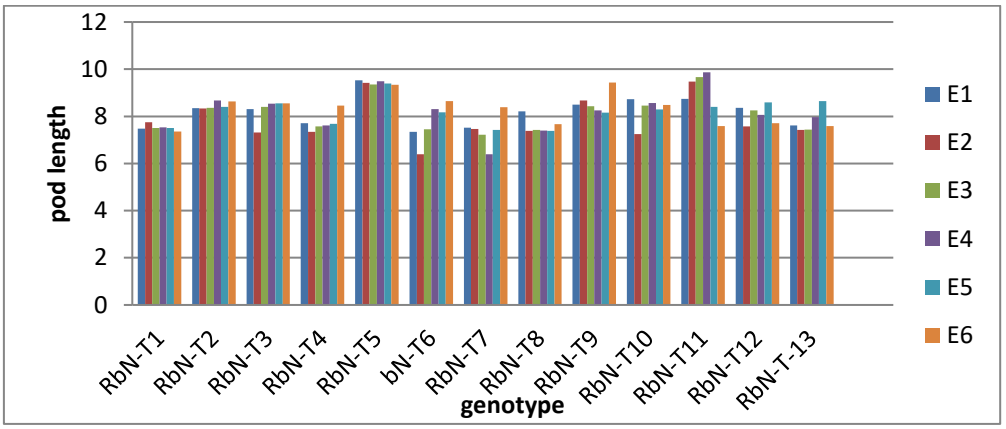


Fig .6. Mean performance of pod length across six environments

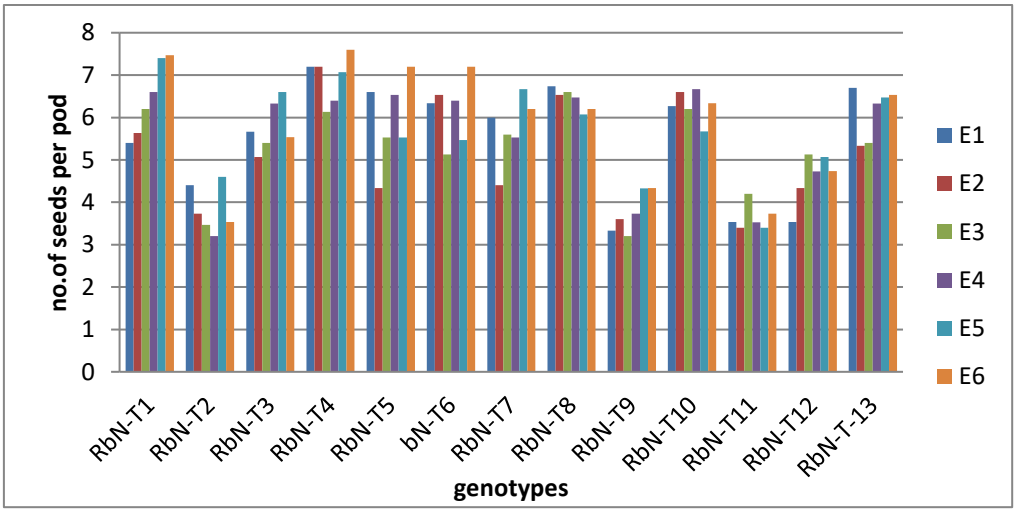


Fig. 7. Mean performance of number of seeds across six environments

Pod length

Highly significant differences for pod length among the genotypes were recorded in the study. The longest pod length recorded was 9.48 cm in genotype RbnG5 and lowest pod length recorded is 7.4 cm in genotype RbnG7. The general mean recorded was 8.15 cm. Comparison of environments means revealed that Env 2 recorded lowest pods per length and Env 6 recorded maximum number of pods per plant.

Number of seeds per pod

Highly significant differences for number of seeds per pod among the genotypes were recorded in the study. The maximum number of pods recorded was 6.93 in genotype RbnG4 and lowest recorded is 3.63 in genotype RbnG11. The general mean recorded was 5.52. Comparison of environments means revealed that Env 2 recorded minimum number of seeds per pod and Env 6 recorded maximum number of seeds per pod.

Plant height

The genotype exhibited significant difference in respect of plant height. The highest plant height was recorded in genotype RbnG10 (167.59 cm) while genotype RbnG2 (98.07 cm) recorded lowest plant height. General mean was recorded 130.01 cm for plant height. Comparison of environments means revealed that Env 2 recorded lowest plant height and Env 4 recorded maximum plant height.

Days to 80% maturity

The genotype exhibited significant difference in respect of days to 80% maturity. The maximum day for maturity was recorded in genotype

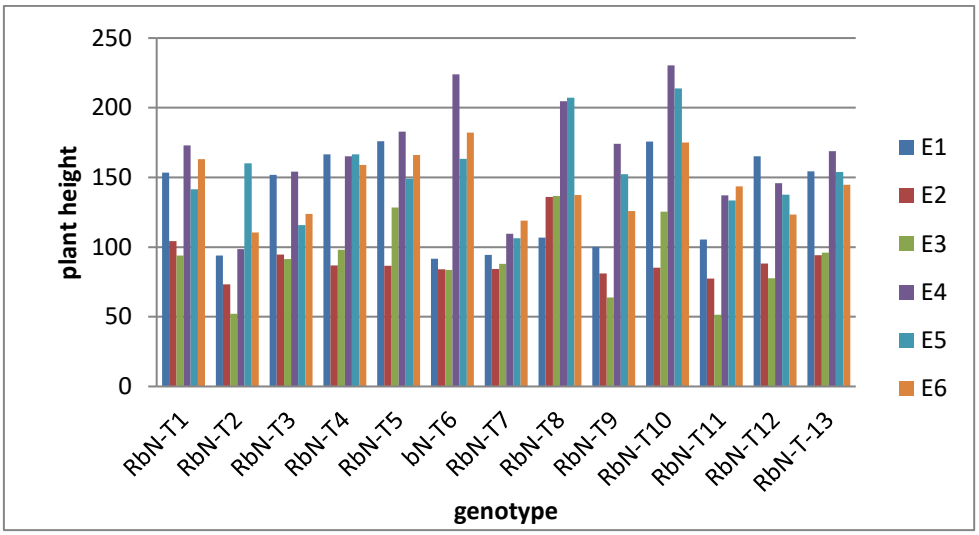


Fig .8. Mean performance of plant height across six environments

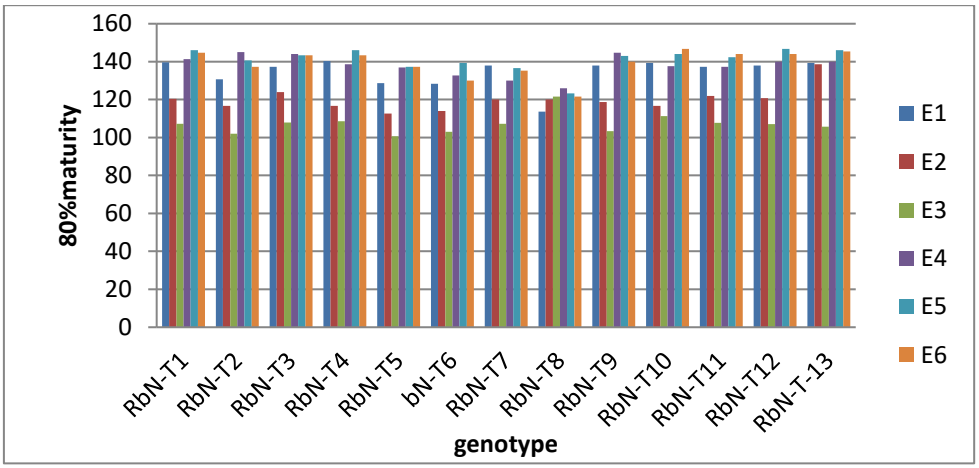


Fig .9. Mean performance of 80% maturity across six environments

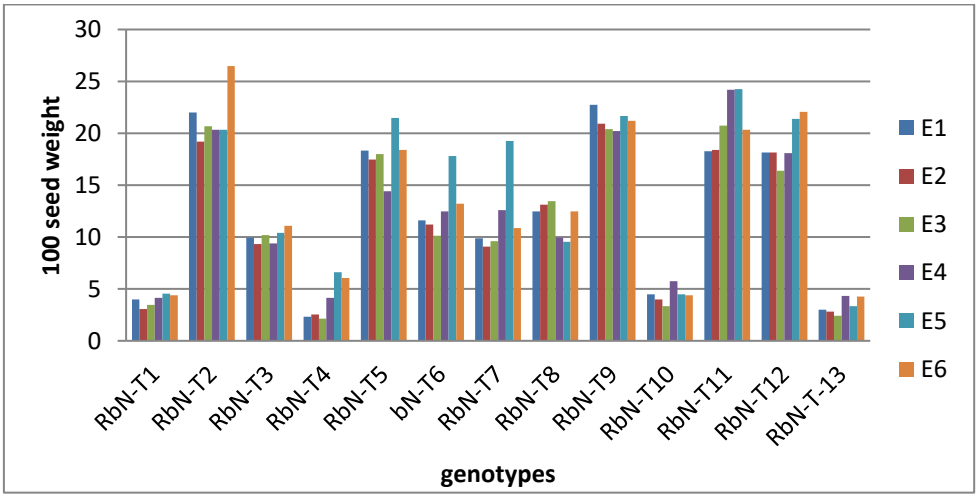


Fig .10. Mean performance of 100 seed weight across six environments

RbnG13 (135.83 days) while genotype RbnG8 (121.06 days) recorded minimum days for maturity. General mean was recorded 130.07 days for maturity. Comparison of environments means revealed that Env 3 recorded minimum days to maturity and Env 6 recorded maximum days to maturity.

Protein content (%)

The genotype exhibited significant difference in respect to protein content. The highest protein content was recorded in genotype RbnG3 (21.24%) while genotype RbnG4 (12.23%) recorded lowest protein content. General mean was recorded at 15.96%. Comparison of environments means revealed that Env 3 and Env 4 recorded lowest protein content and Env 6 recorded highest protein content.

100 seed weight (g)

Highly significant differences for 100 seed weight among the genotypes were recorded. The highest 100 seed weight recorded was 21.5 gm in genotype RbnG2 while the lowest 1000 seed weight recorded was 3.36 gm in genotype RbnG13. The general mean recorded was 12.53 gm. Comparison of environments means revealed that Env 2 recorded lowest 100 seed weight and Env 5 recorded maximum 100 seed weight.

Seed yield per plant (g)

Significant differences were exhibited for seed yield per plant. The highest seed yield per plant recorded was 79.93 gm in genotype RbnG5 while the lowest seed yield per plant recorded was 35.29gm in genotype RbnG13.The general mean recorded was 49.16gm. Comparison of environments means revealed that Env 3 recorded lowest seed yield per plant and Env 6 recorded maximum seed yield per plant.

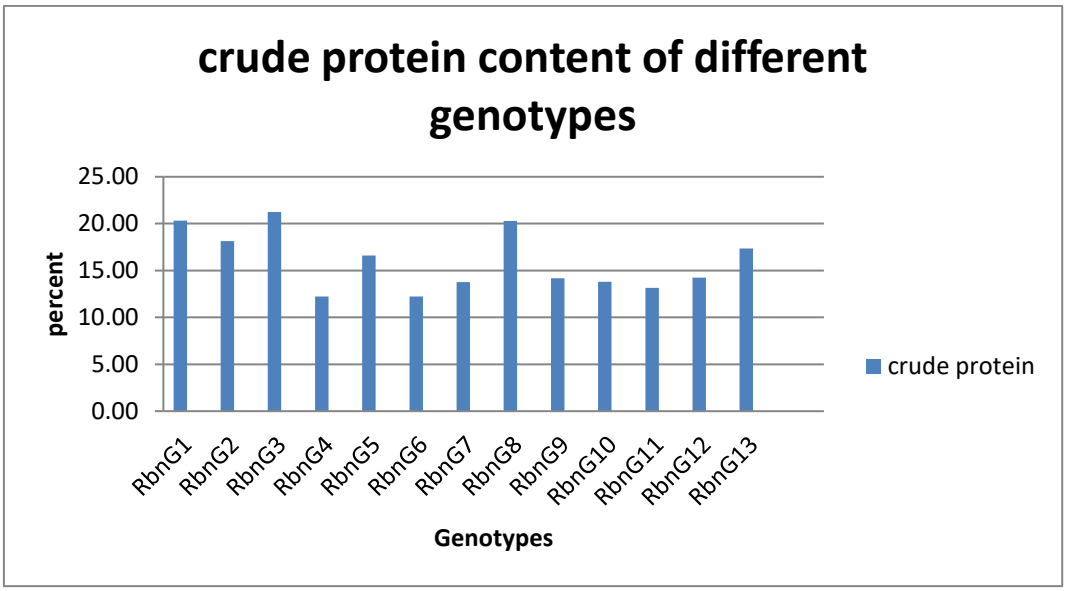


Fig .11. Crude protein content of different genotypes

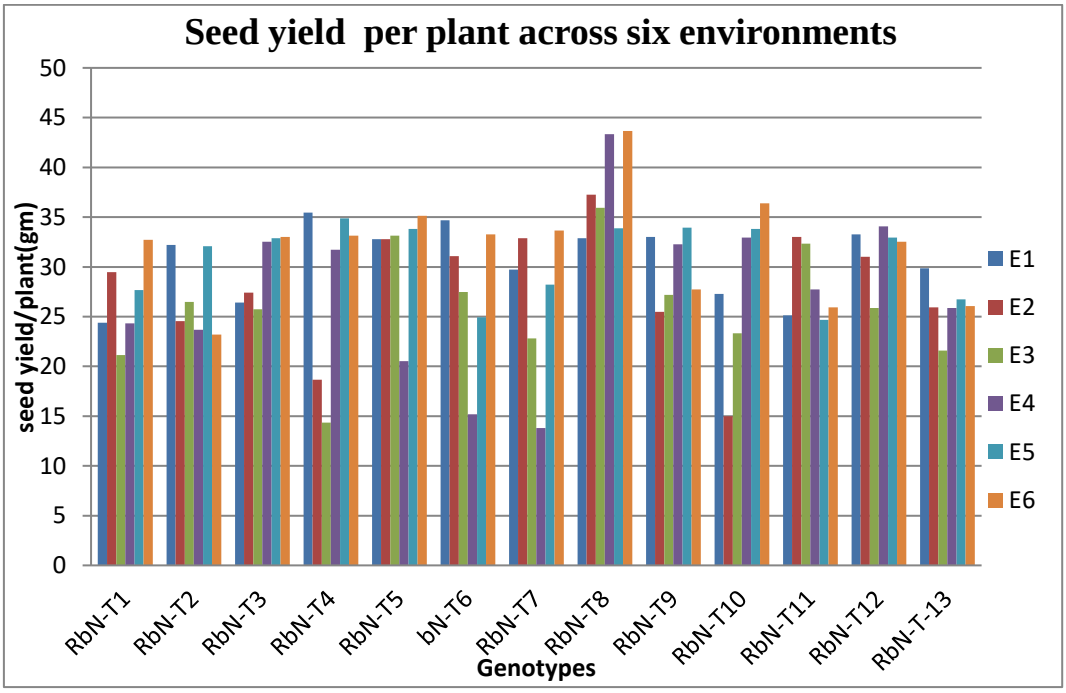


Fig .12. Mean performance of seed yield per plant across six environments

4.3. Estimation of different parameters of genetic variability

Genetic parameters viz. genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2_{bs}) and genetic (GA) advance as a percentage of mean were estimated for all the traits under study and the results are presented in Table 6.

4.3.1. Phenotypic coefficient of variations

The result from the findings indicated that primary branches (31.49%), pods per cluster (47.78%), number of pods per plant (69.27%), pod length (31.59%), plant height (68.77 %), protein content (74.96%) and seed yield per plant (46.12%) reported high PCV. Low PCV was recorded for number of seeds per pod (8.02%). Moderate for 50% flowering (19.52%), days to 80% maturity (13.75%) and 100 seed weight (18.49%).

4.3.2. Genotypic coefficient of variation

From the results finding it is recorded that primary branches (30.72%), pods per cluster (47.13%), number of pods per plant (68.96%), pod length (31.38%), plant height (68.65%), protein content (74.03%) and Seed yield per plant (45.68%) exhibited high GCV. A moderate estimate of GCV was exhibited in days to 50% flowering (18.82%), days to 80% maturity (13.68%) and 100 seed weight (18.48%). Low estimate of GCV was observed in number of seeds per pod (8.02%).

4.4. Heritability

The heritability was computed for each of the characters by the variance components for estimating their relative magnitudes of genotypic and phenotypic variability contributed through environmental factors.

The (Table 6) results indicated that the heritability estimates were observed high for days to 50% flowering (85.29%), number of pods per plant (99.08%), pod length (98.67%), number of seeds per pods (93.89%), plant height (99.65%), days to 80% maturity (93.97%), 100 seed weight (97.74%), protein content (98.75%) and seed yield per plant (91.70%). Low heritability was recorded for number of primary branches (43.78%).

High heritability coupled with GCV was recorded in number of pods per plant (68.96%, 99.08%)), Pod length (31.38%, 98.76%), plant height (68.65%, 99.65%), protein content (74.03%, 98.75%) and seed yield per plant (45.68%, 91.70%) recorded highest GCV coupled with high heritability.

4.5. Genetic advance

To attained relative comparison of the characters in relation to environment, genetic advance as percentage of mean was calculated for prediction of genetic gain (Table 6).

The high estimates of genetic advance as percentage of mean was recorded in days to 50% flowering (35.33%), number of pods per plant (72.45%), plant height (83.54%), and days to 80% maturity (36.51), 100 seed weight (62.02%) and seed yield per plant (27.16%).

High heritability coupled with high genetic advance mean was recorded in days to 50% flowering (85.29%, 35.33%), number of pods per plant (99.08%, 72.45%), plant height (99.65%, 83.54%), days to 80% maturity (93.97%, 36.50%), 100 seed weight (97.74%, 62.10%)) and seed yield per plant(91.70%, 27.16%).

Table 6. Genetic Parameters of Variability (pooled) for various traits in Rice bean genotypes for six environments

Characters	Mean	Min	Max	PCV (%)	GCV (%)	h^2_{bs} (%)	GA	GA as % of mean
50%flowering	94.47	80.33	103.3	19.52	18.82	85.29	5.16	35.33
Primary branches	2.64	2.2	3.6	31.49	30.72	43.78	0.53	1.63
Pods/cluster	49.98	2.4	3.6	47.75	47.13	63.59	0.59	2.66
No. of pods/plant	51.24	30.63	68.8	69.27	68.96	99.08	0.51	72.45
Pod length(cm)	8.13	6.75	9.54	31.59	31.38	98.67	0.28	5.22
Number of seeds/pod	5.51	3.10	7.33	8.02	8.02	93.89	0.37	11.82
Plant height(cm)	130.05	84.13	252.53	68.77	68.65	99.65	0.31	83.54
80% maturity	130.11	120.00	148	13.75	13.68	93.97	0.10	36.50
Protein content (%)	15.96	12.23	21.24	74.96	74.03	98.75	2.03	12.76
100 seed weight(gm)	12.53	4.00	26.8	18.49	18.48	97.74	0.45	62.01
seed yield/plant(gm)	29.15	22.6	46	46.12	45.68	91.70	6.36	27.16

Note: GCV: Genotypic coefficient of variation, PCV: Phenotypic coefficient of variation, GA: Genetic advance

4.6. Correlation coefficient analysis

A study on character association was carried, to assess the relationships among yield and it's components and to have an insight the causes for higher yield in genotypes under different environments and for identification of a stable character influencing the yield, the genotypic correlation coefficient was estimated for close measure of association between characters and also to provide an indication of characters useful for improvement of crop. The estimates of genotypic correlation coefficients were computed for different characters and presented in Table 7.

Correlation between yield and yield attributing characters

Correlation studies indicates seed yield per plant is significant and positively associated for primary branches, pods per clusters, number of pods per plant, pod length, number of seeds per pod, plant height, days to 80% maturity, 100 seed weight and crude protein.

Correlation between component characters

4.6.1. Days to 50 per cent flowering

50 per cent flowering was recorded highly significant and positive correlation with plant height (0.80*) and positive significant with pod length (0.17), and 100 seed weight (0.06).whereas primary branches recorded negative significant (-2.6*).

4.6.2. Number of primary branches

A significant positive relationship of primary branches were observed with pods per clusters (0.27*), number of seeds per pod (0.37*) and plant

height (0.41*) and negative significant with pod length (-0.27*) and 100 seed weight (-0.35).

4.6.3. Number of pods per cluster

The correlation coefficient of pods per cluster was found to be highly significant and positive with number of pods per plant (0.74*) and moderately positive significant with pod length (0.43*), number of seeds per pod (0.39*), plant height (0.33*) and days to 80% maturity (0.44*).

4.6.4. Number of pods per plant

Number of pods per plant exhibited high significant positive correlation with number of seeds per pod (0.78*) and plant height (0.77*) and also show positive significant correlation with days to 80% maturity (0.27*). Negative significant association with 100 seed weight (-0.65*) was also recorded.

4.6.5. Pod length (cm)

Pod length exhibited positive significant correlation with and 100-seed weight (0.36*). It was also observed positive significant with plant height and crude protein.

4.6.6. Number of seeds per pod

Number of seeds per pod exhibited high positive significant correlation with plant height (0.73*) and crude protein (0.61*) and high negative significant correlation with 100 seed weight (-0.78*).

Table 7. Estimates of genotypic correlation (Pooled) coefficients in Rice bean over the environment

Characters	Days to 50% flowering	Primary branches	Pods/cluster	No. of pods per plant	Pod length (cm)	No. of seed per pod	Plant height (cm)	Days to 80% maturity	100 seeds weight (gm)	Crude protein	Seed yield/plant(gm)
Days to 50%flowering	1	-0.26*	-0.01	-0.14	0.17	-0.21	-0.18	0.80*	0.06	-0.18	-0.60*
Primary branches		1	0.27*	0.18	-0.27*	0.37*	0.41*	-0.10	-0.35*	-0.12	0.27*
Pods/cluster			1	0.74*	0.43*	0.39*	0.33*	0.44*	-0.53	0.28*	0.23*
No.ofpods /Plant				1	0.06	0.78*	0.77*	0.27*	-0.65*	0.06	0.36*
Pod length(cm)					1	-0.04	0.02	-0.13	0.36*	0.14	-0.07
No.of seeds/pod						1	0.73*	-0.11	-0.78*	0.61*	0.58*
Plant height(cm)							1	0.04	-0.53*	0.33*	0.34*
Days to 80% maturity								1	-0.21	0.19	-0.52*
100 seeds weight (gm)									1	0.45*	-0.39*
Crude protein										1	-0.46*

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

4.6.7. Plant height (cm)

Plant height exhibited negative significant association with 100 seed weight (-0.53*) and positive significant association with crude protein (0.33*).

4.6.8. Days to 80% maturity

Days to 80 % maturity exhibited negative relationship with 100 seed weight (-0.21) and positive with crude protein (0.17)

4.6.9. 100 seeds weight (gm)

Association at genotypic correlation revealed positive significant association with crude protein (0.45*).

4.7. Path coefficient analysis

4.7.1. Genotypic path coefficient

Path coefficient analysis was carried out to separate the direct and indirect effects of different characters on yield at genotypic level (Table 8). The result of various causes influencing yield are described below:

Direct effect

The genotypic path coefficient revealed that number of primary branches (0.08), number of pods per plant (0.24), pod length (1.28), number of seeds per pods(0.28), plant height (1.42), days to 80% maturity (0.41), 100 seed weight (0.07) and crude protein (0.33) recorded positive direct effect on seed yield per plant. Negative direct effect on yield was contributed by days to 50% flowering (-0.27) and pods per cluster (-1.52).

Indirect effect

4.7.2. Days to 50% flowering

Days to 50% flowering showed negative significant association with seed yield per plant (-0.60*). It showed moderate positive indirect effect via pod length (0.48). The indirect effects via other traits were of low magnitude.

4.7.3. Primary branches

Primary branches showed positive significant association with seed yield per plant (0.27*) and exhibited high indirect positive effect with pod length (0.49) and plant height (0.62). The indirect effects via others traits were negligible with negative association.

4.7.4. Pods per cluster

Pods per cluster showed positive significant association with seed yield (0.23*). It shows high indirect effect with pod length (0.99) and moderate indirect positive with number of seeds per pod (0.21) and plant height (0.39).

4.7.5. Number of pods per plant

Number of pods per plant exhibit positive significant association for seed yield (0.36*). It shows indirect effects via, days to 50% flowering (0.07) and days to 80% maturity (0.17). The indirect effects via others traits are of low magnitude.

4.7.6. Pod length (cm)

Pod length showed positive indirect effects via, number of seeds per pod (0.20) and also low positive indirect effect with primary branches (0.03)

Table 8.Direct and Indirect effects (pooled) for yield and its component characters at genotypic path level

Character	Days to 50% flowering	Primary branches	pods/cluster	No. of pods per plant	pod length (cm)	No.of seed per pod	plant height (cm)	Days to 80% maturity	100 seeds weight (gm)	Crude Protein	G correlation with seed yield seed yield per plant(g)
50%flowering	**-0.27**	0.02	0.01	-0.06	0.48	0.11	-0.14	-0.14	0.02	-0.27	-0.60*
Primary branches	-0.07	**0.08**	-1.12	0.10	0.49	0.09	0.62	-0.22	0.02	-0.07	0.27*
pods/cluster	-0.05	0.06	**-1.52**	0.01	0.99	0.21	0.39	-0.26	0.02	-0.05	0.23*
No. of pods per plant	0.07	0.04	-0.09	**0.24**	-0.05	0.01	-0.18	0.15	0.00	0.07	0.36*
pod length(cm)	-0.10	0.03	-1.18	-0.01	**1.28**	0.20	-0.15	-0.32	0.04	-0.10	-0.07
No.of seed per pod	-0.11	0.03	-1.17	0.00	0.93	**0.28**	0.06	-0.22	0.02	-0.11	0.58*
plant height(cm)	0.03	0.04	-0.41	-0.03	-0.14	0.01	**1.42**	-0.09	-0.04	0.03	0.34*
80% maturity	0.10	-0.04	0.98	0.09	-0.99	-0.15	-0.30	**0.41**	-0.03	0.10	-0.52*
100 seeds wgt(gm)	-0.08	0.02	-0.54	-0.02	0.75	0.10	-0.73	-0.03	**0.07**	-0.08	-0.39*
Crude Protein	-0.01	0.00	0.09	0.04	0.00	-0.1	0.03	0.00	0.01	**0.33**	0.46*

*Significant at 5% level of probability Residual effect: 0.24 (genotypic path)

and 100 seed weight (0.04).The indirect effect with other traits are of negative and low in magnitude.

4.7.7. Number of seeds per pod

Number of seeds per pod shows positive significant association with seed yield (0.58*) and high positive indirect effect with pod length (0.93). Low magnitude of positive indirect effect was also observed for primary branches (0.03), plant height (0.06) and 100 seed weight (0.02).

4.7.8. Plant height (cm)

Plant height exhibited positive signification association with seed yield (0.34*). The indirect effects showed low positive indirect effect via, days to 50% flowering (0.03), primary branches (0.04), number of seeds per pod (0.01) and crude protein (0.03).

4.7.9. Days to 80% maturity

The indirect effects showed high positive indirect effect with pods per clusters (0.98) and low magnitude of positive indirect effect with days to 50% flowering, primary branches and number of seeds per pod.

4.7.10. 100 seeds weight (gm)

The indirect effects showed high positive indirect effect with pod length (0.75) while low magnitude positive indirect effects with primary branches (0.02) and number of seeds per pod (0.10). The indirect effects via other traits were of low magnitude.

4.7.11. Crude protein (%)

The indirect effect showed low positive indirect effect with pods per cluster (0.09), number of pods per plant (0.04) and plant height (0.03). The indirect effects via other traits were of low magnitude.

4.8. Genotype x Environmental interaction

4.8.1. Pooled analysis of variance over environments

Analysis of variance (Table 9) exhibits that the variance due to genotypes were significant for all the characters. This indicates the presence of considerable genotypic variability among the genotypes under studied. The mean sum of square due to environments was significant for all the characters which indicated genotypes interacted with environments significantly. Genotypes x Environment interaction were also found to be significant for all the characters. This showed that genotypes react with the environments. Environment wise analyses of variance revealed that mean sum of square due to genotypes were highly significant for all the traits. Similar findings were given by Sinha *et al.* (2000), Singh *et al*. (1998), Lal *et al*. (2010) and Thaware *et al*. (1998).

4.8.2. Estimation of environmental Index

The effect of environment in a stability analysis study is quantified through environmental index. The estimation of environmental indices (I_j) is presented in (Table 10). Perusal of the results revealed that Env1 (1st June-Kharif), Env5 (15th June-Kharif) and Env6 (1st July-Kharif) sowing was best for days to 50% flowering. Env4 (1st June-Kharif) and Env6 (1st July-Kharif) for primary branches. For pods per cluster Env 2(15th July-post Kharif), Env4 (1st June-Kharif), 5(15th June-Kharif) and Env6 (1st July-Kharif) are

Table.9. Analysis of variance over environments for various characters of ricebean genotypes

SOV	df	Days to 50% flowering	Primary branches	Pods per cluster	No. of pods per plant	Pod length (cm)	No. of seeds per pod	plant height (cm)	Days to 80% maturity	Protein content (%)	100 seeds weight (g)	seed yield per plant (g)
Env	5	4312.67*	3.39	2.28	1280.29*	1.02	25.57*	40530.13*	7102.75*	1.22***	46.78*	211.08*
Rep(Env)	12	14.97*	0.07	0.06	20.06*	0.10	0.06	39.08*	17.9*	0.63	5.18	14.97*
Genotypes	12	307.7***	0.66*	4.69***	6393.7***	15.99***	24.96***	7229***	320.3***	123.89***	1237.52***	2428.2***
Genotypes x environment	60	57.8***	9.63***	0.41***	1215.8 ***	0.87*	1.06**	2314***	85.0***	9.63***	14.11 ***	467.1 ***
Error	144	3.0	0.03	0.21	528.0	0.54	0.63	833	0.13	0.02	6.96	182.7

*** Significant at P<0.001,*, ** Significant at 5% and 1% level of significance

favourable environments. For number of pods per plant, pod length, plant height, days to 80% maturity most favourable environments are Env1 (1st June-Kharif), Env4 (1st June-Kharif), 5(15th June-Kharif) and Env6 (1st July-Kharif).For protein content none of the environments were favourable. For 100 seed weight the environments favourable are Env1 (1st June-Kharif) and Env6 (1st July-Kharif). For seed yield per plant environment Env1 (1st June-Kharif), Env4 (1st June-Kharif) and Env6 (1st July-Kharif) are most favourable.

It is observed that from the result obtained Env 2(15th July-post Kharif) and Env3 (1st Aug-post Kharif) was the unfavourable environment for all the traits. When we compare the different environments under studied, it clearly showed that Env1 (1st June-Kharif), Env4 (1st June-Kharif), Env5 (15th June-Kharif) and Env6 (1st July-Kharif) was most favourable sowing for most of the characters.

4.8.3. Joint regression analysis of variance

From the result obtained (Table 11), the variation due to G × E interaction has been partitioned into two, the predictable component due to linear regression and the unpredictable one due to pooled deviations from regression. The variances due to genotypes were highly significant revealing that there are sufficient differences in manifestation of variation among genotypes over environments for the traits under investigation. Similarly, mean squares due to environment + (genotype × environment) on the performance of genotypes was non- significant for all the characters under study. The linear contribution of the environmental effects on the performance of genotypes was significant for days to 50% flowering, Primary branches, Pod length, plant height, days to 80% maturity, 100 seed weight and seed yield per plant. The mean squares due to genotype ×

Table 10. Environment indices for yield and quality components for Six Environment

Characters		Env1	Env2	Env3	Env4	Env5	Env6
50%flowering	Ij	3.02	-3.37	-18.60	-12.94	3.74	2.27
Primary branches	Ij	-0.06	-0.40	-0.28	0.18	-0.25	0.31
Pods/cluster	Ij	-0.06	0.23	-0.33	0.21	0.18	0.22
No.ofpods/plant	Ij	2.19	-11.29	-0.08	4.30	3.29	1.59
Pod length(cm)	Ij	0.05	-0.31	-0.02	0.07	0.06	0.16
No.0f seeds/pod	Ij	0.003	-0.38	-0.27	0.06	0.21	0.38
Plant height (cm)	Ij	3.47	-39.54	-38.70	36.77	23.90	14.10
80% maturity	Ij	9.35	-9.76	-22.91	-7.91	11.01	9.35
100 seeds weight (gm)	Ij	-0.45	0.28	-0.15	0.23	1.70	0.94
Protein content (%)	Ij	-0.38	-0.25	-0.21	-0.09	-0.27	-0.44
seed yield/plant (gm)	Ij	-1.39	1.11	3.20	1.61	-1.65	-2.89

Environment interactions (linear) were significant for all the characters when tested against combined pooled deviations and pooled error. Significant differences due to G x E (linear) indicated that different genotypes differ genetically in their response to different environments. The mean sum of squares due to pooled deviations were first tested against pooled error which showed non-significant pooled deviation for all the traits which revealed the importance contribution of linear component of genotype × environment interaction for these traits.

4.8.4. Stability parameters analysis for different characters

Owing to the presence of significant Genotype X Environment interactions for different characters, the stability parameters as proposed by Eberhart and Russell (1966) viz. mean performance (mi), regression coefficient on environmental indices (bi) and deviation mean squares (S^2di) for each individual genotypes were estimated for all the characters. The mean and deviation from regression of each genotype were considered for stability and linear regression was used for testing the genotype response: (i) genotypes with high mean, bi =1 and non-significant S^2di (not significantly deviating from zero) were considered 'average stability' (adaptable or suitable over all environmental conditions), (ii) genotypes with high mean, regression coefficient greater than unity (bi>1) and non significant S^2di were rated 'highly stable' (suitable for favourable environments but yielding poor in unfavourable environments), (iii) genotypes with high mean, regression coefficient lesser than unity (bi<1) with non significant S^2di were 'low stable' (not favourably responsive to environmental conditions and could be adapted for specifically poor or unfavourable environments) and (iv) genotypes with any bi value with significant S^2di were unstable.

Table. 11. Joint-regression analysis of variance for stability for various characters in Rice bean genotype

SOV	df	Day s to 50% flowering	Primary branches	Pods per cluster	No. of pods per plant	Pod length (cm)	No. of seeds per pod	plant height (cm)	Days to 80% maturity	Protein content (%)	100 seeds weight (g)	seed yield per plant (g)
Genotype (g)	12	308**	0.87**	4.66**	6394***	16**	25**	7229**	320**	124**	1238**	2428**
Env	5	4333.1***	1.22***	4.44***	10489.7***	3.50*	5.40*	113757***	7110.6***	1.22***	91.06***	4858.8***
Rep(Env)	12	14.2 ***	0.67*	0.24	2009.2 ***	1.02*	1.07	4873***	17.9***	0.05*	0.06 *	4.98
Environment + (Genotype x Environment	65	387*	1.65	0.73*	1929*	1.07	1.39	10887*	625*	8.99*	20	805
Environment (linear)	1	21665*	54.7	22	52448*	17.5	27	568784*	35553*	6.14	455	24294
Genotype x Environment (linear)	12	92.2**	1.53**	0.87**	693*	0.56**	1.32**	3008**	256**	7.14**	36.3**	685**
Pooled Deviation	52	45.5	0.65	0.29	0.92	0.88	0.92	1976	39	9.47	7.90	381
Pooled Error	144	2.77	0.31	0.19	0.59	0.50	0.59	769	2.80	0.02	6.43	169

*** Significant at P<0.001,*, ** Significant at 5% and 1% level of significance

It was found that the deviations from linearity were of different magnitude. Character wise findings in respect of stability are present as under in (Table 12).

Days to 50% flowering

Average days to 50% flowering of genotypes ranged between 83.61-100.5 with an average population mean of 94.7 days. Genotype RbnG3 (100.3) recorded maximum days to 50% flowering followed by RbnG7 (97.89) and RbnG1 (96.89) while genotype RbnG8 (83.61) recorded the minimum days. Seven genotypes took more days than the population mean. Days to 50 per cent flowering revealed that genotypes RbnG1 (μ=96.89, bi=-0.96, S^2di=14.51), RbnG3 (μ=100.5, bi=1.01, S^2di=22.63), RbnG4 (μ=94.06, bi= 0.94, S^2di=22.22), RbnG10 (μ=95.67, bi=-0.91, S^2di=4.10), RbnG11 (μ=96.33, bi=-1.09, S^2di=11.10), RbnG12 (μ=96.78, bi=1.07, S^2di=15.51) shows high mean, regression coefficient (b) near/equivalent to unity and non significant deviation from regression equivalent to zero and can be considered as stable and well adapted to all the environments. RbnG2 (μ=96.89, bi=1.40, S^2di=22.63) possessed high mean values over general mean regression and coefficient equivalent greater than unity with non significant deviation from regression equivalent to zero was found to be highly stable and suitable for favourable environment.

Among the Genotypes, RbnG7 (μ=97.89, bi=-0.71, S^2di=13.30), Rbng13 (μ=96.89, bi=-0.87, S^2di=10.34), having high mean with regression coefficient less than unity and non significant deviation from zero found to be adapted to unfavourable environment. Days to 50% flowering exhibited not much variation between the growing seasons across six environment indicating the character is highly stable.

Table 12. Mean and stability parameters of thirteen genotype over six Environment

Genotype	Days to 50%flowering			Primary branches			pods/ cluster		
	Mean	**bi**	**S²di**	**Mean**	**bi**	**S²di**	**Mean**	**bi**	**S²di**
RbnG1	96.89	0.96	14.51	2.82	**1.11**	0.06	3.02	1.69	-0.01
RbnG2	96.89	1.40	22.63	2.30	0.20	0.08	2.56	-0.34	-0.06
RbnG3	100.5	1.01	17.71	2.58	0.68	-0.07	2.96	0.58	-0.06
RbnG4	94.06	0.94	22.22	2.86	1.27	-0.05	3.22	0.71	-0.04
RbnG5	90.78	1.09	14.72	2.50	0.43	-0.08	2.78	1.58	0.10
RbnG6	91.78	1.10	0.84	2.73	0.63	0.03	2.5	0.88	-0.06
RbnG7	97.89	0.70	13.30	2.61	0.94	-0.05	2.36	1.09	-0.02
RbnG8	83.61	0.49	30.95	2.66	2.33	0.69	3	1.53	0.17
RbnG9	93.61	1.31	5.97	2.28	1.58	0.71	2.77	1.89	0.14
RbnG10	95.67	0.91	4.10	2.84	1.54	0.09	3.18	1.26	0.07
RbnG11	96.33	1.09	11.10	2.63	0.18	0.02	2.33	-0.43	0.11
RbnG12	96.78	1.07	15.51	2.68	1.01	-0.01	2.46	1.36	-0.01
RbnG13	96.89	0.87	10.34	2.83	1.06	-0.05	2.98	1.19	-0.06
genotypic mean	94.47	1		2.64	1		2.78	1	-
S.E(bi)	0.16	0.82	-	0.11	1.51		0.19	1	-

Number of primary branches

Genotypes RbnG1 (μ=2.84, bi=1.11, S^2di=-0.06), RbnG12 (μ=2.68, bi=1.11, S^2di=1.01) and RbnG13 (μ=2.83, bi=1.06, S^2di=-0.05) had higher number of primary branches per plant, regression coefficient of unity and deviation from regression-near to unity, which shows average stability and well adapted to all the environments. Genotypes RbnG8 (μ=2.66, bi=2.33, S^2di=0.69), RbnG4 (μ=2.86, bi=-1.27 , S^2di=-0.05) and RbnG10 (μ=2.83, bi=1.54 , S^2di=0.09) showed high mean, regression coefficient more to unity, deviation from regression near to zero and considered to be stable and specially adapted to favourable environments. Genotypes RbnG6 (μ=2.73, bi=-0.63, S^2di=0.03) and RbnG11 (μ=2.63, bi=0.18, S^2di=0.18) recorded high mean, regression coefficient less to unity and deviation from regression to zero and can be considered for unfavourable environments.

Number of pod per clusters

Stability of number of clusters per pod indicated that genotypes Rbng13 (μ=2.98, bi=1.80, 2di=0.08) had higher number of cluster per pod, regression coefficient equivalent to unity and deviation from regression near to zero which shows stable and well adapted to all environments. RbnG1 (μ=3.02, bi=1.69, S^2di=-0.01), RbnG5 (μ=2.78, bi=1.58, S^2di=0.10), RbnG8 (μ=3, bi=1.53, S^2di=0.17) and RbnG10 (μ=3.18, bi=1.26, S^2di=0.07)shows more than one regression coefficient and deviation from regression near zero with high mean, more than unity and so considered stable for favourable environment. Genotype RbnG3 (μ=2.96, bi=0.58, S^2di=-0.06) and RbnG4 (μ=3.22, bi=0.71, S^2di=-0.04) showed less to unity regression coefficient and deviation from regression equivalent to zero along with average number of clusters per plant over general mean and stable for unfavourable environments.

Number of pods per plant

Genotypes RbnG1 (μ=61.63, bi=-1.05, S^2di=322.86), RbnG5 (μ=54.81, bi=1.07, S^2di=554.75) and RbnG8 (μ=59.86, bi=0.90, S^2di=723.62), showed high mean, regression coefficient equivalent to unity, deviation from regression equivalent to zero and these genotypes possessed highest number of pods per plant over general mean and well adapted to all environments. Genotypes RbnG3 (μ=52.4, bi=1.34, S^2di=-30.53), RbnG4 (μ=57.16, bi=1.76, S^2di=218.03) and RbnG10 (μ=58.93, bi=1.28, S^2di=266.18) exhibited high mean, more than one regression coefficient, deviation from regression more to zero and adapted to favourable condition. Genotypes RbnG7 (μ=52.64, bi=0.83, S^2di=645.95) and RbnG13 (μ=57.33, bi=0.67, S^2di=-111.82), exhibits high mean, regression coefficient less to unity and deviation from regression near to zero and can be considered below average stability and adapted specially for unfavourable environment.

Pod length

RbnG10 (μ=8.30, bi=0.89, S^2di=-0.01), RbnG12 (μ=8.09, bi=1.04 , S^2di=0.05) showed high mean and exhibited regression coefficient equivalent to near/ unity, deviation from regression equivalent to zero and show average stability and well adapted to all environments. Genotype RbnG2 (μ=8.46, bi=1.48, S^2di=-0.04), RbnG5 (μ=9.42, bi=1.50, S^2di=0.10), RbnG9 (μ=8.57, bi=1.20, S^2di=0.55) had regression coefficient more to unity with high mean, and non signification deviation and specially adapted for favourable environments. RbnG3 (μ=8.46, bi=1.48, S^2di=-0.04) showed high mean, regression coefficient less to one, deviation from regression to zero which shows below average stability and specially adapted to unfavourable environment.

Table 12. Mean and stability parameters of thirteen genotype over six Environment

Genotype	No. of pods/plant			Pod length (cm)			No. of seeds/pod		
	Mean	bi	S^2di	Mean	bi	S^2di	Mean	bi	S^2di
RbnG1	61.63	1.05	322.86	7.52	0.25	-0.01	6.45	1.80	0.01
RbnG2	39.98	0.25	248.16	8.46	1.48	-0.04	3.82	1.43	0.01
RbnG3	52.40	1.34	-30.53	8.27	0.75	-0.15	5.77	0.77	-0.00
RbnG4	57.16	1.76	218.03	7.73	0.55	-0.08	6.93	1.47	-0.04
RbnG5	54.81	1.07	554.75	9.42	1.50	0.10	5.96	1.78	-0.09
RbnG6	49.41	1.44	42.36	7.72	1.88	0.10	6.18	2.07	0.19
RbnG7	52.64	0.83	645.95	7.40	1.55	-0.10	5.73	0.33	0.03
RbnG8	59.86	0.90	723.62	7.57	1.07	-0.10	6.43	-0.14	-0.16
RbnG9	40.14	1.04	90.40	8.57	1.20	0.55	3.76	0.87	0.06
RbnG10	58.93	1.28	266.18	8.30	0.89	-0.01	6.29	0.69	0.41
RbnG11	36.63	0.39	-140.26	8.95	-0.54	0.87	3.63	-0.52	-0.07
RbnG12	45.18	0.97	267.55	8.09	1.04	0.05	4.59	0.71	0.58
RbnG13	57.33	0.67	-111.82	7.78	1.37	0.27	6.13	1.71	0.28
genotypic mean	51.24	1.00	-	8.15	1.00	-	5.52	1.00	-
S.E(bi)	0.18	0.92	-	0.19	0.88	-	0.19	0.92	-

Number of seeds per pod

Genotypes RbnG3 (μ=5.77, Bi=0.77, S^2di=-0.00), had higher number of seeds per pod, regression coefficient equivalent near to unity and deviation from regression equal to zero which shows stability and well adapted to all environments. Rbng1 (μ=6.45, bi=1.80, S^2di=0.01), RbnG4 (μ=6.93, bi=1.47, S2di=-0.04), RbnG5 (μ=5.96, bi=1.78, S^2di=-0.09), RbnG6 (μ=6.18, bi=2.07, S^2di=0.19) and RbnG13 (μ=6.13, bi=1.71, S^2di=0.28) had high mean seed per pod and regression coefficient more to unity, deviation from regression equivalent to zero, which shows below average stability and adapted to favourable environments condition. Genotypes RbnG7 (μ=5.73, bi=0.33 , S^2di=0.03) and RbnG10 (μ=6.29, bi=0.69, S^2di=0.41) had low mean, regression coefficient less to unity ,deviation from regression equivalent to zero .Its shows below average stability and adapted to unfavourable environments.

Plant height

Genotypes RbnG1 (μ=138.18, bi=0.81, S2di=283.33), RbnG5 (μ=148.18, bi=0.95, S^2di=153.21), RbnG8 (μ=154.77, bi=0.83, S^2di=626.10), RbnG13 (μ=135.33, bi=0.89, S^2di=99.40) had high mean, regression coefficient near to unity, deviation from regression equivalent to zero, which shows average stability and well adapted to all environments. Genotypes RbnG4 (μ=140.33, bi=1.26, S^2di=3.91), RbnG6 (μ=138.12, bi=1.67, S^2di=322.23) and RbnG10 (μ=167.59, bi=1.28, S^2di=34.47) had high mean, regression coefficient more to one and deviation from regression equal to zero which shows average stability and specially adapted to favourable environments. No genotypes shows below average stability and adapted to unfavourable environment.

Table 12. Mean and stability parameters of thirteen genotype over six Environments

Genotype	Plant height (cm)			Days to 80% maturity			100 seed weight (gm)		
	Mean	**bi**	**S^2di**	**Mean**	**bi**	**S^2di**	**Mean**	**bi**	**S^2di**
RbnG1	138.18	0.81	283.33	133.11	1.16	1.08	3.93	0.44	-2.28
RbnG2	98.07	0.76	1134.44	128.83	1.17	15.41	21.50	-1.11	6.64
RbnG3	121.96	0.85	445.15	133.39	1.06	1.83	10.06	1.39	0.27
RbnG4	140.33	1.26	3.91	132.39	1.12	8.46	3.97	1.27	-2.11
RbnG5	148.18	0.95	153.21	125.72	1.13	2.42	18.01	1.22	-0.67
RbnG6	138.12	1.67	322.23	124.67	0.97	6.69	12.73	1.88	-1.24
RbnG7	100.28	0.79	463.35	127.89	0.85	14.95	11.88	2.72	3.58
RbnG8	154.77	0.83	626.10	121.17	0.03	20.19	11.83	-0.38	-1.90
RbnG9	116.22	1.00	-133.59	131.39	1.17	15.41	21.19	1.49	-0.45
RbnG10	167.59	1.28	34.47	132.72	1.05	15.33	4.40	0.46	-1.47
RbnG11	108.09	1.01	1432.03	131.67	1.04	2.79	21.03	1.71	6.84
Rbn12	122.96	0.84	88.06	132.61	1.15	0.90	19.03	1.55	-1.29
RbnG13	135.33	0.89	99.40	135.94	0.99	60.28	3.36	0.34	-1.87
genotypic mean	130.01	1.00	-	130.12	1.00	-	12.53	1.00	-
S.E(bi)	8.89	0.38	-	1.24	0.223	-	0.61	1.32	-

Days to 80% maturity

Genotypes RbnG3 (μ=133.39, bi=1.06, S^2di=1.83), RbnG10 (μ=132.72, bi=1.05, S^2di=15.33), RbnG11 (μ=131.67, bi=1.04, S^2di=2.79), RbnG13 (μ=135.94, bi=0.99, S^2di=60.28) had high mean, regression coefficient equal to unity and non significant deviation from linearity, these genotypes were found to be more stable could perform well in wide range of environments. Genotypes RbnG1 (μ=133.11, bi=1.16, S^2di=1.08), RbnG4 (μ=132.39, bi=1.12, S^2di=8.46), RbnG9 (μ=131.39, bi=1.17, S^2di=15.41), RbnG12 (μ=132.61, bi=1.15, S^2di=0.90) have high general mean and had regression coefficient more to unity and non significant deviation. Hence these genotypes could be preferred for favourable condition. Genotypes RbnG7 (μ=127.89, bi=0.85, S^2di=14.95), RbnG8 (μ=121.17, bi=0.03, S^2di=20.19), had low mean comparing to the average mean, regression coefficient less to unity and deviation from regression equivalent to zero which shows below average stability and adapted to unfavourable environment.

100 seed weight

Genotypes RbnG2 (μ=21.5, bi=1.11, S^2di=6.64) had higher 100 seed weight, regression coefficient equivalent to unity and deviation from regression equivalent to zero. It shows average stability and well adapted to all the environments. Genotypes RbnG5 (μ=18.01, bi=1.22, S^2di=-0.67), RbnG6 (μ=12.73, bi=1.88, S^2di=-1.24), RbnG9 (μ=21.91, bi=1.49, S^2di=-0.45), RbnG12 (μ=19.03, bi=1.55, S^2di=-1.29) and RbnG11 (μ=21.03, bi=1.71, S^2di=6.84) had high mean, regression coefficient more than one and deviation from regression equivalent to zero which is adaptable to favourable environment condition. No genotype shows below average stability and specially adapted to unfavourable environments

Crude protein (%)

Average protein content genotypes (Table.12) ranged between 12.23 to 21.24 with an average general mean of 15.96 percent. Genotype RbnG3 (21.24%) recorded highest protein percent followed by RbnG1 (20.33%) and RbnG8 (20.30%) while genotype RbnG4 (12.23%) recorded the lowest protein content followed by RbnG11 (13.15%). Sadana *et al* (2006) and Myrna et al (1991).Narasinga Rao *et al* (1989) also reported that values for protein content in rice bean were comparable to some cultivated legume seeds like cowpea (24.1%), green gram (24.0%), Bengal gram (17.1%), lentil (25.1%), moth bean (23.6%) and peas (19.7%) but were lower than soy bean (43.2%).

It was observed that none of the genotype was found stable. Genotypes RbnG2 (μ=18.13, bi=-3.94, S^2di=0.09), RbnG3 (μ=21.24, bi=5.66, S^2di=-0.45), RbnG6 (μ=19.79, bi=5.64, S^2di=-0.44), RbnG8 (μ=20.30, bi=-6.43, S^2di=11.13), had high mean, regression coefficient more than one and deviation from regression equivalent to zero which is adaptable to favourable environment condition. Genotype RbnG1 (μ=20.33, bi=-0.07, S^2di=-0.01), had high mean, regression coefficient less to one and Deviation from regression near to zero, which shows below average stability and specially adapted to unfavourable environments.

Seed yield per plant

Genotype RbnG3 (μ=29.66, bi=0.90, S^2di=2.36), exhibits higher seed yield per plant, regression coefficient to unity and deviation from regression equivalent to zero, shows stability and well adapted to all environments. Genotype RbnG5 (μ=31.37, bi=2.32, S^2di=384.80) had high mean, regression coefficient more than unity and non-significant deviation near to

Table 12. Mean and stability parameters of thirteen genotype over six Environments

Genotype	Crude protein (%)			Seed yield/plant (gm)		
	Mean	**bi**	**S^2di**	**Mean**	**bi**	**S^2di**
RbnG1	20.33	0.07	-0.01	26.62	1.05	315.12
RbnG2	18.13	-3.94	0.09	27.02	0.96	74.44
RbnG3	21.24	5.66	0.45	29.66	0.90	2.361
RbnG4	12.23	3.93	14.30	28.03	1.65	-21.46
RbnG5	16.59	-1.89	0.45	31.37	2.32	384.80
RbnG6	19.79	5.64	0.44	27.77	0.86	64.19
RbnG7	13.76	-0.24	0.63	26.84	0.87	87.68
RbnG8	20.30	-6.43	11.13	37.82	0.76	-1.74
RbnG9	14.18	7.11	9.40	29.93	0.73	-25.42
RbnG10	13.80	0.52	0.04	28.12	1.61	-24.27
RbnG11	13.15	1.77	0.21	28.13	-0.23	68.86
RbnG12	14.23	0.16	0.05	31.61	0.58	-15.69
RbnG13	17.35	0.61	3.67	26.01	0.91	-50.11
genotypic mean	15.96	1.00	-	29.15	1.00	-
S.E(bi)	0.56	0.419	-	3.90	0.96	-

Table. 13. Classification of genotypes for different characters based on stability parameters

Sl. no	Characters	Genotypes stable over all environments (bi=1),($S^2di=0$)	Genotypes stable for favourable environments (bi<1), ($S^2di=0$)	Genotypes stable for poor/un environments (bi>1), ($S^2di=0$)
1	**50%flowering**	RbnG1, RbnG3 and RbnG10	RbnG2, RbnG5, RbnG6, RbnG11 and RbnG12	RbnG4, RbnG7, Rbng13
2	**Primary branches**	RbnG1, RbnG11, RbnG13	RbnG4, RbnG8 and RbnG10	RbnG6 and RbnG11
3	**Pods/cluster**	RbnG7	RbnG1, RbnG5, Rbng13	RbnG3, RbnG4, RbnG7 and RbnG8
4	**No. of pods/plant**	RbnG1, RbnG5, and RbnG8	RbnG3, RbnG4 and RbnG10	RbnG7 and RbnG13
5	**Pod length (cm)**	RbnG8 and RbnG12	RbnG2 RbnG5 and RbnG9	RbnG2 and RbnG8
6	**No. of seeds/pod**	RbnG3	Rbng1, RbnG4, RbnG5, RbnG6	RbnG3, RbnG7, RbnG8 and RbnG10
7	**Plant height (cm)**	RbnG1,RbnG5, RbnG9, RbnG13	RbnG4, RbnG6 and RbnG10	RbnG3, RbnG8, RbnG12
8	**80% maturity**	RbnG3, RbnG10, RbnG11, RbnG13	RbnG1, RbnG4, RbnG9, RbnG12	RbnG7 and RbnG8
9	**100 seeds weight (gm)**	RbnG2	RbnG5, RbnG6, RbnG6, RbnG9, and RbnG11	RbnG8
10	**Crude protein (%)**	-	RbnG2, RbnG3, RbnG6 and RbnG8	RbnG1
11	**Seed yield/plant (gm)**	RbnG1 and RbnG3	RbnG4, RbnG5, RbnG10	RbnG8, RbnG9 and RbnG12

zero and considered to be adapted for favourable condition. Genotypes RbnG8 (μ=37.82, bi=0.76, S^2di=-1.74), RbnG9 (μ=29.93, bi=0.73, S^2di=-25.42), RbnG12 (μ=31.61, bi=0.58, S^2di=-15.69) had regression coefficient less than unity, deviation from regression near to zero, with high mean yield and adapted to unfavourable environments.

4.9. AMMI analysis

4.9.1. AMMI analysis of variance

The combined analysis of variance (Table 14) showed that the genotype, environment were significant for all the characters under studies. The G X E interaction was also found to be significant for all the characters under studies. This indicated the presence of variability among the genotypes and the environments. The significant of Genotype x Environment interaction is requisite to carry out stability analysis forward. The presence of significant GxE interaction showed the differential performance of ricebean genotypes across environments and unstable performance of genotype across the different testing environment. Hence AMMI analysis is further partitioned into two interaction principal components (IPCA 1 and IPCA 2) axes analysis. From the result it was observed that IPCA 1 exhibited significant for all the characters. IPCA 2 was also observed to be significant for all the characters except 100 seed weight. Thus it can be concluded that the prediction assessment, is in agreement of Gauch and Zobel, 1996, as accurate model for using the first two IPCAs AMMI model.

4.9.2. AMMI analysis for Yield and yield traits of thirteen Ricebean genotypes across six environments.

Days to 50% flowering

Table 14. AMMI analysis of variance for yield and its components of thirteen Ricebean genotype grown in six environments

Source	DF	Days to 50% flowering		Primary branches		Pods per cluster		No.of pods per plant		Pod length(cm)	
		M SS	Exp. %	MSS	Exp. %	MSS	Exp. %	MSS	Exp. %	MSS	Exp. %
ENV	5	4333.1***	75.15	1.23***	5.24	4.55***	21.58	10489.7**	25.94	3.50*	6.68
REP(ENV)	12	14.2***		0.053*		0.24		2009.2***		1.01*	
GEN	12	307.7***	12.80	123.89***	12.70	4.69***	54.71	6393.7***	37.95	15.99***	73.26
ENV x GEN	60	57.8***	12.03	9.63***	8.23	0.42***	24.18	1215.8***	36.09	0.87*	19.93
PC1	16	84.84 ***	39.9	30.21***	83.6	0.85***	54.8	1650.61***	36.2	1.51**	46.5
PC2	14	81.23***	32.8	3.54***	8.6	0.34	19.6	1621.12	31.1	1.10* *	29.7
Residual	144	3.0		0.03		0.21		528.0		0.54	

*** Significant at P<0.001, IPCA = Interaction principal component axis, MS = Mean squares, DF = Degrees of freedom

		No.of seeds per pod		Plant height(cm)		Days to 80% maturity		Protein content (%)		100 seed weight(g)		Seed yield per plant(g)	
Source	DF	MSS	Exp. %	MSS	Exp. %	MSS	Exp. %	MSS	Exp. %	MSS	Exp. %	MSS	Exp. %
ENV	5	5.40*	6.92	113757***	71.60	7110.6***	79.89	1.23***	0.29	91.06***	2.81	4858.8***	29.82
REP(ENV)	12	1.06		4873***		17.9***		0.05*		4.96		269.6	
GEN	12	24.96***	76.80	7229***	10.91	320.3***	8.63	123.89***	71.79	1237.52***	91.94	2428.2***	35.77
ENV x GEN	60	1.06**	16.32	2314***	17.47	85***	11.46	9.63***	27.90	14.11***	5.24	467.1***	34.40
PC1	16	1.47**	37.1	4672.59***	53.8	202.75***	63.6	30.21***	83.6	37.06***	70	877.96***	50.1
PC2	14	1.39*	30.8	2590.14	26.1	66.08***	18.1	3.54***	8.6	8.64	14.3	473.12	23.6
Residual	144	0.63		833		3.0		0.03		6.96		182.7	

*** Significant at P<0.001, IPCA = Interaction principal component axis, MS = Mean squares, DF = Degrees of freedom

Significant differences were observed for the genotype, environments and genotype X environment interaction. The explained percentage attributed by mean sum of square is observed to be highest in environment 75.15% (Table14) followed by genotype 12.80% and genotype X environment interaction 12.03%. It was observed that the genotypes have less genotype X environment interaction, so predominant difference was due to genotypic effect. Further genotype X environment interaction was partitioned among the first two interaction principal component axis (IPCA). The IPCA 1 explained 39.9% of the interaction while the IPCA 2 explained 32.8%. The first two IPCA cumulatively captured 72.7% of the total genotype X environment interaction using 30 DF. The mean square for the IPCA 1 and IPCA 2 were also found to be significant.

Primary branches

For primary branches the mean squares attributed by genotype effects was highest 12.70% followed by G X E with 8.23% and environment 5.24% (Table.14). The major variation was due to genotypic effects. The IPCA 1 explained 83.6% of the interaction while IPCA 2 explained 8.6%. The first two IPCA cumulatively captured 92.2% of the total G x E interaction. This implied that the interaction of thirteen ricebean genotype with six environments was predicted by the first two components of genotypes and environments.

Pods per cluster

For pods per cluster the mean squares attributed by genotype effects was highest 54.71% followed by G X E with 24.18% and environment 21.58% (Table.14). The major variation was due to genotypic effects. The IPCA 1 explained 54.8% of the interaction while IPCA 2 explained 19.6%.

The first two IPCA cumulatively captured 74.4% of the total G x E interaction.

Number of pods per plant

For number of pods per plant the mean squares attributed by genotype effects were highest 37.95% followed by G X E with 36.09% and environment 25.94% (Table.14). The major variation was due to genotypic effects. The IPCA 1 explained 36.2% of the interaction while IPCA 2 explained 31.1%. The first two IPCA cumulatively captured 67.3% of the total G x E interaction.

Pod length (cm)

For pod length the mean squares attributed by genotype effects were highest 73.26% followed by G X E with 19.93% and environment 6.68% (Table.14). The major variation was due to genotypic effects. The IPCA 1 explained 46.5% of the interaction while IPCA 2 explained 29.7%. The first two IPCA cumulatively captured 76.4% of the total G x E interaction.

Number of seeds per pod

For number of seeds per pod the mean squares attributed by genotype effects were highest 76.80% followed by G X E with 16.32% and environment 6.92% (Table.14). It was observed that the G X E interaction was less than the genotypes, so main difference was due to genotypic influence. The IPCA 1 interaction explained 37.1% while IPCA 2 interaction explained 30.8%. The first two IPCA cumulatively captured 67.9% of the total G x E interaction.

Plant height (cm)

For plant height the mean square attributed by environmental effects was highest 71.60% followed by G X E with 17.47% and genotype with 10.91%. The environments were diverse and showed major variation in plant height. The G X E is more than that of genotypes, which determined substantial differences in genotype response across the six environments. The IPCA 1 explained 53.8% of the interaction while IPCA 2 explained 26.1%. The first two IPCA cumulatively captured 79.9% of the total G x E interaction.

Days to 80% maturity

For days to 80% maturity the mean square attributed by environmental effects was highest 79.89% followed by G X E with 11.46% and genotype with 8.63%.The environments were diverse and showed major variation in days to 80% maturity. The G X E is more than that of genotypes, which determined substantial differences in genotype response across the six environments. The IPCA 1 explained 63.6% of the interaction while IPCA 2 explained 18.1%. The first two IPCA cumulatively captured 81.7% of the total G x E interaction.

Protein content (%)

For protein content the mean squares attributed by genotype effects was highest 71.79% followed by G X E with 27.90% and environment 0.29% (Table.14).The major variation was due to genotypic effects for this character. The IPCA 1 explained 83.6% of the interaction while IPCA 2 explained 8.6%. The first two IPCA cumulatively captured 92.2% of the total G x E interaction.

100 seed weight (g)

For 100 seed weight the mean square attributed by genotype effects was highest 91.94% followed by G X E with 5.24% and environment 2.81% (Table.14). The major variation was due to genotypic effects for this character. The IPCA 1 explained 70% of the interaction while IPCA 2 explained 14.3 %. The first two IPCA cumulatively captured 84.3% of the total G x E interaction.

Seed yield per plant (g)

The explained percentage of mean square of seed yield for genotype is highest with 35.77% followed by G X E with 34.40% and environment 29.82%. The major variation was caused by genotypic effect for seed yield per plant. The IPCA 1 explained 50.1% of the interaction while IPCA 2 explained 23.6%. The first two IPCA cumulatively captured 73.7% of the total G x E interaction.

4.9.3. AMMI biplot for yield and yield attributes

The Genotypes with more responsive and specifically adapted to a certain environment for the interaction effect have greater IPCA score, while the genotypes with smaller IPCA scores have lower interaction and considered as widely adapted genotypes. The genotypes are classified under four distinct classes based on mean value and IPCA 1, namely, Class I: Genotypes with high mean and positive IPCA 1, Class II: genotypes with high mean and negative IPCA1, Class III: genotypes with low mean and negative IPCA1 and Class IV: Genotypes with low mean and positive IPCA1. The genotypes in Class I and environments with positive IPCA values interact positively hence, can be recommended for environments for that particular character.

AMMI 2 biplot scores for IPCA 1 and IPCA 2 are plotted. The environment scores are fixed to the origin by side lines and sites with short arrows excert less interactive force while those with long arrow excert strong interactive force. The genotypes close to origin indicates general adaption whereas the genotypes which are afar indicate for specific adaptation to environments Ebdon and Gauch. (2002).

Days to 50% interpretation

For days to flowering, the IPCA value (Table 16a) for genotype RbnG3 (0.09), RbnG7 (0.01), RbnG4 (0.11), RbnG11 (-0.04) and RbnG13 (-0.04) are placed near to zero, hence the genotypes could be considered stable. The IPCA values present near the origin are RbnG5 and RbnG6 which indicates that these genotypes are non-sensitive to environmental interaction and also exhibited early flowering. Hence, the genotypes can be selected for days to flowering. Considering the genotypes with high mean and positive IPCAI with environment interaction, RbnG2, RbnG3, RbnG4, and RbnG7 and environment Env4, Env 5 and Env6 recorded positive IPCA1 (Table 15a). Hence, this genotype can be recommended for this environment (Table 15a).

From the Fig. 13. It was observed that Env 5 (15th June-Kharif), Env 1(1st June-Kharif), and Env6 (1st July-Kharif) had short arrows and it did not excert strong interactive force while Env 2(15th July-post Kharif), Env3 (1st Aug-post Kharif) and Env4 (1st June-Kharif) having long arrows showing strong interaction. Genotypes near the origin were RbnG4, RbnG6, RbnG10 and RbnG3 are non sensitive to environment and have lower interaction. The genotypes RbnG2, RbnG13, RbnG8, RbnG7 and RbnG9 are more responsive to environment and have taken maximum days to flowering. The genotypes responded to early flowerings in Env 1(1st June-Kharif) are

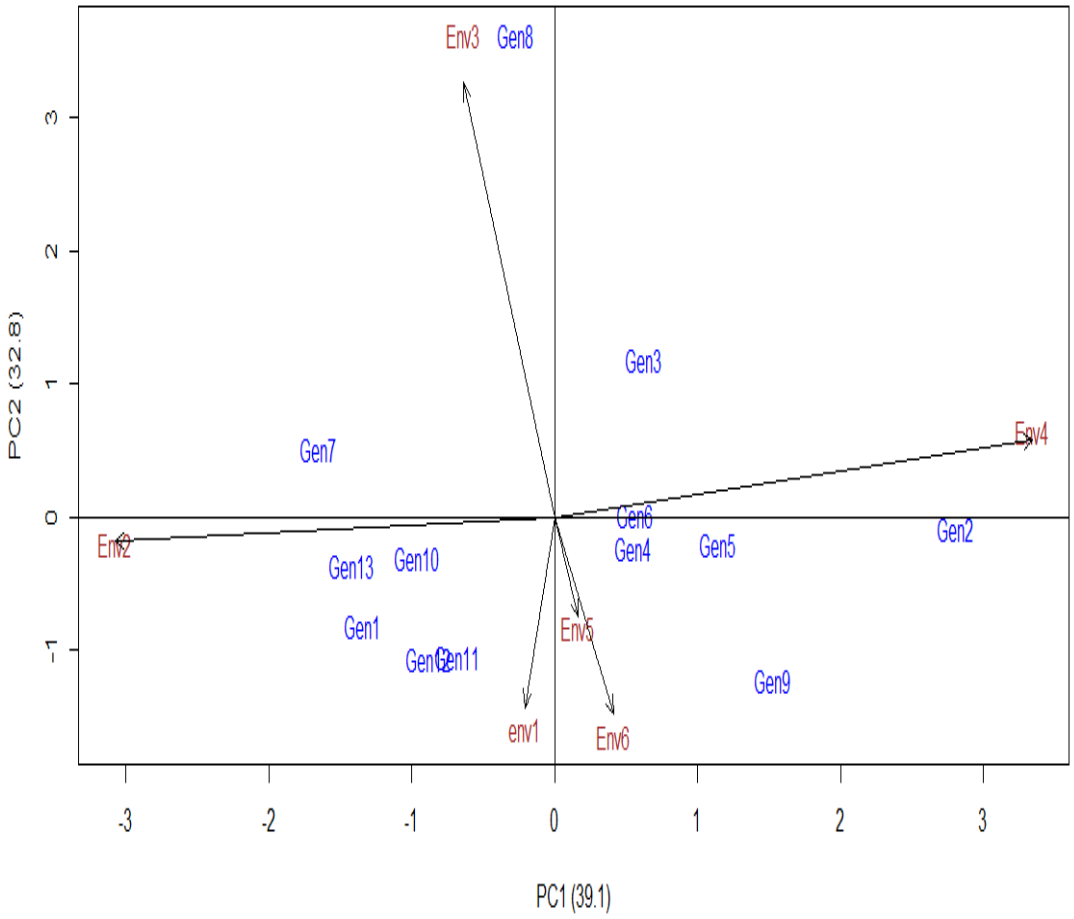


Fig.13. AMMI Biplot for days to 50% flowering showing interaction of PC2 against PC1 scores in six environments.

Legends: **Env1** (1st June 2016), **Env 2**(15th July-post Kharif), **Env3** (1st Aug-post Kharif), **Env4** (1st June-Kharif), **Env 5** (15th June-Kharif), **Env6** (1st July-Kharif).

Gen1-RbnG1, **Gen2**-RbnG2, **Gen3**-RbnG13, **Gen4**-RbnG4, **Gen5**-RbnG5, **Gen6**-RbnG6, **Gen7**-RbnG7, **Gen8**-RbnG8, **Gen9**-RbnG9, **Gen10**- RbnG10, **Gen11**-RbnG11, **Gen12**-RbnG12, **Gen13**-RbnG13.

RbnG11 and RbnG12. Genotypes RbnG1, RbnG7, RbnG10 and RbnG13 is best suited for early flowering in Env 2(15th July-post Kharif). The genotypes RbnG9 is best suited to early flowering in Env 5 (15th June-Kharif) and Env6 (1st July-Kharif).Similarly genotype and RbnG8 is suited for early flowering Env3 (1st Aug-post Kharif) and genotypes RbnG3, RbnG2, RbnG4, RbnG5 and RbnG6 is best adapted to Env4 (1st June-Kharif).

Primary branches

The IPCA value for primary branches with high mean (Table 16a) for genotype RbnG1 (0.00), RbnG4 (0.01), RbnG6 (0.06), RbnG10 (0.05), RbnG12 (0.00) and RbnG13 (0.00) are near to zero and therefore the genotypes could be considered to be stable. The IPCA values of RbnG3 and RbnG11 with moderate mean were present near the origin which indicates that these genotypes were non-sensitive to environmental interaction. Hence, these genotypes can be selected for primary branches. Considering the genotypes and environment interaction genotypes with high mean and positive IPCAI, RbnG1, RbnG4, RbnG6, RbnG10, RbnG12 and RbnG13 and environment Env 1(1st June-Kharif), Env 2(15th July-post Kharif) and Env5 (15th June-Kharif) recorded positive IPCA1(Table 15a). Hence, this genotype can be recommended for this environment.

From the Fig.14. It is exhibited that Env 1(1st June-Kharif), Env4 (1st June-Kharif), Env6 (1st July-Kharif) recorded short arrows showing less interaction. Genotypes near the origin were RbnG1, RbnG4, Rbng5, RbnG10 and RbnG9 are non sensitive to environment and have lower interaction and considered as widely adapted genotypes. The genotypes RbnG12, RbnG3, RbnG6 are more responsive to environment and contributed more to the exhibited G X E interaction. The best genotype in Env1 is RbnG3.

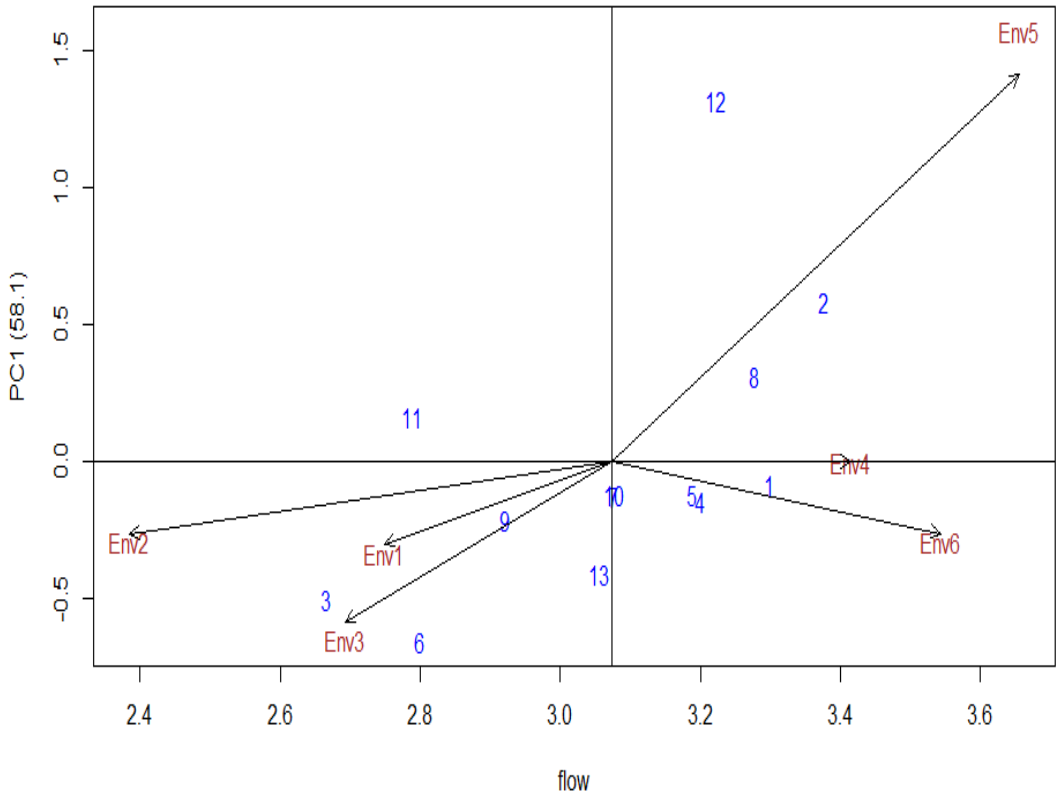


Fig.14. AMMI Biplot for primary branches showing interaction of PC2 against PC1 scores in six environments.

Legends: **Env1** (1st June 2016), **Env 2**(15th July-post Kharif), **Env3** (1st Aug-post Kharif), **Env4** (1st June-Kharif), **Env 5** (15th June-Kharif), **Env6** (1st July-Kharif).

Gen1-RbnG1, **Gen2**-RbnG2, **Gen3**-RbnG13, **Gen4**-RbnG4, **Gen5**-RbnG5, **Gen6**-RbnG6, **Gen7**-RbnG7, **Gen8**-RbnG8, **Gen9**-RbnG9, **Gen10**- RbnG10, **Gen11**-RbnG11, **Gen12**-RbnG12, **Gen13**-RbnG13.

Genotypes RbnG6, and RbnG9 is best suited for Env3 (1st Aug-post Kharif). The genotypes RbnG1, RbnG7, Rbng8 and Rbng10 is best adapted to Env 5 (15th June-Kharif) and RbnG1, RbnG5, RbnG6 for Env6 (1st July-Kharif). Similarly genotype RbnG11 is suited for Env 2(15th July-post Kharif) and genotypes RbnG12, RbnG2, RbnG8 is best adapted to Env5 (15th June-Kharif).

Pods per cluster

The IPCA value for pods per cluster with high mean (Table 16b) for genotype RbnG1 (-0.05), RbnG3 (0.01), RbnG4 (0.01), RbnG6 (0.00), RbnG10 (0.04), and RbnG13 (0.00) was near to zero and therefore the genotypes could be considered as stable genotype. Considering the genotypes and environment interaction genotypes with high mean and positive IPCAI, RbnG3, RbnG4 and RbnG13 and environment Env 1(1st June-Kharif), Env 3(1st June-Kharif), Env 2(15th July-post Kharif), Env4 (1st June-Kharif) and Env6 (1st July-Kharif) recorded positive IPCA1 (Table 15a). Hence, this genotype can be recommended for this environment.

From the Fig. 15. It was observed that Env 2(15th July-post Kharif), Env3 (1st Aug-post Kharif) and Env6 (1st July-Kharif) had short arrows and it did not excert strong interactive force while Env 1(1st June-Kharif), Env4 (1st June-Kharif) and Env 5 (15th June-Kharif) having long arrows showing strong interaction. Genotypes near the origin were RbnG3, RbnG4, RbnG6, RbnG7 and RbnG13 are non sensitive to environment and have lower interaction and considered as widely adapted genotypes. The genotypes RbnG2, RbnG5, RbnG8, and RbnG11 are more responsive to environment. The best genotype in Env 1(1st June-Kharif) and Env6 (1st July-Kharif) is RbnG11.The genotypes RbnG2is best adapted to Env2 (15th July-post Kharif) and Env3 (1st Aug-post Kharif).Similarly genotype RbnG5 and

Table 15a.Environmental IPCA scores of the six environments for different characters of ricebean genotypes

	Days to 50%flowering				Primary branches			Pods per clusters		
Environment code	**Environment**	**Mean**	**IPCAe1**	**IPCAe2**	**Mean**	**IPCAe1**	**IPCAe2**	**Mean**	**IPCAe1**	**IPCAe2**
Env1	Kharif (1st fortnight)-1st July, 2016-17	97.49	-0.06	-1.14	2.58	0.08	1.02	2.72	0.56	-0.62
Env2	post Kharif (2nd fortnight)-15th July, 2016-17	91.11	-3.21	-0.04	2.23	1.06	0.03	2.55	0.50	-0.02
Env3	post Kharif (1st fortnight)-1st August, 2016-17	75.87	-0.56	3.22	2.36	-0.06	-1.04	2.45	0.08	0.52
Env4	Kharif (1st fortnight)-1st June, 2017-18	107.41	3.52	0.08	2.82	1.18	-0.06	2.99	-0.60	0.48
Env5	Kharif (2nd fortnight) -15th June, 2017-18	98.21	0.33	-0.08	2.89	-1.16	0.04	2.96	-0.80	-0.58
Env6	Kharif (1st fortnight) -1st July, 2017-2018	96.75	0.81	-1.56	2.94	-1.14	0.03	3.00	0.04	-0.02

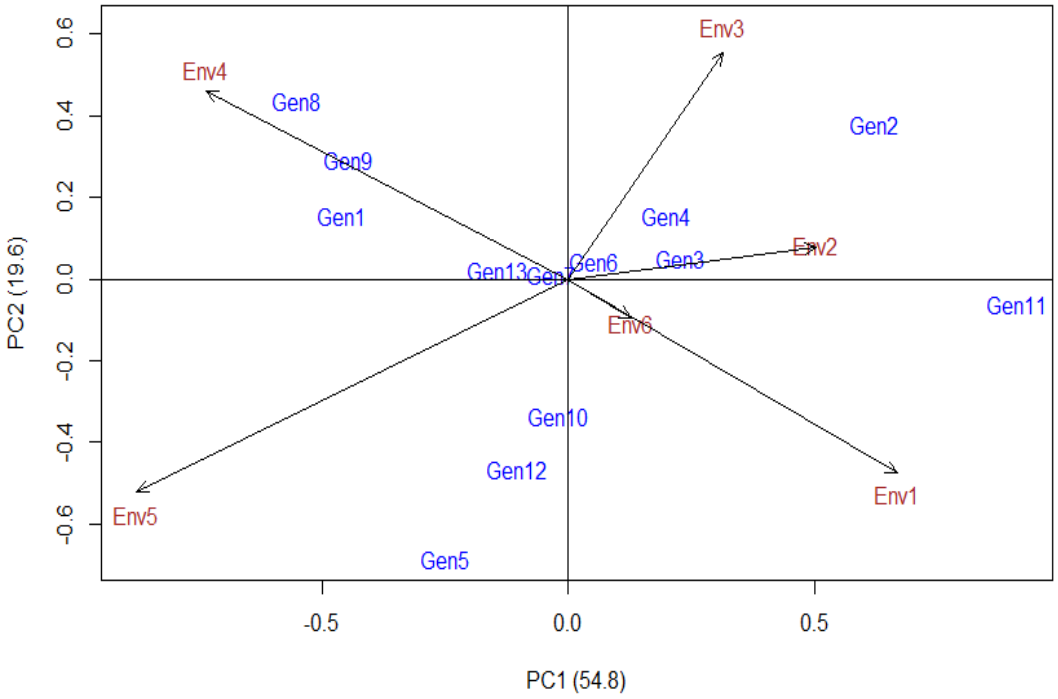


Fig.15. AMMI Biplot for pods per clusters showing interaction of PC2 against PC1 scores in six environments.

Legends: **Env1** (1st June 2016), **Env 2**(15th July-post Kharif), **Env3** (1st Aug-post Kharif), **Env4** (1st June-Kharif), **Env 5** (15th June-Kharif), **Env6** (1st July-Kharif).

Gen1-RbnG1, **Gen2**-RbnG2, **Gen3**-RbnG13, **Gen4**-RbnG4, **Gen5**-RbnG5, **Gen6**-RbnG6, **Gen7**-RbnG7, **Gen8**-RbnG8, **Gen9**-RbnG9, **Gen10**- RbnG10, **Gen11**-RbnG11, **Gen12**-RbnG12, **Gen13**-RbnG13.

RbnG12 is suited for Env 5 (15th June-Kharif) and genotypes RbnG1, RbnG8 and RbnG9 is best adapted to Env4 (1st June-Kharif).

Number of Pods per plant

The IPCA value with high mean (Table 16b) for genotype were RbnG1 (0.08), RbnG3 (0.04), RbnG7 (0.09), RbnG10 (-0.08) and RbnG13 (-0.01) for number of pods per plant which are near to zero, these genotypes could be considered as stable genotypes. Considering genotypes and environment interaction genotypes with high mean and positive IPCAI, RbnG1, RbnG3, RbnG7 and RbnG8 and environment Env 1(1st June-Kharif), Env4 (1st June-Kharif) and Env6 (1st July-Kharif) recorded positive IPCA1 (Table 15b). Hence, this genotype can be recommended for this environment.

It was observed that (Fig.16), Env 2(15th July-post Kharif), Env3 (1st Aug-post Kharif) and Env 5 (15th June-Kharif) had short arrows and it did not excert strong interactive force, while Env 1(1st June-Kharif), Env4 (1st June-Kharif) and Env6 (1st July-Kharif) having long arrows showing strong interaction. Genotypes near the origin were RbnG3, RbnG9, RbnG11, and RbnG13 are non sensitive to environment and have lower interaction and considered as widely adapted genotypes. The genotypes RbnG1, RbnG5, RbnG8 and RbnG10 are more responsive to environment. The best genotype in Env 1(1st June-Kharif) recorded are RbnG4, RbnG6 and RbnG7. Genotypes RbnG1, RbnG8 are best suited for Env4 (1st June-Kharif). The genotypes RbnG10 are best adapted to for Env 5 (15th June-Kharif).Similarly genotype RbnG12, RbnG5 are suited for Env3 (1st Aug-post Kharif) and RbnG2 for Env6 (1st July-Kharif) indicating higher number of pods per plant in their respective environment.

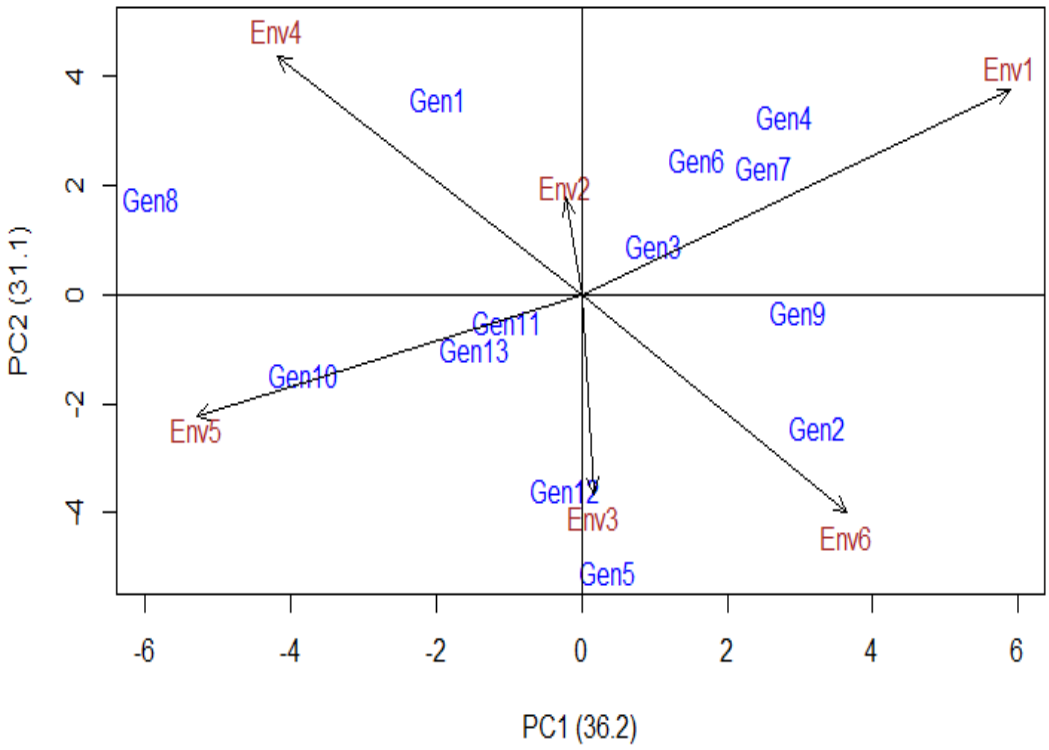


Fig. 16. AMMI Biplot for pods per plant showing interaction of PC2 against PC1 scores in six environments.

Legends: **Env1** (1st June 2016), **Env 2**(15th July-post Kharif), **Env3** (1st Aug-post Kharif), **Env4** (1st June-Kharif), **Env 5** (15th June-Kharif), **Env6** (1st July-Kharif).

Gen1-RbnG1, **Gen2**-RbnG2, **Gen3**-RbnG13, **Gen4**-RbnG4, **Gen5**-RbnG5, **Gen6**-RbnG6, **Gen7**-RbnG7, **Gen8**-RbnG8, **Gen9**-RbnG9, **Gen10**- RbnG10, **Gen11**-RbnG11, **Gen12**-RbnG12, **Gen13**-RbnG13.

Pod length (cm)

The IPCA value with high mean (Table 16c) for genotype RbnG2 (0.02), RbnG3 (0.00), RbnG4 (0.00), RbnG6 (0.04), RbnG10 (0.00), RbnG12 (0.01) for number of pods per plant were place near to zero and therefore the genotypes could be considered as stable genotypes. The IPCA values of RbnG3, RbnG4, RbnG8 and RbnG10 with high mean was place near to the origin which indicates that these genotypes were non- sensitive to environmental interaction. Hence, these genotypes can be selected for pod length. Considering the genotypes and environment interaction genotypes with high mean and positive IPCAI, RbnG2, RbnG6, RbnG10 and RbnG12 and environment Env 1(1st June-Kharif), Env4 (1st June-Kharif) and Env6 (1st July-Kharif) recorded positive IPCA1 (Table 15b). Hence, this genotype can be recommended for this environment.

AMMI 2 biplot for pod length represented (Fig.17) the IPCA1 and IPCA2 scores of the genotype and G x E interaction. The biplot recorded 66.4% of the total variations. It was observed that Env2 (15th July-post Kharif) had short arrows indicating less interaction comparing to Env 1(1st June-Kharif), Env3 (1st Aug-post Kharif) and Env4 (1st June-Kharif) with moderate interaction force. Similarly Env 5 (15th June-Kharif) and Env6 (1st July-Kharif) exhibit longer arrows indicating more interaction forces. Genotypes near the origin were RbnG3, RbnG4, RbnG10, RbnG8 and RbnG12 are non sensitive to environment and have lower interaction and considered as widely adapted genotypes. The genotypes Rbng1, RbnG5, RbnG9, RbnG11, and RbnG13 are more responsive to environment. The best genotype in Env 1(1st June-Kharif) recorded are RbnG7, RbnG8 and RbnG12. Genotypes RbnG11is best suited for Env3 (1st Aug-post Kharif). The genotypes RbnG1, RbnG2 and RbnG13 are best adapted to Env 5 (15th June-Kharif).Similarly genotype RbnG5, RbnG6 and RbnG9 are suited for

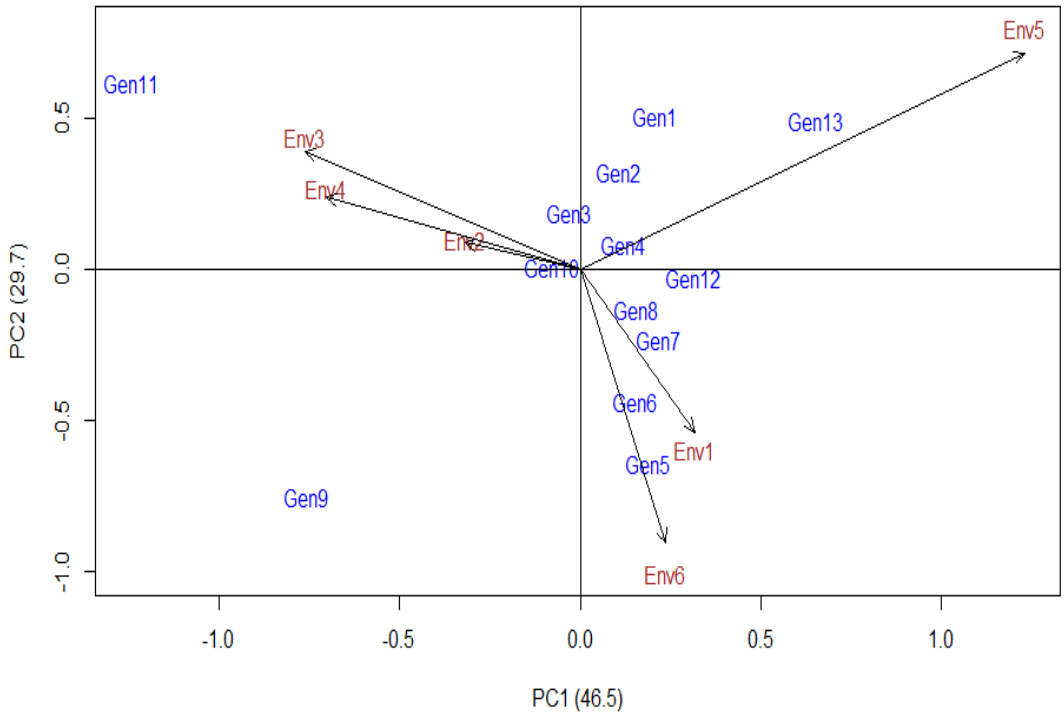


Fig.17. AMMI Biplot for pod length (cm) showing interaction of PC2 against PC1 scores in six environments.

Legends: **Env1** (1st June 2016), **Env 2**(15th July-post Kharif), **Env3** (1st Aug-post Kharif), **Env4** (1st June-Kharif), **Env 5** (15th June-Kharif), **Env6** (1st July-Kharif).

Gen1-RbnG1, **Gen2**-RbnG2, **Gen3**-RbnG13, **Gen4**-RbnG4, **Gen5**-RbnG5, **Gen6**-RbnG6, **Gen7**-RbnG7, **Gen8**-RbnG8, **Gen9**-RbnG9, **Gen10**- RbnG10, **Gen11**-RbnG11, **Gen12**-RbnG12, **Gen13**-RbnG13

Env6 (1st July-Kharif) indicating higher number of pos per plant in their respective environment.

Number of seeds per pod

The IPCA value with high mean (Table 16c) for genotype RbnG1 (-0.05), RbnG3 (-0.01), RbnG4 (0.04), RbnG5 (0.02), RbnG7 (-0.07) and RbnG8 (0.01) for number of seeds per pod which are placed near to zero and therefore the genotypes could be considered as stable. IPCA values with high mean present near to the origin indicates that the genotype was non-sensitive to environmental interaction. Hence, this genotype can be selected for pod length. Considering the genotypes and environment interaction genotypes with high mean and positive IPCA1, RbnG1, RbnG3, RbnG4, Rbng5, and RbnG8 and all the environment recorded positive IPCA1(Table 15b). Hence, this genotype can be recommended across the environment.

AMMI 2 biplot for number of seeds per pod represented (Fig.18) the IPCA1 and IPCA2 scores of the genotype and G x E interaction. The biplot recorded 67.9% of the total variations. It was observed that Env6 had short arrows indicating less interaction and Env4 with moderate interaction comparing to Env 1(1st June-Kharif), Env2 (15th July-post Kharif), Env3 (1st Aug-post Kharif) and Env 5 (15th June-Kharif which exhibits longer vector and contribute more interaction. Genotypes near the origin were RbnG1, RbnG3, RbnG4, RbnG5, RbnG8 are non sensitive to environment and have lower interaction and considered as widely adapted genotypes. The genotypes Rbng6, RbnG7, RbnG10, RbnG11, RbnG12 and RbnG13 are more responsive to environment. The best genotypes in Env 1(1st June-Kharif) recorded is RbnG6. Genotypes RbnG9 and RbnG11 are best suited for Env2. RbnG7 and RbnG12 is best genotypes for Env3 (1st Aug-post

Table 15b.Environmental IPCA scores of the six environments for different characters of ricebean genotypes

	Number of pods per plant				Pod length(cm)			Number of seeds per pod		
Environment code	Environment	Mean	IPCAe1	IPCAe2	Mean	IPCAe1	IPCAe2	Mean	IPCAe1	IPCAe2
Env1	Kharif (1st fortnight)-1st July, 2016-17	53.43	5.09	3.80	8.18	0.04	-0.52	5.52	0.98	0.58
Env2	post Kharif (2nd fortnight)-15th July, 2016-17	39.95	3.08	1.19	7.83	-0.32	0.02	5.13	0.46	-0.54
Env3	post Kharif (1st fortnight)-1st August, 2016-17	51.16	0.04	-4.01	8.12	-0.04	0.48	5.25	0.26	-0.90
Env4	Kharif (1st fortnight)-1st June, 2017-18	55.54	-4.20	4.10	8.20	-0.08	0.36	5.57	-0.30	0.52
Env5	Kharif (2nd fortnight) -15th June, 2017-18	54.53	-5.08	-2.01	8.20	1.08	0.58	5.72	-1.08	0.18
Env6	Kharif (1st fortnight) -1st July, 2017-2018	52.83	3.80	-4.20	8.29	0.32	0.90	5.89	0.36	0.28

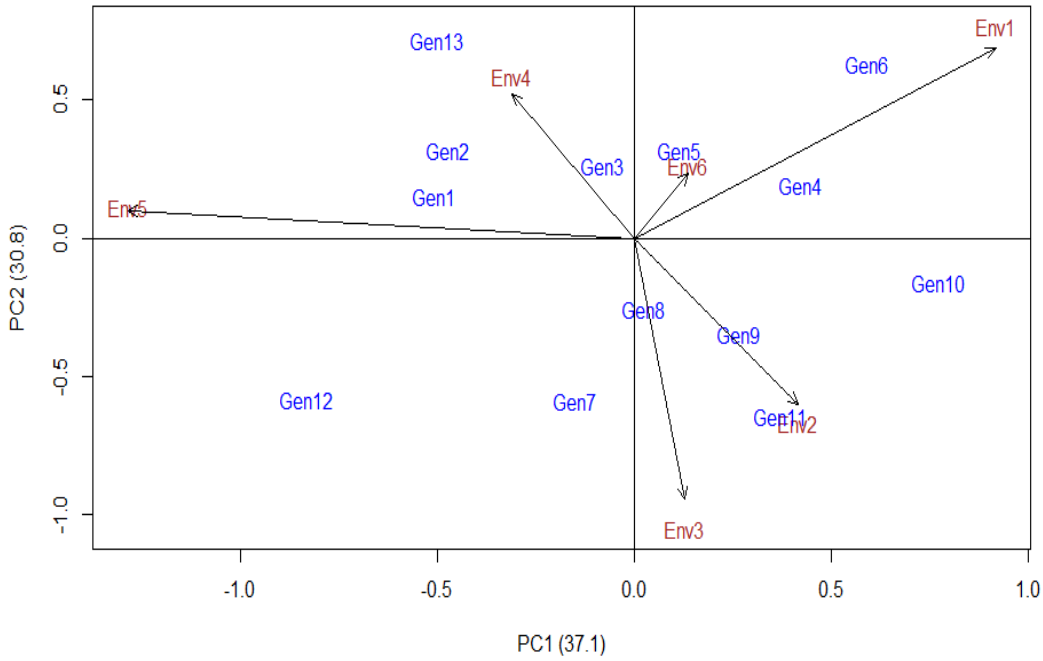


Fig.18. AMMI Biplot for number of seeds per pod showing interaction of PC2 against PC1 scores in six environments.

Legends: **Env1** (1st June 2016), **Env 2**(15th July-post Kharif), **Env3** (1st Aug-post Kharif), **Env4** (1st June-Kharif), **Env 5** (15th June-Kharif), **Env6** (1st July-Kharif).

Gen1-RbnG1, **Gen2**-RbnG2, **Gen3**-RbnG13, **Gen4**-RbnG4, **Gen5**-RbnG5, **Gen6**-RbnG6, **Gen7**-RbnG7, **Gen8**-RbnG8, **Gen9**-RbnG9, **Gen10**- RbnG10, **Gen11**-RbnG11, **Gen12**-RbnG12, **Gen13**-RbnG13.

Kharif). The genotypes best suited for Env4 (1st June-Kharif) is RbnG13 indicating higher number of seeds per pod in their respective environment.

Plant height (cm)

The IPCA value with high mean (Table 16d) for genotype RbnG1 (0.05), RbnG4 (0.04), RbnG5 (-0.02), RbnG7 (0.04), RbnG9 (0.01), RbnG10 (0.06) for plant height was near to zero and therefore the genotypes could be considered as stable. It is also observed that genotype RbnG2 recorded the minimum plant height across the environment with IPCA values near to zero and hence this genotype is considered to be stable. Considering the genotypes and environment interaction genotypes with high mean and positive IPCAI, RbnG1, RbnG4, RbnG5 and RbnG10 and environment Env 1(1st June-Kharif), Env2 (15th July-post Kharif), Env 5 (15th June-Kharif) and Env6 (1st July-Kharif) recorded positive IPCA1 (Table 15c). Hence, this genotype can be recommended for this environment.

AMMI 2 biplot for plant height represented the IPCA1 and IPCA2 scores of the genotype and G x E interaction (Fig. 19). The biplot recorded 79.9% of the total variations. It was observed that Env 1(1st June-Kharif), Env3 (1st Aug-post Kharif) and Env6 (1st July-Kharif) had short arrows indicating less interaction. Env2 (15th July-post Kharif), Env4 (1st June-Kharif) and Env 5 (15th June-Kharif) which exhibits longer vector and contribute more interaction. Genotypes near the origin were RbnG3, RbnG5, RbnG8, RbnG9, RbnG13 and RbnG12 are non sensitive to environment and have lower interaction and considered as widely adapted genotypes. The genotypes Rbng1, RbnG2, RbnG6 and RbnG11 are more responsive to environment. The best genotypes in Env 1(1st June-Kharif) recorded is RbnG1. Genotypes RbnG7 is best suited for Env2 (15th July-post Kharif) and

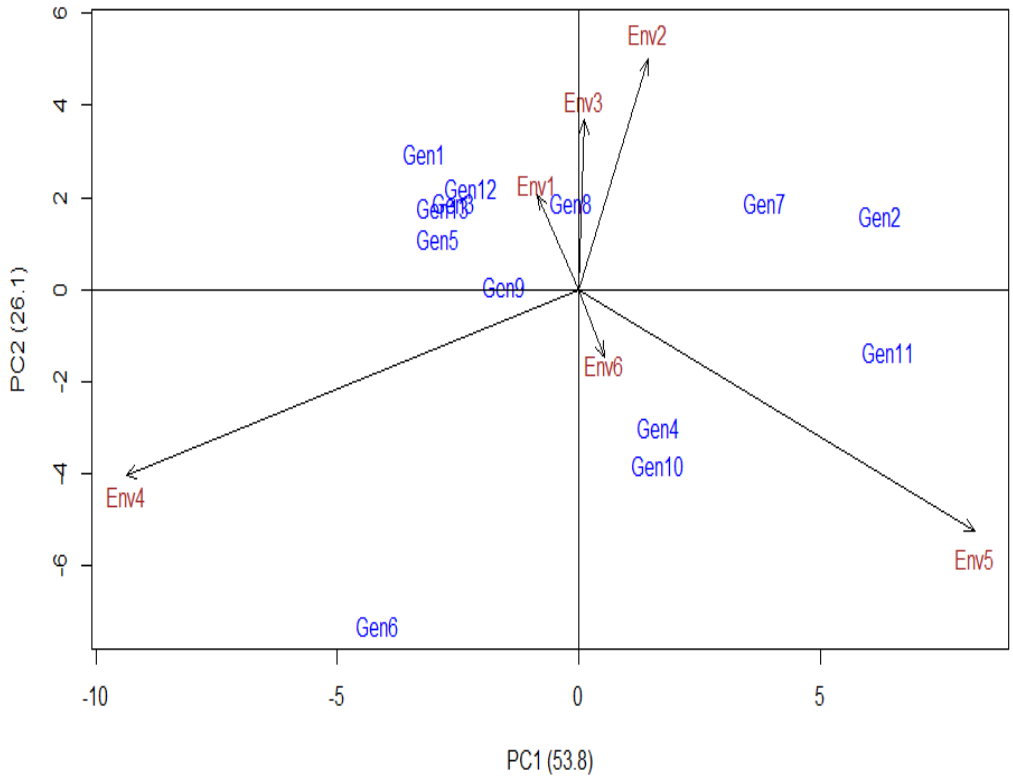


Fig.19. AMMI Biplot for plant height (cm) showing interaction of PC2 against PC1 scores in six environments.

Legends: **Env1** (1st June 2016), **Env 2**(15th July-post Kharif), **Env3** (1st Aug-post Kharif), **Env4** (1st June-Kharif), **Env 5** (15th June-Kharif), **Env6** (1st July-Kharif).

Gen1-RbnG1, **Gen2**-RbnG2, **Gen3**-RbnG13, **Gen4**-RbnG4, **Gen5**-RbnG5, **Gen6**-RbnG6, **Gen7**-RbnG7, **Gen8**-RbnG8, **Gen9**-RbnG9, **Gen10**- RbnG10, **Gen11**-RbnG11, **Gen12**-RbnG12, **Gen13**-RbnG13.

RbnG2 and RbnG 11for Env 5 (15th June-Kharif). The genotypes best suited for Env4 (1st June-Kharif) is RbnG6. Similarly genotype RbnG10 is suited for Env6 (1st July-Kharif).

Days to 80% maturity

The IPCA value with high mean (Table 16d) for genotype RbnG1 (-0.0), RbnG3 (-0.02), RbnG4 (-0.03), RbnG10 (-0.07), RbnG11 (-0.02) and RbnG12 (-0.03) for days to 80% maturity was present near to zero and therefore the genotypes could be considered as stable. It is also observed that genotype RbnG5, RbnG6, Rbng7 and RbnG8 recorded the minimum days to maturity with positive IPCA across the environment with IPCA values near to zero and hence these genotypes are considered to be stable. Considering the genotypes and environment interaction genotypes with high mean and positive IPCAI, RbnG5, RbnG6, RbnG7 and RbnG8 and environment Env 1(1st June-Kharif), Env4 (1st June-Kharif), Env 5 (15th June-Kharif) and Env6 (1st July-Kharif) recorded positive IPCA1 (Table 15c). Hence, this genotype can be recommended for this environment.

AMMI 2 biplot for days to 80% maturity represented the IPCA1 and IPCA2 scores of the genotype and G x E interaction (Fig.20). The biplot recorded 82.5% of the total variations. It was observed that Env1 (1st June-Kharif), Env4 (1st June-Kharif), Env 5 (15th June-Kharif) and Env6 (1st July-Kharif) had short arrows indicating less interaction and has closer association between the environments. Env2 (15th July-post Kharif) and Env3 (1st Aug-post Kharif) which exhibits longer vector and contributes more interaction. The genotypes near the origin are RbnG2, RnG3, RbnG6, RbnG7 and RbnG11 and have less interaction. The genotypes RbnG8, RbnG10 and Rbng13 are more responsive to environment. The best genotypes in Env3 recorded is RbnG8. Genotypes RbnG13 is best suited for

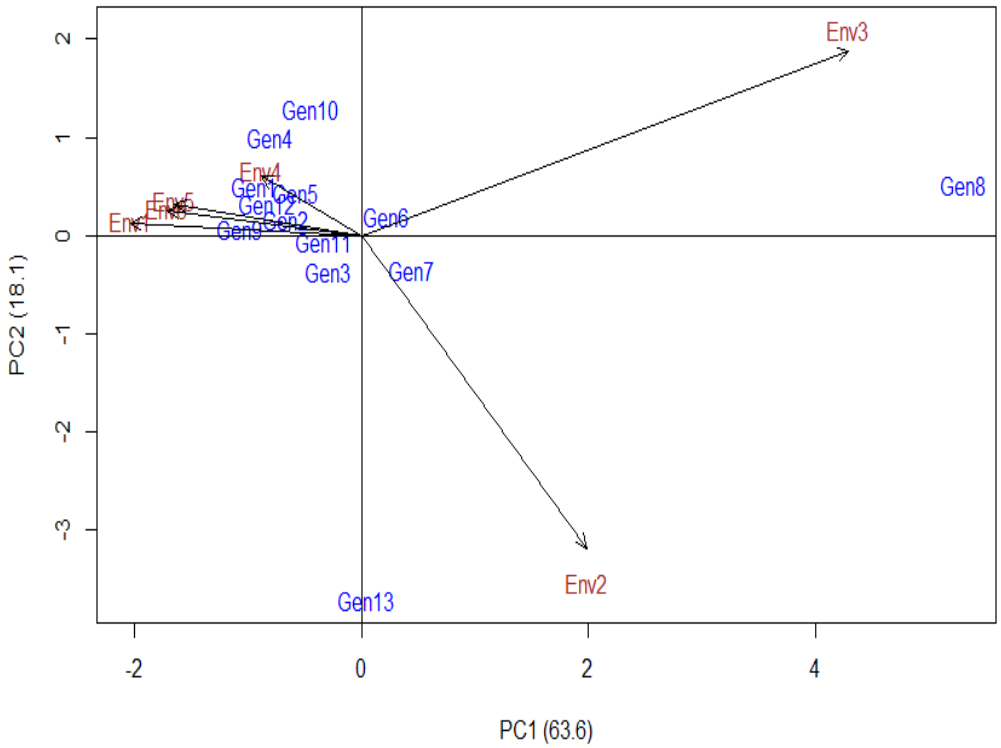


Fig.20. AMMI Biplot for days to 80% maturity showing interaction of PC2 against PC1 scores in six environments.

Legends: **Env1** (1st June 2016), **Env 2**(15th July-post Kharif), **Env3** (1st Aug-post Kharif), **Env4** (1st June-Kharif), **Env 5** (15th June-Kharif), **Env6** (1st July-Kharif).

Gen1-RbnG1, **Gen2**-RbnG2, **Gen3**-RbnG13, **Gen4**-RbnG4, **Gen5**-RbnG5, **Gen6**-RbnG6, **Gen7**-RbnG7, **Gen8**-RbnG8, **Gen9**-RbnG9, **Gen10**- RbnG10, **Gen11**-RbnG11, **Gen12**-RbnG12, **Gen13**-RbnG13

Env2 (15th July-post Kharif). Env 1(1st June-Kharif), Env 5 (15th June-Kharif) and Env6 (1st July- Kharif) are cluster together and reveal similar pattern of interaction for genotype RbnG1, RbnG2, RbnG5, RbnG9, RbnG12 which also cluster together and have similar pattern of interaction.

100 seed weight (g)

The IPCA value with high mean (Table 16e) for genotype RbnG5 (0.01), RbnG9 (0.02), RbnG11 (0.06) and RbnG12 (0.01) for 100 seed weight was present near to zero and therefore the genotypes could be considered as stable. Considering genotypes and environment interaction genotypes with high mean and positive IPCAI, RbnG1, RbnG4, RbnG5, RbnG9 and RbnG12 and environment Env3 (1st Aug-post Kharif), Env4 (1st June-Kharif), Env 5 (15th June-Kharif) and Env6 (1st July-Kharif) recorded positive IPCA1 (Table 15c).Hence, this genotype can be recommended for this environment.

AMMI 2 biplot for 100 seed weight represented the IPCA1 and IPCA2 scores of the genotype and G x E interaction (Fig.21). The biplot recorded 84.3% of the total variations. It was observed that Env2 (15th July-post Kharif), Env4 (1st June-Kharif) and Env6 (1st July-Kharif) had short arrows indicating less interaction. Env 1(1st June-Kharif), Env3 (1st Aug-post Kharif) and Env 5 (15th June-Kharif), which exhibits longer vector and contributes more interaction. Genotypes near the origin were RbnG1, RbnG3, RbnG4, RbnG5, Rbng10 and Rbng13 are non sensitive to environment and have lower interaction and considered as widely adapted genotypes. The genotypes Rbng2, RbnG7, RbnG9 and RbnG11 are more responsive to environment. The best genotypes in Env 1(1st June-Kharif) recorded is RbnG9. Genotypes RbnG2 is best suited for Env6 (1st July-Kharif). Similarly genotypes RbnG11 is suited Env4 (1st June-Kharif)

Table 15c.Environmental IPCA scores of the six environments for different characters of ricebean genotypes

	Plant height(cm)				Days to 80% maturity			100 seed weight(g)		
Environment code	Environment	Mean	IPCAe1	IPCAe2	Mean	IPCAe1	IPCAe2	Mean	IPCAe1	IPCAe2
Env1	Kharif (1st fortnight)-1st July, 2016-17	133.47	-2.98	1.88	134.51	-1.98	0.29	12.09	-1.06	-1.48
Env2	post Kharif (2nd fortnight)-15th July, 2016-17	90.462	2.08	5.67	120.07	2.01	-3.42	11.48	-0.08	-0.58
Env3	post Kharif (1st fortnight)-1st August, 2016-17	91.303	0.08	3.78	107.21	4.12	1.86	11.61	-0.17	1.64
Env4	Kharif (1st fortnight)-1st June, 2017-18	166.78	-9.89	-4.84	138.03	-0.09	0.86	12.30	0.28	0.64
Env5	Kharif (2nd fortnight) -15th June, 2017-18	153.91	8.67	-5.68	141.13	-1.86	0.64	14.24	3.02	-0.48
Env6	Kharif (1st fortnight) -1st July, 2017-2018	144.108	1.12	-2.38	139.46	-1.94	0.48	13.48	0.98	0.42

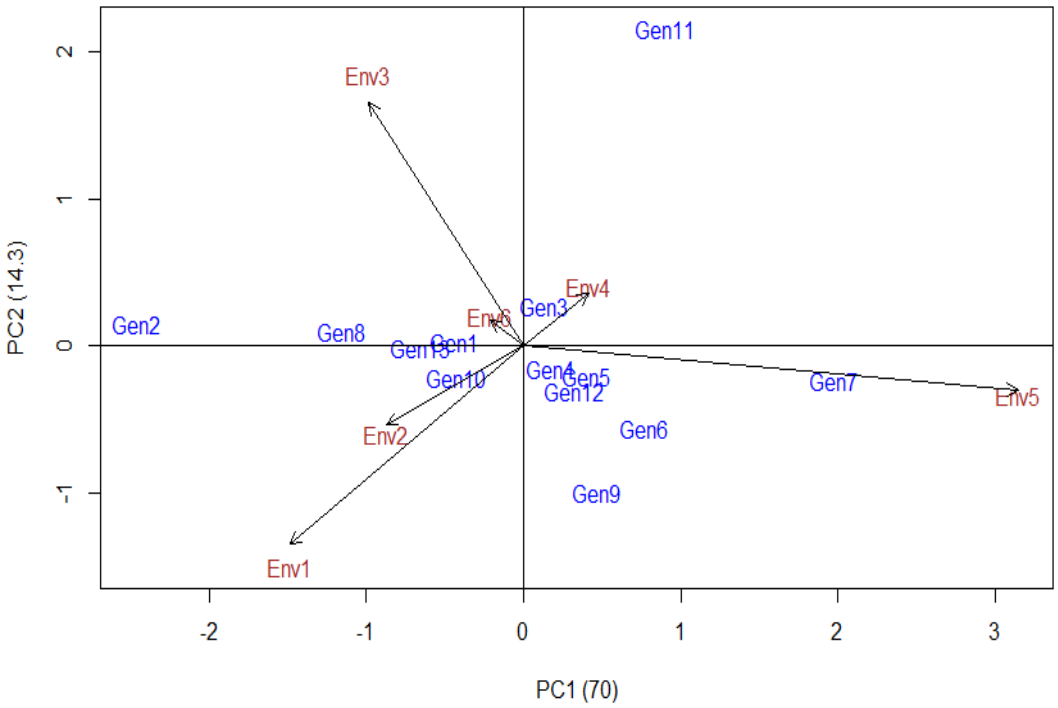


Fig.21. AMMI Biplot for 100 seed weight (g) showing interaction of PC2 against PC1 scores in six environments.

Legends: **Env1** (1st June 2016), **Env 2**(15th July-post Kharif), **Env3** (1st Aug-post Kharif), **Env4** (1st June-Kharif), **Env 5** (15th June-Kharif), **Env6** (1st July-Kharif).

Gen1-RbnG1, **Gen2**-RbnG2, **Gen3**-RbnG13, **Gen4**-RbnG4, **Gen5**-RbnG5, **Gen6**-RbnG6, **Gen7**-RbnG7, **Gen8**-RbnG8, **Gen9**-RbnG9, **Gen10**- RbnG10, **Gen11**-RbnG11, **Gen12**-RbnG12, **Gen13**-RbnG13

Whereas the best genotypes suited for Env 5 (15th June-Kharif) are RbnG6, and RbnG7.

Protein content (%)

The IPCA value with high mean (Table 16e) for genotype RbnG1 (0.00) and RbnG2 (0.08) for protein content was present near to zero and therefore the genotypes could be considered as stable. It is also observed that genotype RbnG3, RbnG6, RbnG8 and RbnG9 recorded the maximum protein content with positive IPCA across the environment with IPCA values near to zero and hence these genotypes are considered to be stable. Considering the genotypes and environment interaction genotypes with high mean and positive IPCAI, RbnG1, RbnG2, RbnG10, RbnG11 and RbnG12 environment Env 1(1st June-Kharif), Env2 (15th July-post Kharif), Env 5 (15th June-Kharif) and Env6 (1st July-Kharif) recorded positive IPCA1 (Table 15d).Hence, this genotype can be recommended for this environment.

AMMI 2 biplot for protein content represented the IPCA1 and IPCA2 scores of the genotype and G x E interaction (Fig.22). The biplot recorded 92.2% of the total variations. It was observed that Env2 (15th July-post Kharif) and Env6 (1st July-Kharif) exhibits shorter vector and contributes less interaction. Genotypes near the origin were RbnG1, RbnG7, RbnG10, RbnG11 and RbnG12 and are non sensitive to environment and have lower interaction and considered as widely adapted genotypes. The genotypes Rbng2, RbnG4, RbnG6, RbnG8, RbnG9 and RbnG13 are more responsive to environment. The best genotypes in Env 1(1st June-Kharif) recorded are RbnG3 and RbnG6. Genotypes RbnG9 is best suited for Env2 (15th July-post Kharif). Similarly RbnG4 is best suited for Env4 (1st June-Kharif). The genotypes RbnG2 is best suited for Env3 (1st Aug-post Kharif) and RbnG8

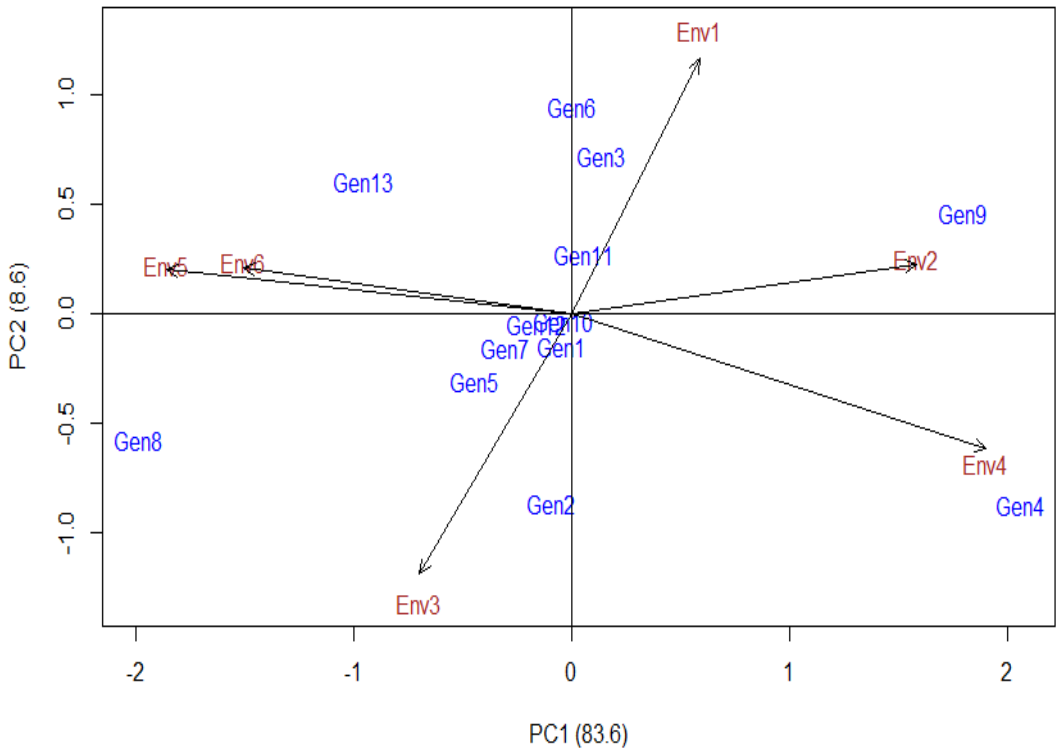


Fig22. AMMI Biplot for protein content (%) showing interaction of PC2 against PC1 scores in six environments.

Legends: **Env1** (1st June 2016), **Env 2**(15th July-post Kharif), **Env3** (1st Aug-post Kharif), **Env4** (1st June-Kharif), **Env 5** (15th June-Kharif), **Env6** (1st July-Kharif).

Gen1-RbnG1, **Gen2**-RbnG2, **Gen3**-RbnG13, **Gen4**-RbnG4, **Gen5**-RbnG5, **Gen6**-RbnG6, **Gen7**-RbnG7, **Gen8**-RbnG8, **Gen9**-RbnG9, **Gen10**- RbnG10, **Gen11**-RbnG11, **Gen12**-RbnG12, **Gen13**-RbnG13

for Env 5 (15th June-Kharif). The genotypes RbnG13 is best suited for Env6 (1st July-Kharif).

Seed yield per plant (g)

The IPCA value with high mean (Table 16f) for genotype RbnG2 (0.07), RbnG3 (-0.01), RbnG6 (0.07) and RbnG7 (0.07) for seed yield per plant were present near to zero and therefore the genotypes could be considered as stable. Considering genotypes and environment interaction genotypes with high mean and positive IPCAI, RbnG2, RbnG6 and RbnG7 and environment that Env 1(1st June-Kharif), Env4 (1st June-Kharif) and Env6 (1st July-Kharif) recorded positive IPCA1 (Table 15d). Hence, this genotype can be recommended for this environment.

AMMI 2 biplot for seed yield per plant represented the IPCA1 and IPCA2 scores of the genotype and G x E interaction (Fig.23). The biplot recorded 73.7% of the total variations. It was observed that Env 1(1st June-Kharif), Env4 (1st June-Kharif) and Env3 (1st Aug-post Kharif) had short arrows indicating less interaction forces Env2 (15th July-post Kharif), Env 5 (15th June-Kharif) and Env6 (1st July-Kharif) which exhibits longer vector and contributes more interaction. Genotypes near the origin were RbnG3, RbnG4, RbnG6, RbnG10, RbnG13 are non sensitive to environment and have lower interaction and considered as widely adapted genotypes. The genotypes Rbng1, RbnG5, RbnG8 and RbnG11 are more responsive to environment. The best genotypes in Env 1(1st June-Kharif) is RbnG12 and Env3 (1st Aug-post Kharif) recorded is RbnG8. Genotypes RbnG9, RbnG7 are best suited for Env2 (15th July-post Kharif). Similarly genotypes RbnG11 is suited for Env4 (1st June-Kharif). Whereas the best genotypes suited for Env 5 (15th June-Kharif) is RbnG5. RbnG1 and RbnG2 is best for Env6 (1st July-Kharif).

Table 15 d.Environmental IPCA scores of the six environments for different characters of rice bean genotypes

	Protein content (%)				Seed yield per plant(g)		
Environment code	Environment	Mean	IPCAe1	IPCAe2	Mean	IPCAe1	IPCAe2
Env1	Kharif (1st fortnight)-1st July, 2016-17	16.34	0.58	1.38	30.54	1.09	-1.42
Env2	post Kharif (2nd fortnight)-15th July, 2016-17	16.22	1.56	0.36	28.04	4.64	0.02
Env3	post Kharif (1st fortnight)-1st August, 2016-17	16.17	-0.62	-0.19	25.95	-1.14	-1.28
Env4	Kharif (1st fortnight)-1st June, 2017-18	16.06	1.82	-0.62	27.54	1.86	-2.36
Env5	Kharif (2nd fortnight) -15th June, 2017-18	16.23	-1.64	0.24	30.79	-5.76	-1.96
Env6	Kharif (1st fortnight) -1st July, 2017-2018	16.41	-1.44	0.18	32.04	-1.84	5.28

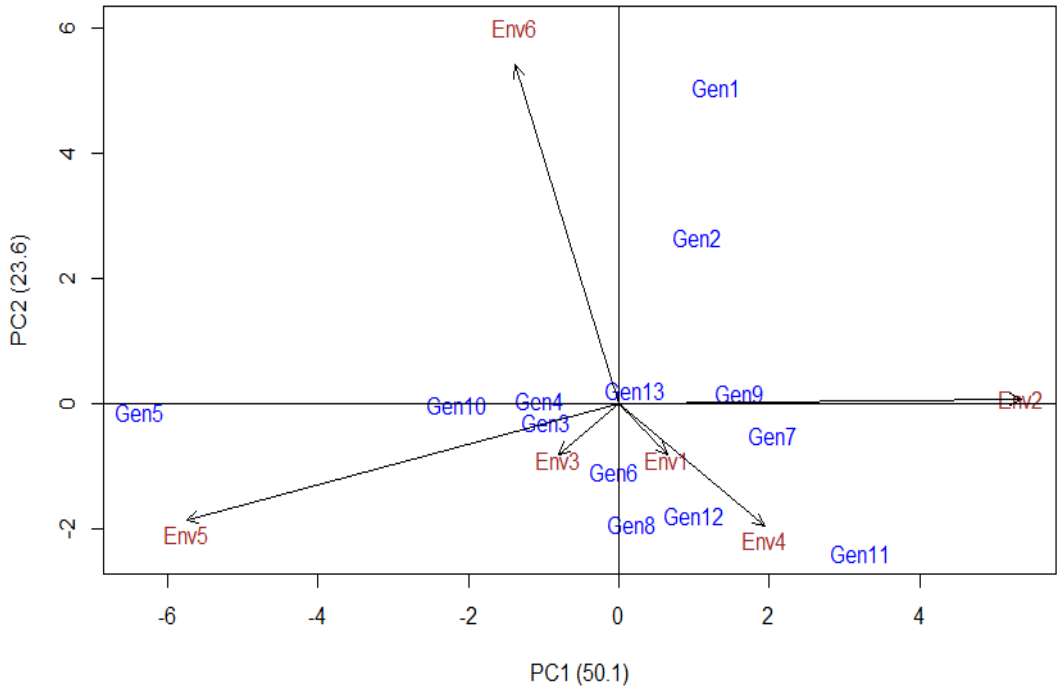


Fig.23. AMMI Biplot for seed yield per plant (g) showing interaction of PC2 against PC1 scores in six environments.

Legends: **Env1** (1st June 2016), **Env 2**(15th July-post Kharif), **Env3** (1st Aug-post Kharif), **Env4** (1st June-Kharif), **Env 5** (15th June-Kharif), **Env6** (1st July-Kharif).

Gen1-RbnG1, **Gen2**-RbnG2, **Gen3**-RbnG13, **Gen4**-RbnG4, **Gen5**-RbnG5, **Gen6**-RbnG6, **Gen7**-RbnG7, **Gen8**-RbnG8, **Gen9**-RbnG9, **Gen10**- RbnG10, **Gen11**-RbnG11, **Gen12**-RbnG12, **Gen13**-RbnG13

4.9.4. AMMI stability values for different traits

Quantitative stability measure is important to quantify and rank genotypes according to their stability. The two principal components have their own extremis, but calculating the AMMI stability value (ASV) is a balanced measure of stability. For this, AMMI stability value was proposed by Purchase (1997). The genotype with low ASV values is considered as stable genotype.

The datas pertaining to AMMI'S stability value were presented in Table 16a to 16f and the results were discussed below.

Days to 50% flowering

For mean performance across six environments, RbnG3, RbnG7 and RbnG13 were found to be superior. For ASV it is observed that genotypes RbnG6, RbnG4 and RbnG10 were found to be stable and promising. Genotype RbnG3 and RbnG7 were also found to be stable when Stability index is measured.

Primary branches

For mean performance across six environments, RbnG1, RbnG3 were found to be superior. For ASV it is observed that genotypes RbnG1, RbnG13 and RbnG3 were found to be stable and promising. Genotype RbnG1 and RbnG3 were also found to be stable when Stability index is measured.

Pods per cluster

For mean performance across six environments, RbnG10, RbnG4 and RbnG1 were found to be superior. For ASV it is observed that genotypes

Table 16a. Estimation of AMMI stability parameters of individual Ricebean genotype based on AMMI model

	Days to 50% flowering							Primary branches						
Genotypes	MV	ICPA1	ICPA2	ASV	rASV	YSI	rYSI	MV	ICPA1	ICPA2	ASV	rASV	YSI	rYSI
RbnG1	96.88	-0.20	-0.20	1.79	9	12.5	3	2.82	0.00	0.03	0.20	1	3	1
RbnG2	93.33	0.09	0.30	3.34	12	22.0	10	2.30	-0.08	-0.25	1.58	11	8	3
RbnG3	100.50	0.09	0.23	1.39	6	7.0	1	2.58	0.00	0.04	0.30	3	8	2
RbnG4	94.05	0.11	-0.19	0.69	2	10.0	8	2.86	0.01	-0.10	0.75	8	21	8
RbnG5	91.66	0.06	-0.20	1.37	5	17.0	12	2.50	-0.03	-0.12	0.59	6	21	12
RbnG6	91.77	0.01	0.08	0.67	1	12.0	11	2.73	0.06	0.12	0.59	7	10	6
RbnG7	97.88	-0.01	0.25	2.03	10	12.0	2	2.61	0.00	-0.07	0.40	5	21	13
RbnG8	83.61	-0.16	0.32	3.63	3	26.0	13	2.66	-0.28	-0.46	3.15	13	17	5
RbnG9	93.61	0.05	-0.24	2.19	11	20.0	9	2.28	0.40	0.34	1.58	12	15	4
RbnG10	95.66	-0.01	-0.12	1.18	3	10.0	7	2.84	0.05	0.20	1.39	10	10	9
RbnG11	96.33	-0.01	-0.20	1.32	4	10.0	6	2.63	0.04	0.17	1.20	9	13	10
RbnG12	96.7	-0.07	-0.23	1.49	7	12.0	5	2.68	0.00	0.06	0.35	4	18	11
RbnG13	96.88	-0.04	-0.18	1.73	8	11.5	3	2.83	0.00	0.04	0.28	2	17	7

Note: ASV=AMMI stability value, rASV= Rank of AMMI stability value, YSI= Stability index, rYSI=Rank stability y index

Table 16b. Estimation of AMMI stability parameters of individual Ricebean genotype based on AMMI model

Genotypes	Pods per cluster							No.of pods per plant						
	MV	ICPA1	ICPA2	ASV	rASV	YSI	rYSI	MV	ICPA1	ICPA2	ASV	rASV	YSI	rYSI
RbnG1	3.02	-0.05	0.20	1.30	10	13	3	61.63	-0.08	0.23	4.25	8	11	3
RbnG2	2.56	0.14	0.29	1.78	12	24	12	39.98	0.10	-0.26	4.48	9	20	11
RbnG3	3.06	0.01	0.09	0.64	7	14	7	52.4	0.04	0.12	1.45	2	6	4
RbnG4	3.58	0.01	0.10	0.57	6	8	2	57.16	0.10	-0.26	4.59	10	11	1
RbnG5	2.90	-0.19	-0.21	0.97	8	16	8	54.81	0.13	-0.23	5.09	12	17	5
RbnG6	2.72	0.00	0.02	0.15	2	11	9	49.41	0.06	0.19	3.09	4	12	8
RbnG7	2.57	0.00	0.01	0.09	1	12	11	52.64	0.09	0.23	3.73	7	13	6
RbnG8	3.30	0.14	0.28	1.69	11	16	5	59.86	-0.13	0.28	7.11	13	20	7
RbnG9	3.12	0.08	0.21	1.29	9	15	6	40.14	0.03	0.13	3.47	5	17	12
RbnG10	4.24	0.04	-0.06	0.34	3	4	1	58.93	-0.08	-0.23	4.68	11	13	2
RbnG11	2.42	0.19	-0.35	2.56	13	26	13	36.63	-0.03	-0.10	1.28	1	14	13
RbnG12	2.58	-0.08	-0.11	0.54	5	15	10	45.18	0.05	0.15	3.58	6	16	10
RbnG13	3.31	0.00	0.05	0.40	4	8	4	57.33	-0.01	-0.10	1.97	3	12	9

Note: ASV=AMMI stability value, rASV= Rank of AMMI stability value, YSI= Stability index, rYSI=Rank stability y index

RbnG7, RbnG6 and RbnG10 were found to be stable and promising. Genotype RbnG10, RbnG4 and RbnG1 were also found to be stable when Stability index is measured.

Number of pods per plant

For mean performance across six environments, RbnG4, RbnG10and RbnG1 was found to be superior. For ASV it is observed that genotypes RbnG11, RbnG3 and RbnG13 were found to be stable and promising. Genotype RbnG4, RbnG10 and RbnG1 were also found to be stable when Stability index is measured.

Pod length (cm)

For mean performance across six environments, RbnG5, RbnG11and RbnG9 was found to be superior. For ASV it is observed that genotypes RbnG10, RbnG3 and RbnG4 were found to be stable and promising. Genotype RbnG5, RbnG11 were also found to be stable when Stability index is measured. With respect to SPIC RbnG10 and RbnG4 were the most stable and considered as a widely adapted.

Number of seeds per pod

For mean performance across six environments, RbnG10, RbnG4and RbnG1 was found to be superior. For ASV it is observed that genotypes RbnG8, RbnG3 and RbnG5 were found to be stable and promising. Genotype RbnG10, RbnG4 and RbnG1 were also found to be stable when Stability index is measured.

Table 16 c. Estimation of AMMI stability parameters of individual Ricebean genotype based on AMMI model

Genotypes	Pod length (cm)							No.of seeds per pod						
	MV	ICPA1	ICPA2	ASV	rASV	YSI	rYSI	MV	ICPA1	ICPA2	ASV	rASV	YSI	rYSI
RbnG1	7.80	0.06	0.15	0.60	9	22	13	7.14	-0.05	0.14	0.63	7	10	3
RbnG2	9.51	0.02	0.09	0.36	5	9	4	4.38	-0.06	0.17	0.65	8	20	12
RbnG3	8.36	0.00	0.04	0.19	2	9	7	6.37	-0.01	0.07	0.28	2	11	9
RbnG4	8.09	0.00	0.04	0.20	3	12	9	7.43	0.04	0.13	0.54	5	7	2
RbnG5	10.95	0.09	-0.17	0.70	10	11	1	6.53	0.02	0.09	0.34	3	11	8
RbnG6	8.85	0.04	-0.12	0.49	8	13	5	6.6	0.14	0.25	0.95	12	17	5
RbnG7	7.90	0.02	-0.10	0.41	6	18	12	6.56	-0.07	-0.15	0.61	6	12	6
RbnG8	7.91	0.00	-0.06	0.27	4	15	11	6.64	0.01	0.06	0.26	1	5	4
RbnG9	9.57	-0.22	-0.35	1.40	12	15	3	4.66	0.04	0.12	0.46	4	15	11
RbnG10	8.33	0.00	0.02	0.11	1	9	8	7.86	0.11	0.20	0.94	11	12	1
RbnG11	9.67	-0.35	-0.46	2.04	13	15	2	4.08	0.11	0.21	0.78	9	22	13
RbnG12	8.80	0.01	0.09	0.49	7	13	6	5.43	-0.19	-0.30	1.16	13	23	1
RbnG13	7.99	0.12	0.27	1.13	11	21	10	6.54	-0.14	0.25	0.93	10	17	7

Note: ASV=AMMI stability value, rASV= Rank of AMMI stability value, YSI= Stability index, rYSI=Rank stability y index

Table 16 d. Estimation of AMMI stability parameters of individual Ricebean genotype based on AMMI model

Genotypes	Plant height (cm)							Days to 80% maturity						
	MV	ICPA1	ICPA2	ASV	rASV	YSI	rYSI	MV	ICPA1	ICPA2	ASV	rASV	YSI	rYSI
RbnG1	161.73	-0.05	0.22	7.22	9	16	7	133.11	-0.01	0.14	3.34	10	13	3
RbnG2	117.75	0.09	0.31	12.91	12	25	13	128.83	-0.08	0.16	2.36	7	16	9
RbnG3	162.17	0.11	0.23	5.70	6	12	6	133.38	-0.02	0.08	1.11	2	4	2
RbnG4	177.27	0.04	-0.16	4.50	3	6	3	132.38	-0.03	0.17	3.01	9	15	6
RbnG5	185.51	-0.02	0.16	6.13	8	10	2	125.72	-0.03	0.12	2.09	6	17	11
RbnG6	173.12	-0.21	-0.38	11.29	11	15	4	124.66	0.13	0.07	0.79	1	13	12
RbnG7	155.27	0.04	0.22	8.10	10	19	9	127.88	0.14	0.15	1.56	4	14	10
RbnG8	165.21	0.20	0.15	1.93	1	6	5	121.05	0.18	0.63	18.57	13	26	13
RbnG9	151.44	-0.01	0.09	3.22	2	12	10	131.38	-0.07	0.18	3.78	12	20	8
RbnG10	192.78	0.06	-0.19	5.06	4	5	1	132.72	-0.07	0.16	2.03	5	9	4
RbnG11	139.58	0.10	-0.33	13.25	13	25	12	131.66	-0.02	0.08	1.15	3	10	7
RbnG12	143.20	-0.03	0.17	5.09	5	16	11	132.61	-0.03	0.12	2.91	8	13	5
RbnG13	156.98	-0.03	0.18	6.06	7	15	8	135.94	0.17	0.18	3.71	11	12	1

Note: ASV=AMMI stability value, rASV= Rank of AMMI stability value, YSI= Stability index, rYSI=Rank stability y index

Plant height (cm)

For mean performance across six environments, RbnG10, RbnG5and RbnG4 was found to be superior. For ASV it is observed that genotypes RbnG8, RbnG9 and RbnG4 were found to be stable and promising. Genotype RbnG10, RbnG5 and RbnG4 were also found to be stable when Stability index is measured.

Days to 80% maturity

For mean performance across six environments, RbnG13, RbnG3and RbnG1 was found to be superior. For ASV it is observed that genotypes RbnG6, RbnG3 and RbnG11 were found to be stable and promising. Genotype RbnG13, RbnG3 and RbnG1 were also found to be stable when Stability index is measured.

Protein content (%)

For mean performance across six environments, RbnG1, RbnG3and RbnG2was found to be superior. For ASV it is observed that genotypes RbnG10, RbnG1 and RbnG11 were found to be stable and promising. Genotype RbnG1, RbnG3 and Rbn2 were also found to be stable when Stability index is measured.

100 seed weight (g)

For mean performance across six environments, RbnG9, RbnG2and RbnG11was found to be superior. For ASV it is observed that genotypes RbnG3, RbnG4 and RbnG12 were found to be stable and promising. Genotype RbnG9, RbnG2 and Rbn11 were also found to be stable when Stability index is measured.

Table 16e. Estimation of AMMI stability parameters of individual Ricebean genotype based on AMMI model

Genotypes	Protein content (%)							100 seed weight (g)						
	MV	ICPA1	ICPA2	ASV	rASV	YSI	rYSI	MV	ICPA1	ICPA2	ASV	rASV	YSI	rYSI
RbnG1	21.03	0.00	-0.02	0.49	2	3	1	4.05	0.01	0.03	2.17	6	18	12
RbnG2	18.64	0.08	-0.08	1.28	5	8	3	25.38	-0.43	0.46	12.08	13	15	2
RbnG3	20.29	0.10	0.10	1.48	6	8	2	11.86	0.00	0.02	0.69	1	10	9
RbnG4	15.74	0.17	-0.55	20.08	13	21	8	4.48	0.00	-0.03	0.85	2	13	11
RbnG5	13.03	-0.01	-0.13	4.38	9	21	12	19.28	0.01	-0.08	1.98	4	9	5
RbnG6	16.74	0.10	0.06	0.94	4	10	6	13.84	0.04	-0.14	3.80	9	15	6
RbnG7	12.83	0.12	-0.10	3.01	8	21	13	12.60	-0.28	-0.37	9.68	12	20	8
RbnG8	16.77	0.12	-0.52	19.43	12	17	5	12.77	-0.10	0.22	5.66	11	18	7
RbnG9	17.72	0.14	0.47	17.52	11	15	4	25.58	0.02	-0.09	2.47	7	8	1
RbnG10	14.38	0.02	0.02	0.32	1	10	9	4.75	-0.01	-0.08	2.10	5	15	10
RbnG11	14.33	0.02	0.04	0.61	3	10	10	24.25	0.06	0.17	4.92	10	13	3
RbnG12	13.97	0.00	0.04	1.56	7	18	11	19.75	0.01	-0.06	1.63	3	7	4
RbnG13	16.23	-0.12	0.27	9.32	10	17	7	3.42	-0.03	0.12	3.19	8	21	13

Note: ASV=AMMI stability value, rASV= Rank of AMMI stability value, YSI= Stability index, rYSI=Rank stability index

Table 16f. Estimation of AMMI stability parameters of individual Ricebean genotype based on AMMI model

Genotypes	Seed yield per plant (g)						
	MV	ICPA1	ICPA2	ASV	rASV	YSI	rYSI
RbnG1	41.44	0.22	0.31	5.76	11	22	11
RbnG2	64.60	0.07	0.19	3.44	8	10	2
RbnG3	51.73	-0.01	-0.08	2.07	4	7	3
RbnG4	42.00	0.06	0.14	2.24	5	15	10
RbnG5	79.93	-0.21	-0.43	13.53	13	14	1
RbnG6	49.53	0.07	0.12	1.08	2	6	4
RbnG7	49.46	0.07	-0.21	4.36	9	14	5
RbnG8	47.04	0.04	0.12	1.96	3	10	7
RbnG9	47.54	0.01	0.11	3.40	7	13	6
RbnG10	41.28	0.02	0.11	4.54	10	22	12
RbnG11	42.15	0.18	-0.37	7.25	12	21	9
RbnG12	46.86	0.03	-0.13	2.79	6	14	8
RbnG13	35.28	0.00	0.03	0.52	1	14	13

MV=Mean value, ASV=AMMI stability value, rASV= Rank of AMMI stability value, YSI= Stability index, rYSI=Rank stability index

Plate no 6.Variability in pod shape size

Seed yield per plant (g)

For mean performance across six environments, RbnG5, RbnG2 and RbnG3 was found to be superior. For ASV it is observed that genotypes RbnG13, RbnG6 and RbnG8 were found to be stable and promising. Genotype RbnG5, RbnG2 and Rbn3 were also found to be stable when Stability index is measured.

Table 17. Stable genotype based on ASV, SI and MV

Sl.no	Characters	ASV	SI	MV
1	Days to 50% flowering	RbnG6, RbnG4 and RbnG8	RbnG1, RbnG3 and RbnG7	RbnG3, RbnG7 and RbnG13
2	Primary branches	RbnG1, RbnG3 and RbnG13	RbnG1 and RbnG3	RbnG1, RbnG3
3	Pods per clusters	RbnG7, RbnG6 and RbnG10	RbnG10, RbnG4 and RbnG1	RbnG10, RbnG4 and RbnG1
4	No.of pods per plant	RbnG11, RbnG3 and RbnG13	RbnG4, RbnG10 and RbnG1	RbnG4, RbnG10 and RbnG1
5	Pod length(cm)	RbnG10, RbnG3 and RbnG4	RbnG5, RbnG9, RbnG11	RbnG5, RbnG11and RbnG9
6	No.of seeds per pod	RbnG8, RbnG9 and RbnG4	RbnG10, RbnG4 and RbnG1	RbnG10, RbnG4 and RbnG1.
7	Plant height	RbnG6, RbnG3 and RbnG11	RbnG10, RbnG5 and RbnG4	RbnG10, RbnG5 and RbnG4
8	Days to 80% flowering	RbnG10, RbnG1 and RbnG11	RbnG13, RbnG3 and RbnG1	RbnG13, RbnG3 and RbnG1
9	Protein content	RbnG3, RbnG4 and RbnG12	RbnG1, RbnG3 and RbnG2	RbnG1, RbnG3 and RbnG2
10	100 seed weight	RbnG3, RbnG4 and RbnG12	RbnG9, RbnG2 and RbnG11	RbnG9, RbnG2 and RbnG11
11	Seed yield per plant	RbnG13, RbnG6 and RbnG8	RbnG5, RbnG2 and RbnG3	RbnG5, RbnG2 and RbnG3

Plate no 7. Pods at maturity

Plate no 8. Variability of pod shape at Maturity

DISCUSSION

In Rice bean, a wide variability of genotype character is quite evident, which holds potential for developing high yielding varieties with desirable characters through appropriate breeding methods. It is necessary to carry out breeding experiments in order to determine whether the qualitative variation among the landraces has significant influence on yield. The existence of genetic variability among landraces for the characters to be improved is the most important and basic factor for successful selection in a breeding programme. Since selection operates on phenotypic variability present in the population, hence estimation of phenotypic and genotypic variability is a prelude in any breeding programme. Thus, the first objective of the present investigation was to attain first hand information regarding extent of variability, interrelationship of yield and its components and causal relationship which would be helpful in formulating effective breeding programme in rice bean.

Stable performance of rice bean genotypes across different environment is essential for the successful selection of stable and high yield genotypes. Therefore, there is a necessity to generate relevant information so as to how different genotypes and their genetic parameters relating to seed yield and its component characters get change in different environment and to examine the role of Genotype x environment Interaction through stability analysis in order to identify stable genotype contributing towards stable yield. It is therefore, necessary to evaluate landraces genotypes for their stability in production and to evaluate the amount of variability present which will get a great boost towards an attempt to serve as source material for future breeding programme. A desirable variety should possess high stability of its performance besides high yield. Jinks and Mather (1955) in *Nicotiana rustica,* Finlay and Wilkinson (1963) in barley, and Eberhart and Russell (1966) in

maize have demonstrated that stability of performance is variety specific and also demonstrated that varieties vary greatly in their response to varying environments. Johnson *et al*. (1968) stated that, stability in the performance of a variety is as important as its mean yield

Genetic variability and related parameters

Variability is the pre-requisite for success of any breeding programme and selection of genotype. The estimate of genotypic and phenotypic coefficient of variation provides clear picture of variability present and extent of genetic variation for breeding material under study. Result indicates that the value of phenotypic coefficient of variations were high comparing to genotypic coefficient of variation for all the characters showing that the environment had an important role in influencing the expression of the characters studied under six environments. Similar results were also reported by Khan *et al*. (2015), Geeta *et al*. (2015) and Arshad *et al* (2003).

Mean squares were significant for all the characters studied. It is evident from environment- wise analysis of variance that sufficient genetic variability exists among genotypes for all the characters studied except for primary branches in Env3 (1st Aug-post Kharif sowing) was found to be non-significant and hence desirable improvement can be brought through selection with high mean in these different characters.

The estimate of heritability provides predicting the effectiveness of selection. High estimates of PCV for the characters indicated that sufficient genetic variability exhibited in genotypes and therefore, selection might bring desirable improvement in these characters. A high estimate of phenotypic and genotypic coefficient of variation was observed for primary branches, pods per cluster, number of pods per plant, pod length, plant height and seed yield per

plant. PCV and GCV value was moderate for 50% flowering, days to 80% maturity and 100 seed weight. Number of seeds per pod exhibited low PCV and GCV. These results indicates that the material under study provide ample scope for improvement through selection of these characters.

Similar findings has been made by Lakshmana *et al.* (2010) in ricebean and reported high PCV values for number of pods/plant, number of seeds/pod. Mandal and Dana (1998) reported similar results in rice bean. Khan *et al*. (2015) in cowpea reported PCV and GCV for different characters. Gadekar and Dhumale (1990) reported GCV and PCV high for branches per plant, number of seeds per pod, medium for days to 50 per cent flowering, length of pod, while medium GCV and high PCV for plant height and 100 seed weight. Jadhav *et al.* (1996) reported high GCV and PCV for plant height, branches per plant, pods per cluster, seeds per pod, grain yield per plant. Chaudhari *et al.* (1997) reported moderate estimates of GCV for grain yield per plant and high PCV. Gill *et al.* (2008) reported low PCV and GCV for number of seeds per pod. High PCV values for number of pods per plant, number of seeds per pod was reported by Lakshmana *et al.* (2010). Dodwad *et al.* (1998) reported high PCV values for pods per plant, and 100 seed weight in greengram. Pal *et al.* (2014) in cowpea reported high PCV values for grain yield/plant, number of pods per plant and 100 seed weight. Ahmad and Rabbani (1992) reported high GCV and PCV for yield per plant and 100 seed weight. A similar finding was reported by Dodake and Dahat (2011) in rice bean, Lavanya (2006) in Mungbean and Khan *et al*. (2015) in cowpea.

Heritability and genetic advance

Heritability is the role of heredity for the expression of phenotypes Falconer, (1960).This is to determine how much phenotypic variation is present in a particular generation which is heritable while genetic advance measures the expected genetic progress for particular characters based on

selection procedure to be estimated. The heritability estimates is better indicator of heritable portion of variation Burton and Dewane, (1952). Johnson *et al.* (1955) suggested that estimates of heritability along with genetic advance were found to be useful for predicting the outcome to select the best individuals than heritability alone. Moderate to high heritability with larger magnitude of expected genetic advance for a particular character is consider to be governed by additive gene action while high heritability with low genetic advance and low heritability with low genetic advance for a character, it may be consider for presence of non-additive gene action.

The heritability estimates were found to be very high for days to 50% flowering, pod length, number of pods per plant, number of seeds per pods, plant height, and days to 80% maturity, 100 seed weight, protein content and seed yield per plant. Pods per cluster exhibits moderate heritability and low heritability was recorded for primary branches. The results are in agreement with Das and Dana (1985) reported low heritability for number of branches per plant. Gadekar and Dhumale (1990) observed high heritability for grains per pod and seeds per pod. Jadhav *et al.* (1996) reported high heritability for grain yield per plant. Chaudhari *et al.* (1997) observed high heritability for grain yield per plant and plant height.

Burton (1952) suggested that estimates of genetic variation along with heritability ought to provide right idea about the expected progress of selection. Number of pods per plant, Pod length, plant height, protein content and seed yield per plant exhibits high GCV coupled with high heritability. Therefore a character possessing high GCV with high heritability will be useful in selection of any breeding programme. Ahmad and Rabbani (1992) reported high estimates of GCV coupled with high heritability for number of pods/plant, Seed yield/plant in ricebean, Dodwad *et al.* (1998) in greengram, and Khan *et al*. (2015) in cowpea.

High heritability with high genetic advance mean were observed in days to 50% flowering, number of pods per plant, plant height, days to 80% maturity, 100 seed weight and seed yield per plant. This indicates that, character improvement can be possible by direct selection for the character. Similar findings were reported by Pal *et al*. (2018) for number of pods per plant and 100 seed weight. Lakshmana *et al.* (2010) in rice bean reported high value of genetic advance for days to maturity and days to 50% flowering. Kumar *et al*. (1997) in number of pods per plant and seed yield per plant in ricebean. Majid *et al*. (1982) reported high GA and GA% for number of pods per plant. Dodake and Dahat (2011) in seed yield per plant and pods per plant. Rahim *et al.* (2010) reported similar results for plant height, number of pods per plant, number of seeds per pod and grain yield per plant. Geeta *et.al* **(**2015) for days to 50% flowering, number of pods and seeds per plant.

Primary branches and pods per cluster exhibits low heritability with low genetic advance mean percentage. Deb and Khalaque (2004) reported low heritability with genetic advance percentage of mean for different characters in different crops.

Correlation

After understanding the nature of variation for seed yield and other traits, it would be desirable to know the nature and magnitude of association existing among these traits in order to identify yield components essential for defining an ideal and stable plant type in rice bean, which will be suitable for growing under different environments. This consideration becomes still imperative, when one visualizes yield as a complex trait and product of the interaction of several metric traits. In the present study, correlation among eleven different traits under different environment was studied.

Correlation studies indicated that seed yield per plant was significantly positively associated with primary branches, pods per cluster, number of pods

per plant, number of seeds per pod and plant height. These results are in confrontation with Geeta *et al* (2015) and Gupta *et al*., (2014) for number of pods per plant and number of seeds per pod. Saste (2004) recorded significant positive correlation with number of pods per plant, number of branches per plant, number of pods per cluster, number of seeds per plant with seed yield. Solanke (2001) recorded positive significant correlation for seed yield per plant with plant height, number of branches per plant, number of clusters per plant and number of pods per plant at genotypic correlation. Gadekar *et al.* (1990) reported positive and significant correlation of seed yield per plant with plant height, pods per plant, and pods per cluster while negative significant was recorded for days to 50% flowering and days to 80% maturity which is in agreement with the investigation carried out for days to 50% flowering and 80% maturity.

Correlation among the yield contributing characters

Days to flowering exhibited positive significant relationships with pod length, days to 80% maturity and 100 seed weight. These results are in conformity with Gaurav *et al*. (2017) for days to 50% flowering and days to 80% maturity.

For primary branches positive significant correlations were observed in pods per clusters, number of pods per plant, number of seeds per pod and plant height while negative significant was observed in pod length, 100 seed weight and crude protein. A positive significant correlation for pods per cluster was observed with number of pods per plant, pod length, number of seeds per pods, plant height, days to 80% maturity and crude protein. A high positive significant correlation for number of pods per plant was exhibited with number of seeds per pod, plant height and days to 80% maturity while negative significant with 100 seed weight. Pod length exhibited high positive correlation with plant height, 100 seed weight, and crude protein. For number of seeds per

pod high positive correlation was exhibited with plant height, and crude protein while negative significant correlation with plant height. Plant height exhibited positive correlation with crude protein and negative correlation with 100 seed weight. The result are in conformity with Singh *et al.* (2009) observed a negative and significant correlation between plant height and 100 seed weight. Days to 80% maturity showed negative correlation with 100 seed weight. 100 seed weight exhibited positive significant correlation with crude protein. Similar finding were reported on genotypic correlation coefficients observed that seed yield per plant was significantly positively correlated with pod length and number of seeds per pod. Chaudhari (2000) reported significant positive association with plant height and number of branches per plant while significant negative correlations for protein content for seed yield.

Based on genotypic association between yield and yield attributing characters, selection could be made for the characters having positive significant association for improvement of seed yield per plant in rice bean. Therefore, it can be suggested that yield attributing characters, pod per clusters, pod length, number of pods per plant, number of seeds per pod, plant height, days to 80% maturity, crude protein and 100 seed weight are positively associated, hence selection and improvement of this characters will simultaneously improve the other characters for seed yield as these are in desirable direction for selection.

Path coefficient analysis

For better understanding and index for selection path coefficient analysis was partitioned into direct and indirect effects to find out the cause and effects of correlation on different yield contributing characters at genotypic level.

Direct effect

The high estimate for positive direct effect was recorded for primary branches (0.08), number of pods per plant (0.24), pod length (1.28), number of seeds per pods (0.28), plant height (1.42), days to 80% maturity (0.41), 100 seed weight (0.07) and crude protein (0.33) and these can be considered for direct selection for high seed yield. Negative direct effect on yield was contributed by days to 50% flowering (-0.27) and pods per cluster (-1.52). Even though pods per clusters showed high negative direct effects, its association with seed yield was significant and positive. The character also play indirect role in increasing the seed yield through pod length, number of seeds per pod, plant height and days to 80% maturity.

Similar result for positive direct effects were observed by Hemavathy *et al.* (2015) for plant height, number of pods per plant and 100 seed weight, Gadhak *et al.* (2013) for biological yield per plant, number of seeds per pod, number of primary branches per plant and Tiwari *et al.* (2014) for pod length, plant height and seeds per pod. Sonene *et al*. (1999) for cluster per plant, days to maturity and days to flowering. Mehta *et al*. (2007) for plant height and crude protein. Reddy *et al.* (2013) for number of capsules per plant. Dodake and Dahat (2011) for number of pods per plant.

Indirect effect

Days for 50% flowering exhibited negative direct effects and its correlation with seed yield was also negative. However indirect effect contributing seed yield was moderate with pod length and number of seeds per pod. The other characters did not contribute much through indirect with other yield components. Primary branches show positive significant association with seed yield per plant and positive direct effects. Contribution of indirect effects for seed yield was through pod length and plant height. Dash (2012) revealed that branches per plant and branch length had moderate direct effect. Pods per

cluster showed positive significant association with seed yield and direct negative effect with seed yield. The indirect effect via pod length was high while and moderate indirect positive for number of seeds per pod and plant height. The number of pods per plant exhibited significant positive association for seed yield and positive direct effect. It shows indirect effects with days to 50% flowering and days to 80% maturity. The indirect effects via others traits are of low magnitude. Dodake and Dahat (2011) studied characters association and path coefficient in ricebean and recorded that number of pods per plant had high direct effect and contributed to yield. Pod length show high direct positive effect but correlation with was low and negative. It exhibited positive indirect effects via, number of seeds per pod and also low positive indirect effect with primary branches and 100 seed weight. The indirect effects with other traits are of negative and low in magnitude. Number of seeds per pod shows positive significant association with seed yield and positive direct effect. It shows high positive indirect effect with pod length. Low magnitude of positive indirect effect was also observed for primary branches, plant height and 100 seed weight. Plant height exhibited positive signification association with seed yield and positive direct effect. The indirect effects showed low positive indirect effect via, days to 50% flowering, primary branches, number of seeds per pod and crude protein. Days to 80% maturity exhibits positive direct effects, however correlation with seed yield is negative. The indirect effects showed high positive indirect effect with pods per clusters and low magnitude of positive indirect effect with days to 50% flowering, primary branches and number of seeds per pod.100 seed weight shows direct positive effect but negative correlation with seed yield. The indirect effects showed high positive indirect effect with pod length while low magnitude positive indirect effects with primary branches and number of seeds per pod. The indirect effects via other traits were of low magnitude. Protein content reveals positive direct effect but exhibited negative correlation with seed yield. The indirect effect

shows low positive indirect effect with pods per cluster, number of pods per plant and plant height. The indirect effects via other traits were of low magnitude.

Similar results were reported by Sonene *et al*. (1999) that days for 50% flowering, cluster per plants and pod per plant resulted positive indirect effect via most of the characters for seed yield. Thanki and Sawargaonkar (2010) for number of branches per plant and plant height indirectly contributed via number of pods per plant for seed yield per plant. Thakur and Bhardwaj (2017) revealed that days to maturity have high indirect effect via plant height and positive and significant correlation with seed yield per plant. Dash (2012) revealed days to flowering with high positive direct effect and moderate direct effect for branches per plant and branch length.

It can be suggested that, the indirect effects contributing to seed yield are primary branches, pods per clusters, number of pods per plant, pod length, number of seeds per pod, plant height, 80% maturity and 100 seed weight were emerged as important characters hence, due emphasis should be given for improvement of seed yields.

Stability analysis (Eberhart and Russell (1966)

The phenotype of an individual is the manifestation of its genotype expressed in a particular environment. The environment plays a major role and influences the final expression of the genotype into phenotype. The phenotype of an individual can be expressed as a function of its genotype, the environment and their interaction (G x E). Some genotypes when exposed to different environments such as regions, seasons, years etc, exhibit a more or less uniform performance. When most of the genotypes react to the changing environmental situations it become vulnerable to influence of environment and promptly interacts with it and as a result their performance is influence by varying environments. If a genotype is found to be responding to a particular

favourable environment the genotype can be recommended for growing in that particular environment only. If wider adaptability is desire then genotype's performance should be evaluated over a number of environments and then suitable genotypes which may perform well in all the environments should be selected. For determining adaptability of different genotypes, they should be subjected to multi-environments, yield testing for number of years or seasons as the case may be. This helps to identify genotypes with low G x E interaction at high level of performance over a wider range of environments

In the present investigation thirteen genotypes were evaluated for stability and genotype x environment interaction over six environments following Eberhart and Russel (1966) model.

Analysis of Variance over environments

Analysis of variance showed that the variance due to genotypes were significant for all the characters which revealed the presence of considerable genotypic variability among the genotypes under studied. The genotypes x environment interaction were also all found to be significant for all the characters which showed that genotypes react with the environments. Significant G x E interaction for pods per plant clusters per plant and yield have been reported by Dobhal and Gautam, (1994). Environment wise analyses of variance revealed that mean sum of square due to genotypes were highly significant for all the characters. Similar findings have been reported by Chattopadhyay *et al.* (2001).

Mean performance of genotype on thirteen genotype of rice bean

It is revealed that, the genotype RbnG8 produced flowering earliest in 83.61 days. On the other hand the highest number of days 100.5 to days to 50% flowering was taken by genotype RbnG3. These findings are in conformity of

Salem *et al.* (2004), Singh *et al.* (1991) in chickpea, Singh *et al* (1998) in ricebean.

The maximum number of primary branches was recorded in genotype RbnG4 (2.86) and minimum was observed in RbnG2 (2.30). The maximum number of pods per cluster was recorded in genotype RbnG10 (3.18) and minimum was observed in RbnG11 (2.33). The highest number of pods per plant was recorded in RbnG1 (61.63) and the lowest was observed in RbnG11 (36.63).

The longest pod length recorded was 9.48 cm in genotype RbnG5 and lowest pod length recorded is 7.4 cm in genotype RbnG7. The maximum number of pods recorded was 6.93 in genotype RbnG4 and lowest recorded is 3.63 in genotype RbnG11. The highest plant height was recorded in genotype RbnG10 (167.59 cm) while genotype RbnG2 (98.07 cm) recorded lowest plant height. The maximum day for maturity was recorded in genotype RbnG13 (135.83 days) while genotype RbnG8 (121.06 days) recorded minimum days for maturity. The highest protein content was recorded in genotype RbnG3 (21.24%) while genotype RbnG4 (12.23%) recorded lowest protein content. The highest 100 seed weight recorded was 21.5 gm in genotype RbnG2 while the lowest 100 seed weight recorded was 3.36 gm in genotype RbnG13. The highest seed yield per plant was recorded in genotype RbnG5 (31.37g), RbnG8 (37.82g) and RbnG12 (31.61g) while genotype RbnG13 (26.01g) recorded lowest seed yield per plant. These findings are in conformity by Musa and Taha (1980), Paikaray and Misra (1992) in chickpea.

Mean performance of environments revealed that Env2 and Env3 recorded the least and unfavourable environment for all the characters observed, whereas Env4 and Env6 performed better and was favourable for all the characters. However days to 50% flowering and days to 80% maturity were

effected in terms of early flowering and maturity in unfavourable environment ie.Env2 and Env3.

Environment indices

From the result it is revealed that Env4 (1st June-Kharif), Env5 (15th June-Kharif) and Env6 (1st July-Kharif) sowing was best for days to 50% flowering. Env4 (1st June-Kharif) and Env6 (1st July-Kharif) for primary branches. For pods per cluster Env 2(15th July-post Kharif), Env4 (1st June-Kharif), 5(15th June-Kharif) and Env6 (1st July-Kharif) are favourable environments. For number of pods per plant, pod length, number of seeds per pod, plant height, days to 80% maturity most favourable environments are Env1 (1st June-Kharif), Env4 (1st June-Kharif), 5(15th June-Kharif) and Env6 (1st July-Kharif). For protein content none of the environments were favourable. For 100 seed weight the environments favourable are Env1 (1st June-Kharif) and Env6 (1st July-Kharif). For seed yield per plant environment Env1 (1st June-Kharif), Env4 (1st June-Kharif) and Env6 (1st July-Kharif) are most favourable.

The environment indices for all the traits under study revealed that none of the trait had positive indices in all the six environments. It is observed that from the result obtained Env 2(15th July-post Kharif) and Env3 (1st Aug-post Kharif) was the unfavourable environment for all the traits as most of the negative traits are observed in this environments. When we compare the different environments under studied, it clearly showed that Env1 (1st June-Kharif), Env4 (1st June-Kharif), 5(15th June-Kharif) and Env6 (1st July-Kharif) was most favourable sowing for most of the characters.

Joint regression analysis of variance

The Joint regression analysis of variance was carried out for eleven characters in six environments and reveals the presence of significant differences among the genotypes for all the characters studied. Stability analysis indicates the presence of significant Genotype x Environment (linear) interactions for all the characters study. High magnitude of Genotype x Environment (linear) due to environments differed considerably for all the characters and that these characters were greatly influence by environments, thereby indicates a linear function of environments with significant variance difference between environments along with genotypic response i.e., the environments created by sowing dates with fifteen days interval during the growing season was justifiable and had linear effects and also prediction of performance for the character was possible. This results are in conformity with findings by Gyanendra *et al,* (2007), Shukla *et al*. (2003), Gupta *et al. (*2014), Nath and Dasgupta (2013), Dhillion *et al.* (2009), Jai Dev *et al* (2009), Mohamed *et al*. (2013) and Ramana and Satyanarayana (2005). Non significant effect of genotype × environment (linear) indicates that the different genotypes did not differ genetically in their response to different environments. The pooled deviation when tested against pooled error was found significant for days to 50% flowering, plant height and days to 80% maturity which indicates the important contribution of non predictable component.

The results of the present study were in conformity with the work reported earlier by various workers viz., Patil and Narkheda (1995) for 100 seed weight, pods per plant and seed yield. Kalpande *et al.* (1996) for yield and yield components, Singh and Nanda (1997) for yield, Manivannam et *al.* (1999) for seed yield, Tofu *et al.* (2002) for days to 50% flowering, days to maturity, plant height and 100 Seed weight and Singh *et.al,* (2003) for yield and its components in mung bean. Senthilkumar and Chinna (2012) also had

the same opinion on these traits. Sowmini and Jayamani (2013) and Singh *et al.*, (2013) reported significant variations for days to flowering in black gram.

Stability parameters of individual genotypes

Identification of stable genotypes suitable to different environmental conditions is the ultimate goal for the estimation of the stability parameters of individual genotype. Many stability models have been developed to identify the stable genotypes. However, Eberhart and Russell (1966) model is the one which has been used in most of the crops. According to Eberhart and Russell (1966), a variety with high or low mean, unit regression co-efficient and low deviation mean square is considered as average stable genotype which will perform consistently over environments. Stability of different genotypes for various yield and yield components characters in rice bean is discussed below:

Days to 50% flowering

Earliness to flower in any crop is the desirable character for early harvest. For days to 50% flowering, it is recorded that out of thirteen genotypes seven genotypes took more days for flowering as compared to the average mean (94.7%). Genotype RbnG3 recorded the maximum days for 50% flowering while genotype RbnG8 took the minimum days to flowering and which was earliest to flower. The genotypes RbnG1, RbnG3, RbnG4, RbnG10, RbnG11 and RbnG12 were found to be stable and adapted to all the six environments. While genotypes RbnG2 is above average in response and suitable for favourable environment. The genotypes have higher mean than that of average mean hence this genotype can be selected basing on the environment for early planting. Among the Genotypes RbnG7, Rbng13 were found to be adapted to unfavourable environment. However, genotype RbnG5 and RbnG6 recorded lower mean than average mean but stable since,

regression coefficient near/equal to one, deviation from regression was non-significant and may be utilized for breeding programme for stable genotype.

Number of primary branches

Genotypes RbnG1, RbnG12, RbnG13 had higher number of primary branches per plant, regression coefficient of unity and deviation from regression-near to unity, which shows average stability and well adapted to all the environments. Genotypes RbnG4, RbnG8 and RbnG10 are considered to be stable and specially adapted to favourable environments. Genotypes RbnG6 and RbnG11are considered stable for unfavourable environments. Genotypes RbnG7 can be considered below average stability as it has recorded lower mean comparing to average mean but regression coefficient near to one, deviation from regression was non-significant and can be consider stable genotype.

Number of pod per clusters

Number of clusters per pod indicated that genotypes RbnG13 with high mean, regression coefficient equivalent/close to one, and non-significant deviation from regression shows stable and well adapted to all environments. Genotypes RbnG1, RbnG5, RbnG8, Rbng10 are considered stable for favourable environment. Genotype RbnG3 and RbnG4 are stable for unfavourable environments. Genotypes RbnG7 can be considered below average stability as it has recorded lower mean comparing to average mean but regression coefficient equivalent to one, deviation from regression was non-significant and can be consider stable genotype.

Number of pods per plant

Genotypes RbnG1, RbnG5 and RbnG8 are recorded to be well adapted to all environments. Genotypes RbnG3, RbnG4 and RbnG10 are adapted to favourable condition. Genotypes RbnG7 and RbnG13 are considered below

average stability and adapted specially for unfavourable environment. These results are in agreement with De Rocha *et al*. (2007) and El-Shaieny *et al*. (2015) on cowpea.

Genotypes RbnG9 and RbnG12 can be considered below average stability as it has recorded lower mean comparing to average mean but regression coefficient equivalent/near to one and non-significant deviation from regression and can be consider stable genotype .

Pod length

For pod length genotype RbnG10 and RbnG12 show average stability and well adapted to all environments. Genotype RbnG2, RbnG5 and RbnG9 are recorded for specially adapted for favourable environments. RbnG3 shows high mean and regression coefficient less to one, deviation from regression to zero and specially adapted to unfavourable environment. Similar results were reported by Akande and Balogun (2009). RbnG8 shows low mean comparing to average mean but regression coefficient equivalent to one and non-significant deviation from regression and can be consider stable genotype .

Number of seeds per pod

Genotypes RbnG3 shows stability and well adapted to all environments. Genotypes Rbng1, RbnG4, RbnG5, RbnG6 and RbnG13 shows below average stability and adapted to favourable environments. Genotypes RbnG7 and RbnG10 shows below average stability and adapted to unfavourable environments. These results are in agreement with those obtained from Singh *et al*. (2007), Dahiya *et al*. (2007). Senthilkumar and Chinna (2012) identified three stable genotypes for number of seeds per pod. Nath and Dasgupta (2013) reported seven average stability genotypes in greengram. RbnG9 shows low mean comparing to average mean but regression coefficient nearer to one and non-significant deviation from regression and can be consider stable genotype.

Plant height

Genotypes RbnG1, RbnG5, RbnG8, RbnG13 shows average stability and well adapted to all environments. Genotypes RbnG4, RbnG6 and RbnG10 stability and specially adapted to favourable environments. Genotypes RbnG3, RbnG7, RbnG12 shows below average stability and adapted to unfavourable environment. RbnG9 and RbnG11 shows low mean comparing to average mean but regression coefficient equal to one and non-significant deviation from regression and can be consider stable genotype.

Days to 80% maturity

Genotypes RbnG3, RbnG10, RbnG11, RbnG13 was observed to be more stable compare to other genotypes and could performed better in wide range of environments. Genotypes RbnG1, RbnG4, RbnG9, RbnG12 could be preferred for favourable condition. Genotypes RbnG7 and RbnG8 recorded below average stability and adapted to unfavourable environment. However, genotype RbnG6 recorded lower mean than average mean but stable since, regression coefficient is near to one and deviation from regression was non-significant and may be utilized for breeding programme for stable genotype.

100 seed weight

Genotypes RbnG2 is found to be stable and well adapted to all the environments with high mean than the average mean. Genotypes RbnG5, RbnG6, RbnG9, RbnG11 and RbnG12 are adaptable to favourable environment. Similar results were reported by Akande and Balogun (2009). No genotype shows below average stability and specially adapted to unfavourable environments

Crude protein (%)

Average protein content of genotypes ranges from 12.23% to 21.24% with an average general mean of 15.96 percent. Rodriguez, *et al*. (1991) reported that seeds of rice bean ranged from 17.26% to 21.42% protein content. Genotype RbnG3 recorded highest protein percent followed by RbnG1 and RbnG8 while genotype RbnG4 recorded the lowest protein content followed by RbnG11. It was observed that none of the genotype was found stable. However, Genotypes RbnG2, RbnG3, RbnG6 and RbnG8 are observed to be adaptable to favourable environment condition. Genotype RbnG1 which shows below average stability and specially adapted to unfavourable environments. From the result it is found that no genotypes have found to be stable across the six environments. Senthilkumar and Chinna (2012) reported that no single variety was stable for the traits.

Seed yield per plant

Plant breeders generally select genotypes which are stable that perform well in terms of yield above average in all the environments. Hence, commercially desirable genotypes should be stable for grain yield with high mean value. For seed yield per plant genotype Rbng2, RbnG3, RbG6 and RbnG7 exhibit high seed yield per plant, shows stability and well adapted to all environments. Genotype RbnG5 can be considered to be adapted for favourable condition. Genotypes RbnG8, RbnG9 and RbnG12 recorded with high mean yield and adapted to unfavourable environments. Similar results were reported by Dahiya *et al*. (2007) and Singh *et al*. (2007). RbnG1 and RbnG13 shows low mean comparing to average mean but regression coefficient is equal/near to one and non-significant deviation from regression and can be consider stable genotype.

Seed yield is a complex character and the analysis of individual yield component can lead to streamlining of stability for seed yield. Analysis of

these characters revealed that genotype RbnG1, RbnG3 and RbnG13 was associated with yield contributing characters for 50% flowering, primary branches, number of pods per plant, number of seeds per pods and plant height with high mean and stable genotype.

From the result it is also exhibited that genotypes RbnG1 was stable for days to 50% flowering, primary branches, number of pods per plant, plant height and seed yield. RbnG3 shows stability in days to 50% flowering, number of seeds per pods and seed yield. RbnG5 recorded stable for number of pods per plant and plant height. RbnG7 for pod per cluster.RbnG8 for number of pods per plant. The genotype RbnG9 and RbnG10 for plant height and days to 80% maturity. The genotype RbnG11 for primary branches and days to 80% maturity. RbnG13 has found stable for primary branches, plant height and 80% maturity. This stability in genotypes will provide opportunities for breeders for further crop improvement and other related research in the future.

The overall stability of characters revealed that 50% flowering, primary branches, pods per cluster, number of pods per plant, pod length, number of seeds per pod, plant height, 80% maturity were most stable characters as these remain stable in most of the genotypes. It indicates the characters can be given due importance for hybridization while selecting parents.

AMMI analysis of variance

The additive main effects and multiplicative interaction (AMMI) analysis is widely used for genotype x environment interaction among the multivariate method. AMMI method is effective as it express a large portion of genotype x environment interaction sum of squares. AMMI analysis separates main and interaction effects and provides relevant interpretation of data to assist a breeding program for genotype stability (Gauch and Zobel, 1996 and 1997). The AMMI model applies Principal Component Analysis (PCA) for interaction and gives graphical representation (biplot) to summarize

information for genotypes and environments simultaneously and allows evaluation of interaction effect of genotype in each environment. Using AMMI ANOVA the yield and its attributes sum of squares was partitioned into genotype, environment and Genotype x Environment interaction. Using principal component analysis the genotype x environment interaction was further partitioned.

The result of combined analysis of variance revealed that the performance of thirteen ricebean genotypes is subject to strong influence of genotype, environment, and genotype x environment interaction. Similar findings were reported by Ntawuruhunga and Dixon (2010) and Yadav *et al*. (2016). Significant genotypic variations were observed for growth parameters such as primary branches, pods per cluster, number of pods per plant, number of seeds per pod, protein content, 100 seed weight and seed yield, indicating opportunity for selection. The large mean sum of square for genotypes indicates that the genotypes were diverse, similar findings was reported by Fentie *et al. (*2013) and Akter *et al*. (2014). A large environment variation was observed in days to 50% flowering, plant height and days to 80% maturity. A major part of variation in these characters can be subjected to environmental changes. Similar variations in response to crops to different environments have been reported by Joseph *et al.* (2017), Rakshit *et al*. (2012), and Temesgen *et al*. (2015). Generally, the contribution of genotype x environment interaction to genotypic is small. About 80% or more of the variation is explained by environment (E) and genotype (G) effects which was reported by Yan and Kang. (2003), the presence of G x E interaction was clearly demonstrated by AMMI model in which all the characters were observed to be significant.

AMMI analysis for Yield and yield traits

Significant differences were observed for the genotype, environments and genotype X environment interaction for days to 50% flowering. The explained percentage attributed by mean sum of square are environment 75.15% followed by genotype 12.80% and G X E interaction 12.03%. The maximum environmental mean square indicates a large difference between the environments tested causing different genotypes to perform differently across the trial environments. AMMI analysis variance also revealed that the G X E interaction was less than that of the genotypes, so predominant difference was due to genotypic effect. For primary branches the mean squares attributed by genotype effects was highest 12.70% followed by G X E with 8.23% and environment 5.24%, The major variation was due to genotypic effects. This implies that the interaction of thirteen genotypes of ricebean with six environments which was predicted by first two components of PCA1 and PCA 2. The results are in conformity with Rashidi *et al*. (2013), Dilip and Ramgiry (2015).

For pods per cluster the mean squares attributed by genotype effects was highest 54.71% followed by G X E with 24.18% and environment 21.58%. The major variation was due to genotypic effects. The first two IPCA cumulatively captured 74.4% of the total G x E interaction. The results are in agreement with Thangavel *et al*. (2011).

For number of pods per plant the mean squares attributed by genotype effects were highest 37.95% followed by G X E with 36.09% and environment 25.94%. The major variation was due to genotypic effects. These results are in agreement with Gambhire *et al*. (2018) and Thangavel *et al*. (2011).

For pod length the mean squares attributed by genotype effects were highest 73.26% followed by G X E with 19.93% and environment 6.68%. The major variation was due to genotypic effects. This implies that the interaction

of thirteen genotypes of ricebean with six environments was predicted by the first two components of PCA1 and PCA 2.

For number of seeds per pod the mean squares attributed by genotype effects were highest 76.80% followed by G X E with 16.32% and environment 6.92%. It was observed that the G X E interaction was less than that of the genotypes, so predominant difference was due to genotypic effect. The result is in agreement with Jogendra *et a*l. (2018).

For plant height the mean square attributed by environmental effects was highest 71.60% followed by G X E with 17.47% and genotype with 10.91%. The environments were diverse and show major variation in plant height. The G X E is more than that of genotypes, which determined substantial differences in genotype response across the six environments for this character. The results are in agreement with Dilip and Ramgiry (2015) and Thangavel *et al*. (2011).

For days to 80% maturity the mean square exhibited by environmental effects was highest 79.89% followed by G X E with 11.46% and genotype with 8.63%. The G X E is more than that of genotypes, which determines substantial differences in genotype response across the six environments for this character. The large mean squares for environment indicate diverse environments with large differences among environmental means resulting in variation for days to 80% maturity for the genotypes tested.

For protein content the mean squares attributed by genotype effects were highest 71.79% followed by G X E with 27.90% and environment 0.29%. Bueno *et al*., (2013) indicated that genotypic variance is one of the most important parameters for quantifying the breeding potential and existence of

genotypic variance indicates the possible use of selective techniques in genotypes.

For 100 seed weight the mean square attributed by genotype effects was highest 91.94% followed by G X E with 5.24% and environment 2.81%. The major variation was due to genotypes. The explained percentage of mean square of seed yield for genotype is highest with 35.77% followed by G X E with 34.40% and environment 29.82%. Major variation in seed yield was due to genotypes. A larger mean sum of square for genotypic effect indicates that the genotypes were diverse with major differences among the genotypic means. The less percentage of mean sum of square for environment shows that the difference among the environmental means was not very high. The findings are in agreement with Jogendra *et al*. (2018).

Many researchers witnessed that the best accurate AMMI model prediction can be made using the first two IPCA, Yan (2000). The mean squares for IPCA 1 and IPCA 2 for all the characters under studied cumulatively contributed to more that 70% of the total Genotype x Environment interaction which implies that the interaction of thirteen ricebean genotypes for six environments were predictable by first two components of genotypes and environments which are in agreement of Gauch and Zobel. (1996).The findings are in confirmatory to that of Padmavati (2013), Bharat *et al* (2018), Yadav *et al* (2016) and Daria *et al* (2017).

AMMI biplot interaction for yield and yield attributes

In AMMI model the interaction principal component 1 (IPCA1) scores and the interaction principal component 2 (IPCA 2) are indicators of stability. Genotypes with a large IPCA scores are more responsive for the interaction

and specifically adapted to a specify environments while genotypes with small IPAC scores has low interaction and consider as widely adapted genotypes. From the result it was exhibited that the contribution of IPCA1 to the GE interaction was greater than that of IPCA2 for all the traits. A similar result was reported in barley by Monica *et al.* (2008).

Purchase (1997) showed that AMMI-2 biplot indicated the genotypes score close to the origin of the biplot are more stable. For better understanding of the biplot, the genotypes with end point vector far from the origin more responsive to the interaction than those with end point vector close to the origin. AMMI 2 biplot graphically represent the interaction effect. Marjanovic-Jeromela *et al*. (2011) stated that the differences of genotype distributions in the biplot are consequence of genotype variations in different environments.

Days to 50% flowering

The analysis revealed that IPCA 1 explained 39.9% of the interaction while the IPCA 2 explained 32.8% of the interaction degree of freedom for days to 50% flowering. The first two IPCA cumulatively captured 72.7% of the total G x E interaction.

It was recorded that (Table 15) the genotypes and environment interaction genotypes with high mean and positive IPCAI, RbnG3, RbnG5, RbnG6, RbnG7, RbnG10 and RbnG13 and environment Env 4 (1st June, 2017), Env 5(15th June, 2017) and Env6 (1st July, 2017) recorded positive IPCA1. Hence, this genotype can be recommended for this environment.

Based on (Fig.2), It was observed that Env1 (1st June 2016), Env 5(15th June, 2017) and Env6 (1st July, 2017) had short arrows and it did not excert strong interactive force while Env 2(15th July, 2016), Env3 (1st Aug, 2016) and Env 4 (1st June, 2017) having long arrows showing strong interaction in respect

to days to 50% flowering. Genotypes near the origin were RbnG4, RbnG6, RbnG10 and RbnG13 and identified as most stable. The genotypes in Env1 are RbnG11 and RbnG10. Genotypes RbnG1, RbnG13 and RbnG12 is best suited for early flowering in Env2 (15th july-post Kharif). The genotypes RbnG4, RbnG5 and RbnG9 is best suited to early flowering in Env5 (15th June-Kharif) and Env6 (1st July-Kharif).Similarly genotype RbnG7 and RbnG8 is suited for early flowering Env3 (1st Aug-post Kharif) and genotypes RbnG3, RbnG2 and RbnG6 is best adapted to Env4 (1st June-Kharif).

Primary branches

The IPCA 1 explained 83.6% of the interaction while IPCA 2 explained 8.6%. The first two IPCA cumulatively captured 92.2% of the total G x E interaction (Fig. 3). Considering the genotypes and environment interaction genotypes with high mean and positive IPCAI, RbnG1, RbnG3, RbnG4, RbnG6, RbnG7, RbnG10, RbnG11 and RbnG13 and environment Env 1(1st June-Kharif), Env 2(15th July-post Kharif) and Env5 (15th June-Kharif) recorded positive IPCA1. Hence, this genotype can be recommended for this environment.

Based on (Fig 3), Env 1(1st June-Kharif), Env 2(15th July-post Kharif), Env3 (1st Aug-post Kharif), 5 (15th June-Kharif) recorded short arrows showing less interaction Genotypes RbnG1, RbnG3, RbnG4, Rbng12 and RbnG13 are near the origin and have lower interaction and also consider more stable than other genotypes. The genotypes RbnG2, RbnG6, RbnG8 and RbnG9 are more responsive to environment. The best genotypes in Env1 are RbnG5, RbnG12. Genotypes RbnG2, and RbnG11 is best suited for Env3 (1st Aug-post Kharif). The genotypes RbnG1, RbnG7, Rbng8 and Rbng10 is best adapted to Env 5 (15th June-Kharif) and Rbng13 for Env6 (1st July-Kharif).Similarly genotype RbnG2 is suited for Env 2(15th July-post Kharif) and genotypes RbnG9 is best adapted to Env4 (1st June-Kharif).

Pods per clusters

Considering the genotypes and environment interaction genotypes with high mean and positive IPCAI (Table 15), RbnG3, RbnG4, RbnG6, RbnG10 and RbnG13 and environment Env 1(1st June-Kharif), Env 3(1st June-Kharif), Env 2(15th July-post Kharif), Env4 (1st June-Kharif) and Env6 (1st July-Kharif) recorded positive IPCA1. Hence, this genotype can be recommended for this environment.

The IPCA 1 explained 54.8% of the interaction while IPCA 2 explained 19.6%. The first two IPCA cumulatively captured 74.4% of the total G x E interaction (Fig 4). It was observed that Env 2(15th July-post Kharif), Env3 (1st Aug-post Kharif) and Env6 (1st July-Kharif) had short arrows and it did not excert strong interactive force while Env 1(1st June-Kharif), Env4 (1st June-Kharif) and Env 5(15th June-Kharif) having long arrows showing strong interaction. Genotypes near the origin were RbnG3, RbnG4, RbnG6, rbnG7 and RbnG13 and have lower interaction and considered as widely adapted genotypes. The genotypes RbnG2, RbnG3, RbnG4 and RbnG6 is best adapted to Env 2(15th July-post Kharif), and Env3 (1st Aug-post Kharif).Similarly genotype RbnG5 and RbnG12 is suited for Env 5 (15th June-Kharif) and genotypes RbnG1, RbnG7, RbnG8 and RbnG9 is best adapted to Env4 (1st June-Kharif). For Env 1(1st June-Kharif) and Env6 (1st July-Kharif) best suited is RbnG11.

Number of Pods per plant

Considering the genotypes and environment interaction genotypes with high mean and positive IPCAI, RbnG1, RbnG3, RbnG7, RbnG10 and RbnG13 and environment Env 1(1st June-Kharif), Env4 (1st June-Kharif) and Env6 (1st July-Kharif) recorded positive IPCA1. Hence, this genotype can be recommended for this environment.

The IPCA 1 explained 36.2% of the interaction while IPCA 2 explained 31.1%. The first two IPCA cumulatively captured 67.3% of the total G x E interaction .It was observed that Env 2(15th July-post Kharif) and Env3 (1st Aug-post Kharif) had short arrows and it did not excert strong interactive force, while Env 1(1st June-Kharif), Env4 (1st June-Kharif), Env 5 (15th June-Kharif) and Env6 (1st July-Kharif) having long arrows showing strong interaction. RbnG3, RbnG9, RbnG11, RbnG13 and RbnG13 are non sensitive to environment and have lower interaction and considered as widely adapted genotypes. The best genotype in Env 1(1st June-Kharif) recorded are RbnG3, RbnG4, RbnG6 and RbnG7. Genotypes RbnG1, RbnG8 are best suited for Env 2(15th July-post Kharif) and Env4 (1st June-Kharif). The genotypes RbnG10, RbnG11, RbnG13 are best adapted to Env 5 (15th June-Kharif).Similarly genotype RbnG2, RbnG5 and RbnG9 are suited for Env3 (1st Aug-post Kharif) and Env6 (1st July-Kharif) indicating higher number of pods per plant in their respective environment.

Pod length (cm)

Considering the genotypes and environment interaction genotypes with high mean and positive IPCAI, RbnG2, RbnG5, RbnG6, and RbnG12 and environment Env 1(1st June-Kharif), Env4 (1st June-Kharif) and Env6 (1st July-Kharif) recorded positive IPCA1. Hence, this genotype can be recommended for this environment.

The IPCA 1 explained 46.5% of the interaction while IPCA 2 explained 29.7%.The first two IPCA cumulatively captured 76.4% of the total G x E interaction. It was observed that Env 2(15th July-post Kharif), Env 1(1st June-Kharif), Env3 (1st Aug-post Kharif) and Env4 (1st June-Kharif) had short arrows indicating less interaction and the genotypes that fall under the same environments will perform more or less similar to each other. Env 5 (15th June-Kharif) and Env6 (1st July-Kharif) exhibit longer arrows indicating more

interaction forces. Genotypes near the origin were RbnG3, RbnG4, and RbnG10 which are less sensitive to environment and would perform well across the environments. The genotypes Rbng1, RbnG5, RbnG9, RbnG11, and RbnG13 are more responsive to environment hence will adapt to specific environment. The best genotype in Env 1(1st June-Kharif) recorded are RbnG7, RbnG8 and RbnG12. Genotypes RbnG11, RbnG10 are best suited for Env 2(15th July-post Kharif), Env3 (1st Aug-post Kharif) and Env4 (1st June-Kharif). The genotypes RbnG1, RbnG2, RbnG4 and RbnG13 are best adapted to Env 5 (15th June-Kharif).Similarly genotype RbnG5, RbnG6 and RbnG9 are suited for Env6 (1st July-Kharif) indicating higher number of pos per plant

Number of seeds per pod

Considering the genotypes and environment interaction genotypes with high mean and positive IPCA1, RbnG1, RbnG3, RbnG4, Rbng5, RbnG8 and RbnG10 and all six environments recorded positive IPCA1. Hence, this genotype can be recommended across the environment.

The IPCA 1 explained 37.1% of the interaction while IPCA 2 explained 30.8%.The first two IPCA cumulatively captured 67.9% of the total G x E interaction. It was observed that Env6 (1st July-Kharif) and Env4 (1st June-Kharif) had short arrows indicating less interaction comparing to Env 1(1st June-Kharif), Env 2(15th July-post Kharif), Env3 (1st Aug-post Kharif) and Env 5 (15th June-Kharif) which exhibits longer vector and contribute more interaction. Genotypes near the origin were RbnG3, RbnG8, and RbnG15 and are non sensitive to environment and have lower interaction, hence considered as widely adapted genotypes. The genotypes Rbng6, RbnG7, RbnG10, RbnG11, RbnG12 and RbnG13 are more responsive to environment. The best genotypes in Env 1(1st June-Kharif), recorded are RbnG6, RbnG4 and RbnG10. Genotypes RbnG9, and RbnG11 are best suited for Env 2(15th July-post Kharif). RbnG7 and RbnG8 are best genotypes for Env3 (1st Aug-post

Kharif). The genotypes best suited for Env4 (1st June-Kharif) are Rbng3 and RbnG13. The genotypes RbnG1, RbnG2, RbnG12 are best adapted to Env 5 (15th June-Kharif).Similarly genotype RbnG5 is suited for Env6 (1st July-Kharif) indicating higher number of seeds per pod in their respective environment.

Plant height (cm)

Considering the genotypes and environment interaction genotypes with high mean and positive IPCAI, RbnG2, RbnG4, and RbnG10 and environment Env 1(1st June-Kharif), Env2 (15th July-post Kharif), Env 5 (15th June-Kharif) and Env6 (1st July-Kharif) recorded positive IPCA1. Hence, this genotype can be recommended for this environment.

The IPCA 1 explained 53.8% of the interaction while IPCA 2 explained 26.1%. The first two IPCA cumulatively captured 79.9% of the total G x E interaction. It was observed that Env 1(1st June-Kharif), Env3 (1st Aug-post Kharif) and Env6 (1st July-Kharif) had short arrows indicating less interaction. Env 2(15th July-post Kharif), Env4 (1st June-Kharif) and Env 5 (15th June-Kharif) which exhibits longer vector and contribute more interaction. It is revealed that almost all the genotypes are near the origin which are non sensitive to environment and have lower interaction and considered as widely adapted genotypes. The genotypes that occur close together on the plot will show similar maturity for all the environments. Genotypes RbnG6, RbnG8, RbnG10 and Rbng13 are more responsive to environment. The best genotypes in Env3 (1st Aug-post Kharif) recorded are RbnG6 and RbnG8. Genotypes RbnG7 is best suited for Env 2(15th July-post Kharif). It is revealed that all the remaining genotypes are best suited for Env 1(1st June-Kharif), Env4 (1st June-Kharif), Env 5 (15th June-Kharif) and Env6 (1st July-Kharif).

80% maturity

Considering the genotypes and environment interaction genotypes with high mean and positive IPCAI, RbnG5, RbnG6, RbnG7 and RbnG8 and environment Env 1(1st June-Kharif), Env4 (1st June-Kharif), Env 5 (15th June-Kharif) and Env6 (1st July-Kharif) recorded positive IPCA1.Hence, this genotype can be recommended for this environment.

For days to 80% maturity the IPCA 1 explained 63.6% of the interaction while IPCA 2 explained 18.1%. The first two IPCA cumulatively captured 81.7% of the total G x E interaction. It is revealed that almost all the genotypes are near the origin which are non sensitive to environment and have lower interaction and considered as widely adapted genotypes. The genotypes that are close together on the plot will show similar maturity for all the environments. It is revealed that the genotypes RbnG6, RbnG8, RbnG10 and Rbng13 expressed the highest interaction indicating their narrow adaptability to certain environments and high sensitivity to environmental interactive forces while the genotypes RbnG3, RbnG6 and RbnG11 were the closest to the centre of the biplot expressing the lowest interaction with environments and indicating their stability or broad adaptability. The best genotypes in Env3 (1st Aug-post Kharif) are RbnG6 and RbnG8 exhibiting longer spokes with high interaction. Genotypes RbnG7 is best suited for Env 2(15th July-post Kharif) with high contribution to interaction forces. It is revealed that most of the genotypes are grouped together exhibiting similar adaptation on the other hand four environment were grouped together have similar environment interaction with the genotypes and Env 1(1st June-Kharif), Env4 (1st June-Kharif), Env 5 (15th June-Kharif) and Env6 (1st July-Kharif) with shorter spokes and less interaction are best suited for RbnG1, RbnG2, RbnG4, RbnG5, RbnG9 and RbnG10.This findings is in Conformity by Kempton (1984)

Protein content (%)

Considering the genotypes and environment interaction genotypes with high mean and positive IPCAI, RbnG1, RbnG2, RbnG10, RbnG11 and RbnG12 and environment Env 1(1st June-Kharif), Env2 (15th July-post Kharif), Env 5 (15th June-Kharif) and Env6 (1st July-Kharif) recorded positive IPCA1.Hence, this genotype can be recommended for this environment.

For protein content the IPCA 1 explained 83.6% of the interaction while IPCA 2 explained 8.6%.The first two IPCA cumulatively captured 92.2% of the total G x E interaction. It was observed that all the environments under studied exhibits longer vector and contributes more interaction. Genotypes RbnG1, RbnG10, RbnG911 and RbnG12 are close to origin expressing the lowest interaction with environments and indicating their stability or broad adaptability. The genotypes Rbng2, RbnG4, RbnG6, RbnG8, RbnG9 and RbnG13 are more responsive to environment indicating their narrow adaptability to certain environments and high sensitivity to environmental interactive forces. Similar findings are reported by Pratap *et al*. (2009) in their stability studies using AMMI model in green gram and observed that four genotypes out of 12 were stable for protein content. Babu *et al*. (2009) reported and identified three genotypes as stable for protein content using AMMI model in black gram.

100 seed weight (g)

Considering the genotypes and environment interaction genotypes with high mean and positive IPCAI, RbnG3, RbnG5, RbnG9, RbnG11 and RbnG12 and environment Env3 (1st Aug-post Kharif), Env4 (1st June-Kharif), Env 5 (15th June-Kharif) and Env6 (1st July-Kharif) recorded positive IPCA1.Hence, this genotype can be recommended for this environment.

For 100 seed weight the IPCA 1 explained 70% of the interaction while IPCA 2 explained 14.3 %. The first two IPCA cumulatively captured 84.3% of the total G x E interaction. Genotypes RbnG1, RbnG3, RbnG4, RbnG5 and Rbng10 are close to origin expressing the lowest interaction with environments and indicating their stability or broad adaptability. Genotypes Rbng2, RbnG7, RbnG9 and RbnG11 are more responsive to environment. It was observed that Env 2(15th July-post Kharif), Env4 (1st June-Kharif) and Env6 (1st July-Kharif) had short arrows indicating less interaction. Env 1(1st June-Kharif), Env3 (1st Aug-post Kharif) and Env 5 (15th June-Kharif) which exhibits longer vector and contributes more interaction. The best genotypes in Env 1(1st June-Kharif) recorded are RbnG6, RbnG9 and RbnG12. Genotypes RbnG1, RbnG2, RbnG8 and RbnG10 are best suited for Env 2(15th July-post Kharif) and Env6 (1st July-Kharif). Similarly genotypes RbnG3 and RbnG3 are suited for Env3 (1st Aug-post Kharif) and Env4 (1st June-Kharif) whereas the best genotypes suited for Env 5 (15th June-Kharif) are RbnG4, RbnG5 and RbnG7.

Seed yield per plant (g)

Considering the genotypes and environment interaction genotypes with high mean and positive IPCAI, RbnG2, RbnG3, RbnG6, RbnG7, RbnG12 and RbnG13 and environment that Env 1(1st June-Kharif), Env4 (1st June-Kharif) and Env6 (1st July-Kharif) recorded positive IPCA1. Hence, this genotype can be recommended for this environment.

For seed yield per plant the IPCA 1 explained 50.1% of the interaction while IPCA 2 explained 23.6%. The first two IPCA cumulatively captured 73.7% of the total G x E interaction. It showed that the genotypes Rbng1, RbnG5 and RbnG11 expressed the highest interaction for seed yield per plant indicating their narrow adaptability to specific/certain environments and high responsive to environmental interactive forces while the genotypes RbnG3, RbnG4, RbnG6, RbnG10 and RbnG13 were the closest to the centre of origin

expressing the lowest interaction with environments and indicating wider adaptability and stability. The best genotypes in Env 1(1st June-Kharif) and Env3 (1st Aug-post Kharif) recorded are RbnG6 and this two environments exhibited shorter pokes indicating less interaction forces. Genotypes RbnG9, RbnG7are best suited for Env 2(15th July-post Kharif) with high interaction forces. Similarly genotypes RbnG8, RbnG11 and RbnG12 are suited for Env4 (1st June-Kharif) with moderate spokes resulting in moderate interaction. Whereas the best genotypes suited for Env 5 (15th June-Kharif) are RbnG3, RbnG4, RbnG5 and RbnG10 with long spokes and contribute high interaction forces. For Env6 (1st July-Kharif) RbnG1 and RbnG2 genotypes are suitable with high contribution to interaction forces. Similar findings has been made by Babu *et al.,* (2009) using AMMI model and identified three stable genotypes for seed yield per plant in black gram. Pratap *et al.*, (2009) in green gram reported seven genotypes out of twelve were stable for seed yield per plant using AMMI model for stability.

Stability analysis by AMMI stability values

In order to quantify and rank the genotypes according to their yield stability AMMI stability values were calculated suggested by Zobel *et al*. (1998) and Purchase *et al. (*2000). In fact, ASV is the distance from zero in a two dimensional scatter gram of IPCA 1 scores against IPCA 2. In ASV method, a genotype with least ASV score will be more stable. The concept of stability using ASV could be useful for selection of yield and stability at the same time Dehghani *et al*, (2010). Ranking of genotypes based on the stability index (SI) with mean value and AMMI stability value together could be more fruitful than considering AMMI stability values alone Bajpai and Prabhakaran. (2000). Therefore the genotypes characters are considered with estimation of yield stability index. The concepts of interaction classifications strongly determinants whether the best genotype in one environment is also the best in

other environments which is required by breeders. The result thus shows the potential usefulness of AMMI model to identify the genotypes having wider adaptability or specific adaptability which can be used as a genetic resource for breeding. An attempt was made in the present investigation to select the stable genotype based on ASVs by considering eleven characters (Table.15). And results were discussed as follows.

From the result obtain it was observes that mean yield performance across the environments, genotypes RbnG3, RbnG7 and RbnG13 were found superior and stable for days to 50% flowering. For primary branches genotypes RbnG1, RbnG3 was found superior. It is observed that for pods per cluster genotypes RbnG10, RbnG4 and RbnG1 were found to be superior. For number of pods per plant genotype RbnG4, RbnG10 and RbnG1. For pod length genotypes, RbnG5, RbnG11and RbnG9 was found to be superior. For number of seeds per pod genotypes RbnG10, RbnG4 and RbnG1. For plant height genotypes RbnG10, RbnG5 and RbnG4. For days to maturity genotypes RbnG13, RbnG3 and RbnG1.For protein contents genotypes RbnG1, RbnG3 and RbnG2 was stable. For 100 seed weight genotypes RbnG9, RbnG2 and RbnG11 was found to be superior and for seed yield per plant genotypes RbnG5, RbnG2 and RbnG3. From the overall performance of mean yield across six environments it is observed that RbnG1 (96.88) contributed in six associated characters for yield, RbnG3 (100.50) contributed in 4 yield associated characters, RbnG10 (95.66) is associated in four yield characters and RbnG4 (94.05) contributed in three associated characters for yield. Based upon the 10 characters under studied and mean performance across the six environments genotypes RbnG1, RbnG3, RbnG4 and RbnG10 were found to be superior and stable.

AMMI stability value (ASV)

Purchase, (1997) stated that AMMI stability value (ASV) measures and rank genotypes according to their yield stability.

According to ASV ranking, genotypes RbnG6, RbnG4 and RbnG10 are the lowest and stable, whereas RbnG2, RbnG7 and RbnG9 were unstable for days to 50% flowering. For primary branches RbnG1, RbnG3 and RbnG13 are the stable genotypes whereas RbnG2, RbnG8 and RbnG9 were unstable. For pods per cluster RbnG7, RbnG6 and RbnG10 are more stable and genotypes RbnG2, RbnG8 and RbnG8 are unstable. For number of pods per plant RbnG11, RbnG3 and RbnG13 are lowest and stable and genotypes RbnG5, RbnG8 and RbnG11 are unstable. For pods length RbnG10, RbnG3 and RbnG4 are lowest and stable and genotypes RbnG5, RbnG9 and RbnG11 are unstable. For number of seeds per pod RbnG10, RbnG3 and RbnG4 are lowest and stable and genotypes RbnG5, RbnG9 and RbnG11 are unstable. For plant height RbnG8, RbnG9 and RbnG4 are lowest and stable and genotypes RbnG2, RbnG11 and RbnG6 are unstable. For days to 80% maturity RbnG6, RbnG3 and RbnG11 are lowest and stable and genotypes RbnG8, RbnG9 and RbnG13 are unstable. For protein content RbnG10, RbnG1 and RbnG11 are lowest and stable and genotypes RbnG4, RbnG8 and RbnG9 are unstable. For 100 seed weight RbnG3, RbnG4 and RbnG12 are lowest and stable and genotypes RbnG2, RbnG7and RbnG8 are unstable. For seed yield per plant RbnG13, RbnG6 and RbnG8 are lowest and stable and genotypes RbnG5, RbnG11and RbnG10 are unstable. The lower ASVs and near zero IPCA scores are associated with great stability of genotypes. According to these criteria, RbnG1, RbnG3, RbnG4, RbnG8, RbnG10 and RbnG13 are the most stable genotypes as they had the lowest ASVs and near zero IPCA scores. These genotypes could potentially be used to breed for stability in breeding programmes.

Yield stability index (YSI)

The parameters for selection of genotypes is not only stability, because the most stable genotypes might not necessarily give the best yield performance, incorporation of both mean yield and stability in a single criterion measures to identify genotypes for different environmental conditions. The lower YSI with high mean is regarded as the most stable genotype. This method has been successfully used in other crops, such as wheat, Farshadfar, (2008), which stated that this criterion agreed with the biplot analysis

On the basis of Yield stability index, genotypes RbnG1, RbnG3 and RbnG7 were found to be stable when Stability index is measured for days to 50% flowering. Genotype RbnG1 and RbnG3 were observed to be stable for primary branches. For pods per cluster genotype RbnG10, RbnG4 and RbnG1 were also found to be stable when Stability index is measured. For number of pods per plant genotype RbnG4, RbnG10 and RbnG1 were also found to be stable when Stability index is measured. For pod length genotype RbnG5, RbnG11 were also found to be stable when Stability index is measured. For number of seeds per pod genotype RbnG10, RbnG4 and RbnG1 were also found to be stable when Stability index is measured. For plant height genotype RbnG10, RbnG5 and RbnG4 were also found to be stable when Stability index is measured. For days to 80% maturity genotype RbnG13, RbnG3 and RbnG1 were also found to be stable when Stability index is measured. For protein content genotype RbnG1, RbnG3 and RbnG2 were also found to be stable when Stability index is measured. For 100 seed weight genotype RbnG9, RbnG2 and RbnG11 were also found to be stable when Stability index is measured. For seed yield per plant genotype RbnG5, RbnG2 and RbnG3 were also found to be stable when Stability index is measured. As per the criteria obtained from YSI, it was observed that genotypes RbnG1 RbnG3, RbnG4,

RbnG5 and RbnG10 were found to be stable for overall performance of the genotypes across the six environments under studies. Similar studied was applied to identify high yielding stable genotypes in cereal crops like maize and durum wheat.

It was observed that the in some characters under studies the genotypes showed high mean yield and also had high IPCA scores as compared to the other genotypes, an indication that they were not stable (Table16a -16f). Pacheco *et al*. (2005) stated lower mean yields results in selection for better stability while selection for higher mean yields may results to poor stability. Abalo *et al.*, (2003) and Asio, (2004) similarly reported that yield stability could only be expected from low yielding genotypes which do not exploit favourable environment.

SUMMARY AND CONCLUSION

The present investigation entitled **"Studies on Genotypic x Environmental Interaction on Rice bean [(*Vigna umbellata* Thunb.) Ohwi and Ohashi] Landraces of Nagaland "** was carried out in School of Agricultural Sciences and Rural Development Nagaland University, Medziphema, Department of Genetics and Plant Breeding to assess the variability and stability of landraces genotypes of rice bean, with regard to yield and it's contributing characters in Rice bean and also to estimate the variability present in the material in six environments. Observations were recorded on days to 50% flowering, primary branches (nos), pods per cluster (nos), number of pods per plant (nos), plant height (cm), pod length (cm), number of seeds per pod, 100 seed weight (gm), crude protein and seed yield per plant (gm).

The important findings from the investigation are summarized below:

- Genotypes were highly variable among most of the traits studied. It is evident from environment- wise analysis of variance that sufficient genetic variability exists among genotypes for all the characters studied except for primary branches in Env3 (1st Aug-post Kharif sowing) was found to be non-significant . Hence desirable improvement can be brought through selection in these different characters.
- Significant analysis of variance among the genotype reveal that days to 50% flowering and days to 80% maturity reveal non-synchronized flowering and maturity.

- Mean performance reveal that RbnG8 and RbnG5 were the earliest to flower and maturity. The highest protein content was recorded in genotype RbnG3 (21.24%) while genotype RbnG4 (12.23%) recorded lowest protein content.

- The highest seed yield per plant was recorded in genotype RbnG5 (79.93g), RbnG2 (64.6g) and RbnG3 (51.73g) while genotype RbnG13 (35.29g) recorded lowest seed yield per plant.

- The estimation of phenotypic and genotypic coefficient of variation was high for primary branches, pods per cluster, number of pods per plant, pod length, plant height, protein content, and seed yield per plant, hence the selection based on phenotypic performance would be effective for improvement of these characters.

- PCV and GCV values were moderate for days to 50% flowering, days to 80% maturity and 100 seed weight. The estimates of PCV as well as GCV were lowest for number of seeds per pod

- The heritability estimates were found to be very high for days to 50% flowering, number of pods per plant, pod length, number of seeds per pods, plant height, days to 80% maturity, 100 seed weight and seed yield per plant. Pods per cluster exhibits moderate heritability and low heritability was recorded for primary branches.

- High heritability with high genetic advance mean were observed for days to 50% flowering, number of pods per plant, plant height, days to 80% maturity, 100 seed weight and seed yield per plant. This indicated that this character can be improved upon by direct selection since the character is

under control of additive gene effect. Primary branches and pods per cluster exhibits low heritability with low genetic advance mean percentage

- Correlation studies indicated that seed yield per plant were significant and positively associated with days to primary branches, pods per cluster, number of pods per plant, number of seeds per pod and plant height.

- Correlation studies indicated that yield contributing characters was significantly positively associated with pod per clusters, pod length, number of pods per plant, number of seeds per pod, plant height, days to 80% maturity, crude protein and 100 seed weight. This result indicated that the characters which are positively associated improvement of this trait will simultaneously improve the other traits

- The estimate for positive direct effect was recorded number of primary branches, pods per clusters, number of pods per plant, number of seeds per pod, plant height, days to 80% maturity, 100 seed weight and crude protein therefore these can be considered for direct selection for high seed yield.

- It can be suggested that, the indirect effects contributing to seed yield are primary branches, pods per clusters, number of pods per plant, pod length, number of seeds per pod, plant height, days to 80% maturity, crude protein and 100 seed weight were emerged as important characters for the improvement of seed yields.

- Analysis of variance showed that the variance due to genotypes were significant for all the characters which revealed the presence of considerable genotypic variability among the genotypes under studied. The genotypes x environment interaction were also all found to be significant for all the

characters which showed that genotypes react with the environments. Environment wise analyses of variance revealed that mean sum of square due to genotypes were highly significant for all the characters.

- Stability analysis indicates the presence of significant genotype x Environment (linear) interactions for all the characters study. High magnitude of Genotype x Environment (linear) due to environments differed considerably for all the characters and that these characters were greatly influence by environments, thereby indicates a linear function of environments with significant variance difference between environments along with genotypic response .

- The environment indices for all the traits under study revealed that none of the trait had positive indices in all the six environments. It is observed that from the result obtained Env 2(15th July-post Kharif) and Env3 (1st Aug-post Kharif) was the unfavourable environment for all the traits as most of the negative traits are observed in this environments. When we compare the different environments under studied, it clearly showed that Env1 (1st June-Kharif), Env4 (1st June-Kharif), 5(15th June-Kharif) and Env6 (1st July-Kharif) was most favourable sowing for most of the characters.

- From the result it is revealed that Env1 (1st June-Kharif), Env5 (15th June-Kharif) and Env6 (1st July-Kharif) sowing was best for days to 50% flowering. Env4 (1st June-Kharif) and Env6 (1st July-Kharif) for primary branches. For pods per cluster Env 2(15th July-post Kharif), Env4 (1st June-Kharif), Env5 (15th June-Kharif) and Env6 (1st July-Kharif) are favourable environments. Most favourable environments for number of pods per plant, pod length, number of seeds per pod, plant height, days to 80% maturity are Env1 (1st June-Kharif), Env4 (1st June-Kharif), Env5 (15th June-Kharif) and

Env6 (1st July-Kharif). For protein content none of the environments were favourable. For 100 seed weight the environments favourable are Env1 (1st June-Kharif) and Env6 (1st July-Kharif). For seed yield per plant environment Env1 (1st June-Kharif), Env4 (1st June-Kharif) and Env6 (1st July-Kharif) are most favourable.

- The overall stability of characters revealed that 50% flowering, primary branches, pods per cluster, number of pods per plant, pod length, number of seeds per pod, plant height, 80% maturity, 100 seed weight and seed yield per plant were most stable traits as these remained stable in most of the genotypes.

- From the result it is also exhibited that genotypes RbnG1 was stable for days to 50% flowering, primary branches, number of pods per plant, plant height and number of seed per pod. RbnG3 shows stability in days to 50% flowering, number of seeds per pods, days to 80% maturity and seed yield. RbnG5 recorded stable for number of pods per plant, number of seeds per pod and plant height. RbnG8 for number of pods per plant and plant height. The genotype RbnG10 days to 50% flowering, pod length and days to 80% maturity. The genotype RbnG11 for days to 50% flowering and days to 80% maturity. RbnG13 has found stable for primary branches, pods per cluster, number of seeds per pod, plant height, days to 80% maturity and seed yield per plant. This stability in genotypes will provide opportunities for breeders for further crop improvement and other related research in the future

- Genotypes RbnG1, RbnG3, RbnG10 and RbnG13 revealed stability in different character and stable over all environments and this stability in genotypes will provide opportunities for breeders for further crop improvement and other related research in the future. .

- Seed yield revealed that genotype RbnG1 and RbnG3 was associated with yield attributing characters for 50% flowering, primary branches, number of pods per plant, number of seeds per pods and plant height with high mean and stable genotype.

- Genotype RbnG3 recorded highest protein percent followed by RbnG1 and RbnG8 while genotype RbnG4 recorded the lowest protein content followed by RbnG11.

- From the result it is found that no genotypes for protein content have found to be stable across the six environments.

- In AMMI analysis the genotype, environment was significant for all the characters. The G X E interaction was also significant for all the characters. This indicated the presence of variability among the genotypes and the environments.

- Significant genotypic variations were observed for growth parameters such as primary branches, pods per cluster, number of pods per plant, number of seeds per pod, protein content, 100 seed weight and seed yield, indicating opportunity for selection. The large mean sum of square for genotypes indicated that the genotypes were diverse.

- A large environment variation was observed in days to 50% flowering, plant height and days to 80% maturity. A major part of variation in these characters can be subjected to environmental changes.

- Genotype X environment interaction was observed over the different environments as indicated by crossover performances for some of the genotypes which imply different adaptation by different genotypes

suggesting the need to identify and select environment specific genotypes for different environments.

- It was observed that IPCA 1 exhibited significant for all the characters. IPCA 2 was also observed to be significant for all the characters except 100 seed weight. The mean squares for IPCA 1 and IPCA 2 for all the characters under studied cumulatively contributed to more that 70% of the total Genotype x Environment interaction which implies that the interaction of thirteen ricebean genotypes for six environments were predictable by first two components of genotypes and environments.

- Based on AMMI biplot analysis, genotype RbnG3 was identified to be the most desirable and stable across different environments for pods per clusters, number of pods per plant, pod length, number of seeds per pod, plant height, days to 80% maturity, 100 seed weight and seed yield per plants.

- Genotypes RbnG10 was identified for stable across the environments for days to 50% flowering, primary branches, pod length, protein content, 100 seed weight and seed yield per plant. Similarly RbnG13 is found to be stable for days to 50% flowering, pods per cluster, number of pods per plant and seed yield per plant.

- RbnG4 was identified for stability on days to 50% flowering, pods per clusters, pod length, 100 seed weight and seed yield per plant. Rbng6 for days to 50% flowering, pods per clusters and days to 80% maturity and RbnG5 for number of seeds per pod, plant height and 100 seed weight.

- From the result observed from AMMI 2 biplot it was indicated that the differences and genotype distributions in the biplot are a consequence of genotype variations in different environments.

- When looking at the environment, it was observed that Env1 (1st June 2016), Env 5(15th June, 2017) and Env6 (1st July, 2017) were more favourable for days to 50% flowering. Env 1(1st June-Kharif), Env 2(15th July-post Kharif), Env3 (1st Aug-post Kharif), 5 (15th June-Kharif) are stable environments for primary branches. For pods per clusters it was recorded that that Env 2(15th July-post Kharif), Env3 (1st Aug-post Kharif) and Env6 (1st July-Kharif) stable environments. For number of pods per plant it was observed that Env 2(15th July-post Kharif) and Env3 (1st Aug-post Kharif) was most stable environments. For pod length it was observed that Env 2(15th July-post Kharif), Env 1(1st June-Kharif), Env3 (1st Aug-post Kharif) and Env4 (1st June-Kharif) was stable environment. For number of seeds per pods it was observed that Env6 (1st July-Kharif) and Env4 (1st June-Kharif) was most stable. For plant height it was observed that Env 1(1st June-Kharif), Env3 (1st Aug-post Kharif) and Env6 (1st July-Kharif) was most stable. For days to 80% maturity, Env 1(1st June-Kharif), Env4 (1st June-Kharif), Env 5 (15th June-Kharif) and Env6 (1st July-Kharif) were more stable. For 100 seed weight it was observed that Env 2(15th July-post Kharif), Env4 (1st June-Kharif) and Env6 (1st July-Kharif) were more stable. For seed yield per plant, Env 1(1st June-Kharif), Env4 (1st June-Kharif) and Env3 (1st Aug-post Kharif) are stable environment.

- From the AMMI biplot analysis it was revealed that Env2 (15th July-post Kharif) and Env6 (1st July-Kharif) were stable for protein content.

- Genotypes near the origin were RbnG1, RbnG7, RbnG10, RbnG11 and RbnG12 and are non sensitive to environment and have lower interaction and considered as widely adapted genotypes.

- From the result it can be revealed that that IPCA 1 scores across six environments for characters contributed to yield under studied were RbnG1, RbnG3, RbnG13, RbnG10, GbnG4 with least interaction and stable for wide adaptability. Genotypes RnbG2, RbnG4, Rbng5, RbnG7, Rbng8 and RbnG11 contributed largely to the interaction across the six environments and may be considered for specifically adapted genotypes.

- The lower ASVs and near zero IPCA scores are associated with great stability of genotypes. According to these criteria, RbnG1, RbnG3, RbnG4, RbnG8, RbnG10 and RbnG13 are the most stable genotypes as they had the lowest ASVs and near zero IPCA scores. These genotypes could potentially be used to breed for stability in breeding programmes.

- As per the criteria obtained from YSI, it was observed that genotypes RbnG1, RbnG3, RbnG4, RbnG5 and RbnG10 were found to be stable for overall performance of the genotypes across the six environments under studies.
- Based from ASV, Stability index and Mean values, the genotype RbnG3 and RbnG7 was found to be stable for days to 50% flowering. For primary branches genotypes RbnG1 and RbnG3 was stable. RbnG4, RbnG10 and RbnG1 were found to be stable for pods per clusters. For number of pods per plant genotypes RbnG4, RbnG10 and RbnG1 were found to be stable. The genotypes RbnG5, RbnG9, RbnG11 were reported to be stable for pod length. For number of seeds per pod genotypes RbnG10, RbnG4 and RbnG1 were found to be stables. For plant height genotypes RbnG10, RbnG5 and RbnG4 were found to be stable. For days to 80% maturity genotypes

RbnG13, RbnG3 and RbnG1 were found to be stable**.** For protein content genotypes RbnG1, RbnG3 and RbnG2 were found to be stable. The genotypes RbnG9, RbnG2 and RbnG11 were found to be stable for 100 seed weight. For seed yield genotypes RbnG5, RbnG2 and RbnG3 were found to be stable.

Conclusion

On the basis of above studies and results obtained it may be concluded that-

- Days to 50% flowering, primary branches, pods per cluster, number of pods per plant, pod length, seeds per pod, plant height, 100 seed weight, protein content and seed yield per plant are contributing phenotypic traits for yield and these can be use as an indices for breeding programme.

- The estimates of phenotypic and genotypic coefficient of variation were the highest for pods per plant, number of seeds per pod, plant height, protein content and 100 seed weight. It can be concluded that the character will provide scope for improvement through selection in these characters.

- Days to 50 % flowering, days to 80% maturity, plant height (cm), and length of pod (cm), number of seeds per pod (nos.), number of branches per plant (nos.), seed yield per plant (g), 100 seed weight (g), seed yield per plant (g) expressed high estimate of heritability in broad sense indicating the scope for direct selection of these traits

- Number of pods per plant, Pod length, plant height, protein content and seed yield per plant recorded highest GCV coupled with high heritability which will provide an opportunity for valuable selection in breeding programmes.

- High heritability coupled with high genetic advance mean was recorded for days to 50% flowering, number of pods per plant, plant height, days to 80% maturity, 100 seed weight and seed yield per plant. This indicated that, character can be improved upon by selection since the character is under control of additive gene effect.

- Correlation of seed yield in rice bean can be improved by making selection for pod length, number of seeds per pods, number of pods per plant, plant height, days to 80% maturity and 100 seed weight. seed yield can be improved by making direct selection through pod length, plant height, 80% maturity, pods per cluster, and pods per plant and 100-seed weight for improving seed yield

- The genotype x environment interaction gives a clear understanding that genotype and environment interaction across the environment plays a vital role for breeding adaptable genotypes for wider environment.

- Comparing Eberhart and Russel mode and AMMI model analysis environment showed more or less the same stability in all the characters studied. When both the models are compared, for days to 50% flowering Env1 (1st June, Kharif 2016), Env 5(15th June, Kharif, 2017) and Env6 (1st July, 2017) are more stable environments. For pods per cluster Env 2(15th July-post Kharif) is stable environment. For pod length Env1 (1st June 2016) and Env4 (1st June-Kharif) are more stable environments. For seeds per pod Env4 (1st June-Kharif) and Env6 (1st July-Kharif) are more stable. For plant

height Env1 (1st June, Kharif 2016) and Env6 (1st July-Kharif) are observed to be stable. For days to 80% maturity Env1 (1st June 2016), Env4 (1st June-Kharif), Env 5(15th June, 2017) and Env6 (1st July-Kharif) are more stable environment. For 100 seed weight Env6 (1st July-Kharif) is observed to be stable. For seed yield per plant Env1 (1st June 2016) and Env4 (1st June-Kharif, 2017) is more stable environments. The relationship of traits and environments may give a good idea to construct the suitable ideotype for ricebean improvement.

- In regression Model for protein content none of the genotype and environment was observed to be stable. AMMI studies revealed that genotypes RbnG1, RbnG10, RbnG11 and RbnG12 were the stable genotypes for protein content. The AMMI Stability Value (ASV) Ranking for Protein indicated that RbnG1 and RbnG10 was the most stable genotype and suitable for all the six environments. Genotype RbnG1, RbnG3 and RbnG2 were also found to be stable when Stability index is measured. These genotypes which were found to be stable would be useful for exploitation as elite gene pool materials in future breeding programmes or for commercial exploitation

- Stability of grain yield per plant is possible through manifestation of days to 50% flowering, primary branches, pods per cluster, pod length, plant height, days to 80% maturity, pods per cluster, and pods per plant and 100-seed weight. Selection of genotypes that combine high protein content and grain yield will provide opportunities to a breeder for selection of these genotypes as parents for breeding improvements.

- From the results of this investigation based on Eberhart and Russel model and AMMI biplot analysis it was revealed that the most stable genotypes across the six environments are genotypes RbnG1, RbnG3, RbnG4, RbnG10

and RbnG13 for AMMI analysis RbnG1, RbnG2, RbnG3, RbnG4, RbnG6, RbnG7, RbnG10 and RbnG13 are found to be stable and this stability in genotypes will provide opportunities for breeders for further crop improvement and other related research in the future.

Apart from the results summarized above, there are few more findings as cited below.

From the result it is found that flowering of most of the genotypes for the entire environment appear to flower when day length is shorter, which means the crop ricebean is photosensitive since all the genotypes inspite of different growing environments flowers at specific photoperiod. Most of the genotypes under study are observed to be late maturing. However it was observed that RbnG5 and RbnG8 was early in all six environments and found to be photo- insensitive. From the findings of this study it is also recommended for more experiment and more genotypes of ricebean should be screened for photo insensitivity as this will help in selecting the appropriate genotypes for particular environment or season.

For protein content it was revealed that the differences were inherent (Genotypic). The differences were however not consistent due to significant environmental influence on protein content of ricebean manifested through significant GxE interactions. There was variation in the ranking of the genotypes within individual locations for protein content which made it difficult to identify superior genotypes. However, AMMI analysis techniques help to get more information to assess the stability of the genotypes according to their favourable interaction. AMMI biplot reveal that genotype RbnG1, RbnG10, RbnG911 and RbnG12 are stable and widely adapted to all six environments. The IPCA value with high mean reveal RbnG1, RbnG2,

RbnG10, RbnG11 and RbnG12 could be considered as stable and environment Env 1(1st June-Kharif), Env2 (15th July-post Kharif), Env 5 (15th June-Kharif) and Env6 (1st July-Kharif). Based on ASV RbnG10 and RbnG1 are the most stable genotypes as they had the lowest ASVs and near zero IPCA scores. As per the criteria obtained from YSI, it was observed that genotypes RbnG1 and RbnG3 were found to be stable for overall performance of the genotypes across the six environments. Genotype x environment (G×E) interaction studies focused protein content are very scanty, even when it comes to important commercial pulse crop such as soybean, black gram, Mungbean. So far, studies using ricebean is not reported. Therefore, this study is the first report in this crop species. The results demonstrated the potential of genotype for protein content for utilization in future breeding program or commercial exploitation in ricebean.

The variation exhibited by genotype and environment interaction on various characters was significant which indicates their response to environment condition, hence sowing dates during the growing season do influence seed yield. The findings of this study clearly demonstrated that seed yield decline, this may be due to shattering of the seeds. Furthermore, selection solely for seed yield could result in rejection of several stable genotypes. Thus, planting in the cropping season and considering other environmental aspect was observed to be essential for efficient selection. These results can be put into investigation in future programme and study for further improvement of Rice bean.

The concepts of interaction classifications strongly determinants whether the best genotype in one environment is also the best in other environments which is required by breeders. The result thus shows the potential usefulness of

AMMI model to identify the genotypes having wider adaptability or specific adaptability which can be used as a genetic resource for breeding. AMMI stability value (ASV) and stability index (SI) are suitable stability indices for discriminating stable genotypes with high mean performances. Stability index which incorporate ASV and mean performances is most desirable for discriminating the most stable genotypes with high performance ASV that produce a balanced measurement between the two IPCA scores information.

The collection of rice bean genotypes and their genetic analysis are useful to provide valuable information to research community for further improvement. The stability analysis carried out in the investigation helps in better understanding of crop genotypes for adaptability over a wide range of environment tested and helps in identification of stable genotypes RbnG1, RbnG3, RbnG4, RbnG6, RbnG10 and RbnG13. Use of stable genotypes in the hybridization programme will lead to development of phenotypically high stable potential cultivars in rice bean. The identification of two photo-insensitive genotypes RbnG8 and Rbng5 will be useful for further testing their adaptation across the environment of the region and maybe valuable source for further development of photo-insensitive lines in rice bean. Of the thirteen genotypes tested, RbnG5 and RbnG7 could also be used in cultivation or in breeding for improved seed yield in their favourable environments Env4 (1st June-Kharif) and Env5 (15th June-Kharif). These results could be used for breeding programs, as well as testing for more effective selection.

REFERENCES

Abalo, G., Hakiza, J. J., El- Bedewy., R. and Adipala, E. 2003. Genotype x Environment interactions studies on yield of selected potato genotypes in Uganda. *African Crop Journal.* **11**: 9-15.

Ahmad, Z. and Rabbani, A. 1992. Genetic variability and correlation studies in ricebean. *Pakistan Journal Agricultural Research.* **13**(2): 21-125.

Akhtar, L. H., Kashif, M., Ali, M. and Aziz, T. 2010. Stability analysis for grain yield in mungbean (*Vigna radiata* L. Wilczek) grown in different agro-climatic regions. *Emirates Journal of Food Agriculture.* **22**(6): 490-497.

Akande, S. R., Balogun, M. O. 2009. Multilocational evaluation of cowpea grain yield and other reproductive characters in the forest and southern guinea Savanna agroecologies in Nigeria. *Electron Journal Environmental, Agricultural and Food Chemistry*. **8**: 526-533.

Akter, A., Jamil Hassan, M., Umma Kulsum, M., Islam, M.R., Kamal, H. and Mamunur, R. M. 2014. AMMI Biplot Analysis for Stability of Grain Yield in Hybrid Rice (*Oryza sativa* L.). *Journal of Rice Research*. **2**: 2-4.

Alghamdi, S. S. 2004. Yield stability of some soybean genotypes across diverse environments. *Pakistan Journal of Biological Sciences.* **7(12)**: 2109-2114.

Allard, R. W. and Bradshaw, A. D. 1964. Implications of genotype-environment interactions in applied plant breeding. *Crop science.* **4**:503-508.

Ali, Y., Aslam, Hussian, and Shakur. 2004. Genotype and environmental interaction in cowpea (*Vigna unguiculata* L.) for yield and disease resistance. *International Journal of Environmental Science and Technology*. **1**(2): 119-123.

Al-jibouri, N. A., Miller, P. A. and Robinson, H. F. 1958. Genotypic and environmental variances, covariances in upland cotton cross of interspecific origin. *Agronomy Journal.* **50**: 633-637.

Annual report. 2017-2018.Government of India, Ministry of Agriculture and Farmers welfare, Department of Agiculture, Cooperation and Farmers welfare. Directorate of Pulses Development. pp.3.

Anandan, A. 2010**.** Environmental impact on the combining ability of fibres traits and seed cotton yield in cotton. *Journal of Crop Improvement.* **24:** 310-23.

AOAC. 2000. Approved methods of Association of Official Analytical Chemists.*7th Edition Saint Paul, Minnesotea, U.S.A*, pp .345.

Arora, R. K., Chandel, K .P .S .and Pant, K. C. 1988. Rice bean a potential grain legume. *NPBGR, ICAR, Pusa campus, New Delhi*.

Arslanoglu, F., Aytac, S. and Oner, E. K. 2011. Effect of genotype and environment interactions and stability of soybean (*Glycine max* L. (Merrill) seed. *African Journal of Biotechnology*. **10**:18409-18417.

Asseffa, Tofu, Dahiya, B. N, Deswal, D. P. 2002. Stability analysis for seed yield and its components in green gram. *National Journal of Plant Improvement.* **4** (2): 17-22.

Asio, M. T. 2004. Agronomic evaluation of some local and improved cowpea (*Vigna unguiculata*) lines in Uganda. M.sc Thesis,Makerere University, Kampala, Uganda.

Awasthi, C. P., Thakur, M., Dua, R. P. and Dhaliwal, Y. S. 2011. Biochemical evaluation of some promising varieties/genotypes of rice bean [*Vigna umbellata* (Thunb. Ohwi and Ohashi)]. *Indian Journal of Agricultureal Biochemistry.* **24**: 39-42.

Babu, K. N., Sudarshnam, A., Ramana, J., Srinivasa R. V. and Panduranga, R. C. 2009. Phenotypic stability in black gram (*Vigna mungo* L. Hepper) Using Eberhart and Russell and AMMI Models. *The Andhra Agricultural Journal.***56 (3):** 275-287.

Baker, R. J. 1988**.** Tests for crossover genotype x environment interactions. *Canadian Journal of Plant Science.* **68:**405-410.

Baisakh, B. 1992. Interrelationship between yield and yield attributes in rice bean (*Vigna umbellata*). *Indian Journal of Agricultural Sciences*. **62** (9): 620-622.

Bajpai, P. K. and Prabhakaran, V. T. 2000. A new procedure of simultaneous selection for high yielding and stable crop genotypes. *Indian Journal of Genetics*. **60**: 141-146.

Becker, H.C., J. Leon. 1988. Stability analysis in plant breeding. Plant Breeding. **101**(1): 1-23.

Berger, J. D., Speijers, J., Sapra, R. L., and Sood, U. C. 2007. Genotype by environment interaction and chickpea improvement. In: Chickpea Breeding and Management. Yadav SS, Redden R J, Chen W, Sharma B (eds), CAB International. pp. 617-629.

Bihari, D .S., Birari, S. P. and Jamadagni, B. M. 1993. Stability analysis of promising genotype of cow pea [*Vigna unguculata* (L.) walp] *India Journal of Agriculltural Sciences*. **63** (2):103-106.

Borah, H. K., Deb, choudhury, P. K., Sheikh, I. A.and Barman, B. 2001. Genetic parameters correlations and path analysis among yield and yield characters in ricebean (*Vigna umbellata* (Thumb.) Ohwi and Ohashi). *Madras Agricultural Journal.* **88**: 629-632.

Bose, L. K., Jambhulkar, N. N., Pande, K. and Singh, O. N. 2014. Use of AMMI and other stability statistics in the simultaneous selection of rice genotypes for yield and stability under direct-seeded conditions. *Chilean Journal of Agricultural Research*. **74**(1).

Bose, L. K., Jambhulkar, N. N. and Singh, O. N. 2014. Additive Main Effects and Multiplicative Interaction (AMMI) analysis of grain yield stability in early duration rice. *Journal of Animal and Plant Sciences*. **24**(6): 1885-1897.

Bueno, R.D., Borges, L. L., Arruda, K. M. A., Bhering, L. L., Barros, E.G., Moreira, M. A. 2013. Genetic parameters and genotype x environment

interaction for productivity, oil and protein content in soybean. *African Journal of Agricultural Research*. **8**(38):4853- 4859.

Burton, G .W .and De-vane, C. H. 1952. S S. Biometrical techniques in plant breeding.

Chatterjee, B. N. and Dana, S. 1977. Rice bean (*Vigna umbellata* (Thumb) Ohwi and Ohashi). *Tropical Grain Legume Bulletin*. **10**: 22-25.

Chauduari, G. B., Patil, J. V. and Barhate, K .K. 2000.Character association in rice bean (*Vigna umbellata*) (Thumb, Ohwi and Ohashi*). Legume Research.* **23** (1): 25-28.

Chaudhari, G. B. 1997. Genetic divergence in rice bean. M.Sc. (Agri.) thesis submitted to M.P.K.V., Rahuri (M.S.).

Chaudhari, S. B., Naik, M. R., Patil, S. S. and Patel, J. D. 2013.Stability analysis in Cowpea [*Vigna unguiculata* (L) Walp.]. *Trends in Biosciences.* **6** (4): 450-456.

Chaudhary, K. R. and Wu, J. 2011. Stability analysis for yield and seed quality of soybean [*Glycine max* (L.) Merril]. across different environments in eastern South Dakota. Annual Conference on Applied Statistics in Agriculture Kansas State University.

Chandel, K. P. S., Arora, K. K,, Pant. K. C,. 1988. Ricebean- A potential grain legume. *Science Monogram -12*, National Bureau of Plant Genetic Resources, New Delhi.

Chakrabarti, M. and Bhattacharya, N. M. 2005. Genetic variability in rice bean. *Environment and Ecology* **23**: 534-537.

Chandra, S. 1968. Variability in gram. *Indian Journal Genetics*. **28**: 205-210.

Chattopadhyay, A., Dasgupta, T., Hazra, P. And Som, M.G., 2001, Phenotypic stability for green pod yield and its components in cowpea (*Vigna unguiculata* (L.) Walp.). *Indian Agriculturist*, **45**(3-4): 141-146.

Chandel, K. P. S., Joshi, B. S., Arora, R. K. and Pant, K. C. 1978. Rice bean- a new pulse with higher potential. *Indian Farming* **28**: 19-22.

Comstock, R. E. and Moll, R. H. 1963.Genotype x environment interaction.*Statiscal genetics and plant breeding* pp.164-198.Nad-NRC publ no.912

Crossa, J., Cornelius, P. L. 1997. Sites regression and shifted multiplicative model clustering of cultivar trial sites under heterogeneity of errors variances. *Crop Science*. **37**: 406-415.

Dash, G. B. 2012. Variability and character association studies among micromutants of forage ricebean. *Forage Research* **38**: 119-121.

Das, N. D. 1979. Genetics of *Phaseolus calcaratus* unpublished Ph.D. thesis. BCKVV, Mohanpur, Nodia.

Das, N. D and S, Dana. 1985. Diallel analysis of four characters in rice bean. *Indian agricultural journal*. **29 (2):** 81-5.

Das, N. D. and Dana, S. 1981. Inheritance of seed yield components in rice bean. *Indian Journal of Genetics*. **41(2)**: 264-267.

Danillo, O. M. S., Carlos, A. F. S., Leonardo, S. B. 2016. Adaptability and stability parameters of total seed yield and protein content in cowpea (*Vigna unguiculata*) genotypes subjected to semi-arid conditions. *Australian Journal of Crop Sciences.* **10**(8): 1164-1169.

Dahiya, O. P., Singh, D., Mishra, S. K. 2007. Genotype and environment interaction and stability in cowpea (Vigna unguiculata (L) Walp). *Journal of Arid legumes*. **4**:69-71

Deb, A. C. and M. A. K. 2004. Study of genetic diversity of some of the yield and yield contributing characters in chickpea (*Cicer arietinum* L.). *Journal of Science Foundation*. **2**: 77-82

De, D. K., Bandopadhyay. P., Mazumdar, D. and Panja, B. N. 2007. Estimation of area of ricebean (*Vigna umbellata*) leaf by linear measurements. *Forage Research*. **33** (1): 9-12.

De, Rocha, M. M., Filho, F. R. F., Ribeiro., V. Q., Carvalho, H. W. L., Filho, J. B. 2007.Yield adaptability and stability of semi-erect Cowpea genotypes in Brazil Northeast region. *Pesquisa Agropecuária Brasileira.* **42**:1283-1289.

Deepak, P., Verma, S. K., Panwar, R. K., Anju, A. and Amit, K. G. 2018. Correlation and Path Analysis Studies in advance lines of Pigeonpea [*Cajanus Cajan* (L.) Millspaugh] under different environments**.** *International Journal of Current Microbial. App. Sci*. **7**(4): 378-389.

Dehghani, H, Sabaghpour, S. H., Ebadi, A. 2010. Study of genotype × environment interaction for chickpea yield in Iran. *Agronomy Journal*. **102**(1): 1–8.

DeLacy, I. H., Basford, K. E., Cooper, M., Bull, J. K. and McLaren, C. G. 1996. Analysis of multi-environment trials – An historical perspective. In: Cooper M, Hammer GL (Eds) Plant Adaptation and Crop Improvement. CAB International, Wallingford, UK, PP 39-124

Dewey, D. R and Lu, K. H. 1959. A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agronomy Journal* **51**: 515-518.

Dhillion, S. K., Singh, G., Gill, B. S., and Singh, P. 2009. Stability analysis for grain yield and its components in soybean (*Glycine max*. L. Merrill). *Crop Improvement*, **36**(1): 55-58.

Dobhal, V. K. and Gautam, N. K. 1994. Stability analysis for yield and component characters in ricebean (*Vigna umbellata*). *Indian Journal of Agricultural Sciences* **64**: 237-239.

Dodake, M. M. and Dahat, D. V. 2011. Association of characters and path coefficient analysis studies in rice bean [*Vigna umbellata* (Thumb.) Ohwi and Ohashi]. *International Journal of agricultural Sciences.* **7(2)**: 359-361.

Dodake, M. M. and Dahat, D. V. 2011. Genotypic and phenotypic variability in rice bean.*International Journal of Plant Science* **6** (2): 370-371.

Dodake, M. M. and Dahat, D. V. 2011. Association of characters and path coefficient analysis studies in ricebean [*Vigna umbellata* (Thunb) Ohwi and Ohashi]. *International Journal of Agricultural Sciences,* **2**: 359-361.

Dodwad, I. S., Salimath, P. M. and Patil, S. A. 1998. Evaluation of green gram collections for pod and seed characters. *Legume Research*. **21**(3/4): 183-187.

Ebdon, J. S. and Gauch, H. G. 2002. Additive Main Effect and Multiplicative Interaction Analysis of National Turf grass Performance Trials: II. Cultivar Recommendations, *Crop Science*. **42**:497–506.

Eberhart, S. A and Russell, W. A. 1966. Stability parameters for comparing varieties. *Crop Science, Madiso.* **6** (1): 36-40.

Eisemann, R. L., Cooper, M. and Woodruff, D. R. 1990. Beyond the analytical methodology – Better interpretation of genotype-by-environment interaction. In: Kang MS (ed) Genotype-by-environment Interaction and Plant Breeding. Louisiana State University, Baton Rouge, Louisiana. pp, 108-117.

Eisemann, L. T. 1990. The physiological basis of crop yield. In: L. T. Evans (ed.). Crop Physiology-Some case histories. Cambridge University Press, Cambridge. pp. 345.

El-Shaieny, A. A. H., Abde-Ati, Y. Y., El-Danarary, A. M. and Rashwan, A .M. 2015: Stability analysis of component characters in cowpea. *Journal of Horticulture and forestry* .vol.**7** (2), pp-24-35.

Falconer, D. S. 1960. Introduction to quantitative genetics. Oliver and Boyd, Edinburgh, pp.125-184.

Farshadfar, E. 2008. Incorporation of AMMI stability value and grain yield in single non-parametric index (GSI) in bread wheat. *Pakistan Journal of Biological Sciences.* **11**(14): 1791-1796.

Farshadfar, E., Mahmodi., N. and Yaghotipoor., A. 2011. AMMI stability value and simultaneous estimation of yield and yield stability in bread wheat (*Triticum aestivum* L.). *Australian Journal of Crop Science*. **5**(13). 1837–1844.

Fentie, M., Assefa, A., Belete, K. 2013. Ammi Analysis of Yield Performance and Stability of Finger Millet Genotypes across Different Environments. *World Journal of Agricultural Sciences.* **9**: 231-237.

Finaly, K.W. and Wilkinson, G. N. 1963. The analysis of adaptation in plant breeding programme. *Australian Journal of Agricultural Research*. **14**: 742-751.

Fikru, M. 2004. Genetic variability and inter- relationship of agronomic traits affecting seed yield in desi type Chickpea (Cicer arietinum L.). An M.Sc thesis submitted to the School of Graduate Studies, Addis Ababa University.

Finlay, K. W. and Wilkinson, G. N. 1966. The analysis of adaptation in a plant breeding programme. *Australian Journal Agriculture Research* **14**: 747-754.

Firas, M. and AL-Aysh. 2013 .Analysis of Performance, Genotype-Environment Interaction and Phenotypic Stability for Seed Yield and Some Yield Components in Faba Bean (*Vicia faba* L.) Populations. *Jordan Journal of Agricultural Sciences.* **1**(9**)**:43-50.

Fisher, R. A. 1918. The correlation between relative on the supposition of Mendelian Inhertance. *Trance Royal Society. Edinburgh*, **52**:399-403.

Gabriel, D., Carlos, A. F. S., Peter, O., Mildred, A., Charles, K.W. 2015.Grain Yield and Protein Content of Brazilian Cowpea Genotypes under Diverse Ugandan Environments. *American Journal of Plant Sciences*. **6**: 2074-2084.

Gadekar, P. and Dhumale, D. B. 1990. Study of genetic variability in rice bean. *Annals Plant Physiology*. **4** (1): 92-95.

Gadekar, P., Dhumale, D. B. and Raut, R. S. 1990. Interrelationship between yield and it's components in rice bean. *Indian Journal of agricultural Sciences*. **60** (8): 547-549.

Gadekar, P. and Dhumale, D. B. 1990 . Study the path analysis in rice bean. *Annals Plant Physiology*. **4** (2): 211-214.

Gadhak, S. S., Dethe, A. M. and Kathale, M. N. 2013. Genetic variability, correlations and path analysis studies on yield and its components in Mungbean (*Vigna radiata* (L.) Wilczek). *Journal of Bioinfolet*. **10** (2A): 441-447.

Gauch, H. G .1992. Statistical Analysis of Regional yield Trials: AMMI analysis of factorial designs. Elsevier, Amsterdam, the Netherlands, pp. 53-110.

Gauch, H.G. 1992. Statistical Analysis of Regional Trials, AMMI Analysis of Factorial Designs. Elsevier, Amsterdam, the Netherlands, pp. 278.

Gauch, H.G., Zobel, R.W. 1996. AMMI analysis of yield trials. In M .S. Kang & H.G. Gauch. (eds). Genotype by environment interaction. pp. 85-122. *Gujarat Agricultural University Research Journal*. **22**: 101-102.

Gaurav, K. G., Verma, P. K. and Hari, K. 2017. Genetic Variability, Correlation and Path Analysis in Mungbean [*Vigna radiata* (L.) Wilczek]. *International Journal of Current Microbiology and Applied Sciences.* **6 (**11): 2166-2173.

Gautam, R., N. Kumar., J.P., Yadavendra, S.B., Neog, S., Thakur, A., Khanal, B., Bhandari. and P.A. Hollington. 2007. Food security through ricebean research in India and Nepal (FOSRIN). Report 1. Distribution of ricebean in India and Nepal. Local Initiatives for Biodiversity, Research and Development, Pokhara, Nepal and CAZS Natural Resources, College of Natural Sciences, Bangor University, Wales, UK.

Geeta, P., Rajendra, P .and Birendra, P. P. C. 2015**.** Co-efficient of variation, heritability, genetic advance and variability for ricebean (*Vigna umbellata* (Thunb.) genotypes under mid hill conditions of Uttarakhand. *Journal of Applied and Natural Science* .**7** (2): 794 - 798.

Geeta, P., Rajendra, P., Birendra, P. and Priyamvada, C. 2015. Genotypic and phenotypic correlation between seed yield and its components in Rice bean (*Vigna Umbellata* (Thunb.) Ohwi AND Ohashi). *International Journal of Agricultural Science and Research.* **6**.2250-0057.

Gill, R .K., Singh, S. and Brar, G. S. 2008. Genetic diversity studies in rice bean (*Vigna umbellata* (Thumb) Ohwi and Ohashi) Germplasm. *Crop Improvement* . **35**(1): 41-44.

Grausgruber, H., Oberforster, M., Werteker, M., Ruckenbauer,,P. and Vollmann J. 2000. Stability of quality in Austrian-grown winter wheats. *Field Crop Research.* **66:** 257–267.

Gupta, R. K., Tomer, Y. S., Battan, K. R., Singh, V. R. 1991.Stability analysis in mungbean. *Indian Journal of agricultural Sciences.* **25** (3):15-160.

Gupta, R. K., Tomer, Y. S., Battan, K. R., Singh, V. R. 1999. Stability analysis in Mungbean. *Indian Journal of Agricultural Research* .**5**(3):154-160.

Gupta, S., Pandey, A., Amit, K. and Pattanayak, A. 2014. Evaluation of Genotypic variation and suitability of rice bean for mid-altitudes of Meghalaya, India. *Legume Research-An International Journal*. vol **37**: 568-574.

Gyanendra, S., Chaudhary, B. S. and Singh, S .P. 2007. Stability analysis for seed yield and its component in rice bean. *Indian Journal of crop sciences.* **2**: 1.

Gyanendra, S., Chaudhary, B. S. and Singh, S. P. 1998. Stability analysis of some agro-morphological characters in ricebean *Annals of Agricultural Research.* **19**: 411-414.

Hanson, C. H., Robinson, H. R. and Comstock, R. S. 1956**.** Biometrical studies of yield in segregating population of Korean Lespedeza. *Agronomy Journal* **48**: 268 - 272.

Haware, B. L., Birari, S. P., Dhonukshe, B. L., Jamadagni, B .M. 1998. Stability analysis for grain yield in rice bean. *Indian Journal of Agricultural Research.* **32**(1): 17-20.

Hemavathy, A. T., Shunmugavalli, N. and Anand, G. 2015.Genetic variability, correlation and path co-efficient studies on yield and its components in mungbean [*Vigna radiata* (L.)Wilezek]. *Legume Research.* **38** (4): 442-446.

Hossain, M. A., Rahman, L. and Shamsuddin, A. K. M. 2003. Genotype-Environment and Stability analysis in Soyabean. *Journal of Biological Sciences.* **3**(11): 1026-1031.

Igbedioh, S. O., Shaire, S. and Aderiye, B. J. I. 1995. Effects of Processing on Total Phenols and Proximate Composition of Pigeonpean (*Cajanus cajan*) and Climbing Bean (*Vigna umbellata*). *Journal of Food Science and Technology* . **32**: 497-500.

Jai, D., Anand, D., Kumari, V., Sood, V. K., Singh, A., Singh, A., Kaushal, R. P., Jenjiha, J. K., and Sood, O. P. 2009. Genotype x environment

interaction for yield and maturity in soybean. *Crop Improvement*. **36**(1): 59-63.

Javed, H. I., Masood, M. A. and Chungutai, S. R. 2006. Performance of Maize genotype on basis of stability analysis in Pakistan. *Asian Journal of plant science.* **5**(2): 207-210.

Jadhav, S. J. 1996. Genetic variability and path analysis in rice bean. *Annals of Plant physiology*. **4** (2): 211-214.

Jinks, J. L. and Mather, K. 1955. Stability in development of heterozygotes and homozygotes. *Journal of Proceedings of the Linnean Society. Botany.* **143**: 561-578.

Jilani, A., Qamar, I. A., Ali, A .and Arshad, M. 2001. Performance of summer forage legumes in the sub tropical sub humid Pothwar plateau of Pakistan. *Journal of Biological Sciences* **1**: 573-574.

Jogendra, S., Amit, K., Abdul, F. R. and Muneendra, K. S. 2018. Stability analysis of pigeon pea genotypes by deployment of AMMI model under rainfed environment. *Legume Research*. **41**(2): 182-188.

Johnson, H. W., Robinson, H .E. and Comstock, R. S. 1955. Estimates of genetic and environmental variability in soyabean. *Agronomy Journal.* **47**: 314-318.

Johnson, V. A., Shafer, L. and Schmidt, J. W. 1968. Regression analysis of general adaptation in hard red winter wheat (*Triticum aestivum* L.). *Crop science*. **8**: 187-191.

Joshi, K. D., Bhandari, B., Gautam, R., Bajarcharya, J. and Hollington, P. A. 2006. Ricebean: a multipurpose underutilized legume. Paper presented at 5th International symposium on new crops and uses: Their roles in rapidly changing world. Organized by the centre for underutilized crops, university of Southampton in partnership with National non-food crops centre and the tropical Agricultural Association.

Joshi, S. N. 1969.Variety x environmental interaction in varietal test of green gram (*Phaseolus aureus* Roxb). *Indian Journal of agricultural Sciences*. **39**: 1010-1012.

Joshi, S. N. 1972. Stability parameters for comparing green gram (*Phaseolus aureus* Roxb.) varieties. *Madras Agricultural Journal*. **59**: 195-197.

Joseph, A. D., Joseph, M. A., Vernon, E. G., Isaac, K. A. and Samuel, K .O. 2017. AMMI Stability Analysis and Estimation of Genetic Parameters for Growth and Yield Components in Cassava in the Forest and Guinea Savannah Ecologies of Ghana. *International Journal of Agronomy*. **1**: 10.

Kalpande, H. V., Patil, J .G. and Deshmukh, R. B. 1996. Stability analysis for seed yield and its components in green gram. *Journal of Soils and Crops.* **6** (2): 173-176.

Kamdi, R. E. 2001. Relative stability, performance and superiority of crop genotypes across environment. *Journal of Agricultural*. **6**:449-460.

Katoch, R. 2011. Morpho-physiological and nutritional characterization of rice bean *(Vigna umbellata), Acta Agronomica Hungarica* .**59**(2): 125-136.

Kaur, M. and Kawatra, B .L.2002. Evaluation of iron bioavailability from ricebean (*Vigna umbellata*) by using anameic rats. *Nutritional Research* **22**:633-640.

Kaur, A., Kaur, P. and Singh, N. 2013. Grains, Starch and Protein characterstics of ricebean grown in Indian Himalayas regions. *Food Research International Journal.* **54**(1):102-110.

Kavitha, G., Dhindsa, G. S., Sarvjeet, S. and Johar, S. 2009. Stability analysis of yield and its components in malt barley (hordeum vulgare l.) genotypes. *Crop improvement* .**36** (1): 29-34.

Kempton, R. A. 1984.The used of biplots in interpreting variety by environment interaction. *Journal of Agriculture science*. **103**:123-125.

Khadka, K. and Acharya, B. D. 2009. Cultivation Practices of Ricebean. Local initiatives for biodiversity research and development, 1st edition. Pokhara, Nepal.

Khabiruddin, M., Gupta, S. N. and Tyagi, C. S. 2002. Nutritional composition of some improved genotypes of rice bean (*Vigna umbellata*). *Forage Research* **28**: 104-104.

Khan, H., Viswanatha, K. P. and Sowmya, H. C. 2015. Study of genetic variability parameters in cowpea (*Vigna unguiculata* walp.) germplasm lines. *The Bio-scan*. **10**(2): 747-750.

Kumar, B. M. D., Shambulingappa, K. G., Kulkarni, R. S., Swamy, G. S. K. and Lohidhaswa, H .S. 1997. Analysis of genetic variability and

character association in rice bean [*Vigna umbellata* (Thunb.) Ohwi and Ohashi]. *Mysore journal agricultural science*. **31** (1): 23-28.

Lakshmana, D., Jolli, R.and Madaiah, D. 2010. Genetic variability studies in rice bean [*Vigna Umbellata* (Thunb)]. *Legume Research*.**33** (4): 279-282.

Lal, H. A., Muhammad, K., Muhammad, A., Tariq, A.2010. Stability analysis for grain yield in mungbean grown in different agro climatic region. *Emirates Journal of Food and Agriculture*. **22**(6): 490-497.

Lavanya, G. R. 2006. Evaluation of mungbean germplasm for genetic variability. *Indian Journal of Plant Genetic Resources*. **19** (1): 104-406.

LI_BIRD. 2008. Food security through Rice bean research in India and Nepal (FOSRIN).periodic activity report. Local initiative for Biodiversity, research and developments (LI-BIRD), Pokhara, Nepal.

Lokesh, V., P. K., Gupta, S. N. and Behl, R. K. 2003. Genotypic variation for important morphological characters and seed yield attributes in rice bean. *Forage Research*. **29** (4): 189-191.

Luthra, O. P, Singh, R. K., Kakar, S. N. 1974. *Theoritical Applied Genetics*. **45**:143-149.

Machikowa, T. and Laosuwan, P. 2011. Path coefficient analysis for yield of early maturing soybean. *Songklanakarin Journaln of Science Technololgy* .**33** (4): 365-368.

Mather, K. and Jinks, J. L. 1982. *Biometrical Genetics- the Study of Continuous Variation.* Chapman and Hall, London, New York, pp. 396.

Manivannan, N. 1999. Association between stability parameters in green gram. *Legume Research.* ***23*** (3): 167-171.

Majid, M. A., Khanum. S., Sheik, M. A. Q. and Bhuiya, A. D. 1982. Genetic variability and correlation studies in Black gram. *Journal of Agricultural*.**7**: 98-102.

Mahto, C. S., Kumar, N., Kumar, Y. and Prakash, S. (2016). Genetic diversity Analysis in green gram (*Vigna radiata* (L) Wilkczek). *National seminar on innovative breeding approaches for agricultural security*. **1**(19):26-27.

Masindeni, D. R. 2013. Evaluation of South African high quality protein maize (*Zea mays* L.) inbred lines under optimum and low nitrogen conditions and the identification of suitable donor parents. PhD Thesis, University of the Free State.

Mehta, A. K., Vishnoi, R. and Bilaiya, S. K. 2007. Genetic variability in soybean for green fodder yield and their trait, In National Symposium on A new vista forage crop research. West Ben. pp. 46.

Minimol, J. S, Datke, S. K, Deshmukh, S. N and Satpute, G. N. 2000. Genotype x environment interaction in groundnut *(Arachis hypogaea* L.). *Annals of Plant Physiology.* **14** (1): 74-79.

Mishra, D. 1994. Phenotypic stability for seed yield in rice bean. *Indian Journal of Agricultural Sciences*. **65**(12): 904-906.

Mishra, A., Moduli, K .C., Mishra, B .K. and Patra, A. K. 1995. Interrelationship between yield and it's components in rice bean. *Environmental and Ecology*. **13** (2): 430-432.

Mohanlal, V. A., Saravanan, K. and Sabesan, T. 2020. Additive main effects and multiplicative interaction (ammi) stability analysis for seed yield in black gram (*vigna mungo* l. hepper) genotypes. *Plant Archives*. **20**(1): 1611-1614.

Mohamed, S. H., Mohamed, G. I. A. and Ell-said, R.A.R. 2013. Stability analysis for grain yield and its components of some Durum wheat Genotypes (*Triticum durum*. L) under different environment. *Asian Journal of crop Sciences*. **5**.179-189.

Mohammed, M. I. 2009. Genotype X Environment interaction in Bread wheat in Northern Sudan using AMMI analysis. *American-Eurasian Journal of Agricultural & Environmental Sciences*. **4**:427-433.

Monica, R., Domenico, R., Roberto, P., Giovanna, A. (2008). Genotype by environment interactions in barley (*Hordeum vulgare* L.): different responses of landraces, recombinant inbred lines and varieties to Mediterranean environment. *Euphytica.* **163**: 231–247.

Moldovan, V., Moldovan, M. And Kadar, R. 2000. Item from Romania. S.C.A. Agricultural Research Station. Turda, 3350, str. Agriculturii 27 Jud Chuj, Romania.

Mukai, T. 1988. Genotype-environment interaction in relation to the maintenance of genetic variability in populations of *Drosophila melanogaster*. *Proceedings of the 2nd International Conference on Quantitative Genetics:* 21-31.

Musa, B and Taha. 1980. The effect of sowing dates and plant orientation on yield and yield components of Chickpea. Annual reports of Hudejba Research station. Vol. No.Arc.PP.17-18.

Muhammad, A., Ahmad, B., Haqqani, A .M. and Muhammad, B. 2003. Genotype x Environment interaction for grain yield in chickpea (*cicer arietinum*.L). *Pakistan Journal of Botany*. **38**(3): 683-690.

Myrna, S., Rodriguez and Evelyn, M. T. M. 1991. Nutritional assessment of seed proteins in rice bean, *Vigna umbellata* (Thunb) Ohwi and Ohashi. *Plant Foods for Human Nutrition.* **41(1):** 1-9.

Naidu, N .V., Satyanarayana, A. 1991. Association between mean performance and stability parameters in greengram. *Indian Journal of Agricultural Sciences*. **61** (6):420-421.

Naidu, N. V., Satyanarayana, A. 1991. Stability analysis for seed yields its component in Mungbean. *Legumes Research*. **14** (4):169-174.

Nassar, R. and Huehn, M. 1987. Studies on estimation of phenotypic stability: tests of significance for non nonparametric measures of phenotypic stability. *Biometrics*. **43**: 45–53.

Nath, D. and Dasgupta, T. 2017. Genotype x Environment Interaction and Stability analysis in mung bean. *International Journal of Current Microbiol and Applied Sciences*. **6**(9): 1955-1963.

Navale, P. A. and Solanke, A. U. 2001. Genetic diversity studies in rice bean (*Vigna umbellata* (Thumb) Ohwi and Ohashi). M.P.K.V. Rahuri.

Narasinga, R. B .S., Deosthale, Y. G. and Pant, K. C. 1989. Nutritive value of Indian foods. National Institute of Nutrition, Indian Council of Medical Research (ICMR), Hyderabad, Andhra Pradesh, India.

Nimbalkar, A. P., Baviskar and Bajaj, V. H. 2006. AMMI approach *for* seed yield and stability of French bean (*Phaseolus vulgaris*). *Indian journal of Genetics and Plant Breeding*. **66** (4): 343-344.

Ntawuruhunga, P. and Dixon, A. G. O. 2010. Quantitative variation and interrelationship between factors influencing cassava yield, *"Journal of Applied Biosciences***. 26**: 1594–1602.

Nwofia, G. E., Nwanebu, M. and Agbo, C. U. 2012. Variability and Inter-Relationships between Yield and Associated Traits in Cowpea (*Vigna unguiculata* (L.) Walp as Influenced by Plant Populations. *World Journal of Agricultural Sciences.* **8** (4): 396-402.

Oliveira, E. and Godoy, I. 2006. Pod yield stability analysis of runner peanut lines using AMMI. *Crop Breeding and Applied Biotechnology*. **6**(4). 310–317.

Oliveira, E. J., Xavier, J. P., Jesus, O. N. (2014). AMMI analysis of the adaptability and yield stability of yellow passion fruit varieties. *Agricultural Science*. **71**(2): 139-145.

Pacheco, R. M., Duarte, J. B., Vencovsky, R., Pinheiro, J. B., Oliveira, A. B. 2005. Use of supplementary genotypes in AMMI analysis. *Theoretical and Applied Genetics*. **110**: 812-818.

Paikaray, R. K. and Mishra, R. C. 1992. Performance of Chickpea under different dates of sowing in Orissa. Intern. *Chickpea Newsletter*. **27**: 24-25.

Pal, R., Nautiyal, M. K., Singh, Y. V. and Sharma, C. I. 2014. Evaluation of genetic variability for some quantitative traits in rain cowpea (*vigna unguiculata* (L) Walp.). *International Journal of Basic and applied Agricultural research*. **12**(2): 188-192.

Panse, V. G. and Sukhatme, P. V. (1978). Statistical Methods for Agricultural Workers, ICAR, New Delhi.

Patil, H. S., Narkhede, B. N. 1995. Stability analysis for 100 seed weight pods/plant and seed yield in green gram. *Legume Research*. **18** (1): 41-44.

Paroda, R. S. and Hayes, J. D. 1970. An investigation of genotype environment interaction for rate of ear emergence in spring wheat. *Heredity*. **26**: 157-175.

Perkins, J. M. and Jinks, J. L. 1968. Environmental and genotype-environmental component of variability. III. Multiple lines and crosses. *Heredity*. **23**: 339-356.

Phundan, S and Narayanan. S. S. 1993. Biometrical techniques in plant breeding Kalyani Publishers.

Phundan, S, Narayanan, S. S. 2004. Biometrical techniques in plant breeding. Kalyani Publishers, Ludhiana, New Delhi, India.

Piepho, H. P. 1998. Methods for comparing the yield stability of cropping systems-a review. *Journal of Agronomy Crop Science.* **180**: 193-213.

Pol, K .M., Aawari, V. R., Ugal, S. D. and Thakur, S. 2001. Periodical correlation of various morpho physiological and yield contributing character with grain yield in rice bean (*Vigna umbellate*). *Annals plant physiology*. **15**(2): 159-162.

Pratap, K., Sudarshanam, A., Satyanarayana, R, V., Srinivasa R. V. and Panduranga R. C. 2009. Phenotypic stability analysis in Greengram (*Vigna radiate* L. Wilckzek) using Eberhart and Russell and AMMI Models. *The Andhra Agricultural Journal.* **56**(3)**:** 288-297.

Purchase, J. L., Hatting, H and Vandeventer, C. S. 2000. Genotype X environment interaction of winter wheat (*Triticum aestivum* L) in South Africa: D. Stability analysis of yield performance. *South African Journal of Plant Soil*. **17**:101-107.

Purchase, J. L. 1997. Parametric analysis to describe G×E interaction and yield stability in winter wheat. Ph.D. Thesis, Dept. of Agronomy, Faculty of Agriculture, University of the Orange Free State, Bloemfontein, South Africa.

Ramana, M. V. and Satyanarayana, A. 2005. Stability for yield and component traits in soybean (*Glycine max.* L. Merrill). *J. Oilseeds Research*. **22**: 18-21.

Rahim, M. A., Mia, A. A., Mahmud, F., Zeba, N. and Afrin, K .S. 2010. Genetic variability, character association and genetic divergence in mung bean (*Vigna radiate* L. Wilczek). *Plant omics Gerenal.* **3**(1):1-6.

Rao, Y. K., Durga, K. K., Murthy, S. S. and Reddy, D. M. (2004). Stability for seed yield in Mungbean. *Legume Research.* **27**(1): 11-18.

Raffi, S. A., Newaz, M. A. and Khan, N. 2004. Stability analysis for pod and seed production in dry beans (*Phaseolus vulgaris* L.). *Asian Journal of Plant Science*. **3**(2): 239-242.

Raje, R. S. and Rao, S. K. 2004. Stability analysis for seed yield in mungbean (*Vigna radiate* L.Wilczek). *Legume Research.* **27**(1): 11-18.

Raiger, H. L., Bhandari, B. C. and Phogat, B. S. 2010. Annual report of All India Coordinated Research Network on Under-utilized crops NBPGR, New Delhi, pp. 40816-518.

Rakshit, S., Ganapathy, K., Gomashe, S., Rathore, A., Ghorade, R., Kumar, M .N. 2012. GGE biplot analysis to evaluate genotype, environment and their interactions in sorghum multi-location data. *Euphytica*. **185**: 465-479.

Rashidi, M., Farshadfar, E. and Jowkar, M. M. 2013. AMMI analysis of phenotypic stability in chickpea genotypes over stress and non-stress environments. *International Journal Agricultural Crop Sciences.* **5**(3): 253-260.

Reddy, P. N., Hemantkumar, M., Krishanaiah, S.B .V. 1990. Stability analysis of yield and component characters and correlation of stability in green gram (*Phaeolus radiatus* L.). *Indian Journal of Agricultural Sciences*. **60**(11): 755-757.

Reddy, M. P., Reddy, B. R., Arsul, B. T. and Maheshwari, J. J. 2013. Character Association and Path Coefficient Studies in Linseed. *International Journal of Current Microbial and Applied Sciences.* **2**(9): 250-254.

Rharrabti, Y., Villegas, D., Royo C., Martos-Núñez, V. and García del Moral L.F. 2003. Durum wheat quality in Mediterranean environments II. Influence of climatic variables and relationships between quality parameters. *Field Crop Research*. **80:** 133–140.

Robinson, H. F. 1951. Quantitative genetics in relation to breeding on the contennial of Mendelism. .*Indian Journal of Genetics*. **26** (1): 171-187.

Rodriguez, M. S. and Mendoza, E .M. 1991. Nutritioanl assessment of seed protein in rice bean [*Vigna umbellata* (Thunb). Ohwi and Ohashi]. *Plant Food for Human Nutrition* **41**: 1-9.

Santos., G. Ceccon., E.V. Rodrigues., P. E. Teodoro., P. A. Makimo., V. B. Alves, J.F. Silva., A.M. Corrêa., R.C.F. Alvares and F.E. Torres. 2015.

Adaptability and stability of cowpea genotypes to Brazilian Midwest. *African Journal of Agricultural Research.***10**: 3901-3908

Sarma, B .K., Singh, M .and Pattanayak, A. 1991. Evaluation of rice bean (*Vigna umbellata*) germplasm in upland terraces of Meghalaya. *Indian Journal of Agricultural Sciences* **61**: 182-184.

Sarvamangala, C., Uma, M .S,. Birader, S. and Saliman, P .M. 2010. Stability analysis for yield and yield components over seasons in cow pea [*Vigna unguiculata*L. (Walp)]. *Electronic Journal of plant breeding.* **1(6)**:1392-1395.

Saikia, P., Sarkar, C. R. and Borua, I. 1999. Chemical composition, anti-nutritional factor and effect of cooking on nutritional quality of rice bean [*Vigna umbellate* (Thunb). Ohwi and Ohashi]. *Food Chemistry.* **67**: 347-352.

Saharan, K., Khetarpaul, N. and Bishnoi, S. 2002. Antinutrients and protein digestibility of fababean and ricebean as affected by soaking, dehulling and germination. *Journal of Food Science and Technology*.**39** (4): 418-422.

Sadana, B., Hira, C. K., Singla, N. and Grewal, H. 2006. Nutritional evaluation of rice bean (*Vigna umbellata*) starins. *Journal of Food Science and Technology* **43**: 5.

Salem, S. A. 2004. Yield Stability of Some Soybean Genotypes across Diverse Environment. *Pakistan Journal of Biological Science.* **7**(12): 2109-2144.

Samonte, S. O., Wilson, L. T., McClung, A. M. and Medley, J. C. 2005. Targeting cultivars onto rice growing environments using AMMI and SREG GGE biplot analysis. *Crop science*. **45**(6): 2414-2424.

Sands, D. C., Morris, C .E., Dratz, E .A., Pilgeram, A. L. 2009. Elevating optimal human nutrition to a central goal of plant breeding and production of plant-based foods. *Plant Science*. **177**: 377–389.

Sarkar, A. and Mukherjee, M. 2007. Study on genetic variability in rice bean germplasms under terai region of west Bengal. In National Symposium on "A new vista to forage crop research, West Bengal, PP 34.

Satyan, B. A., Reddy, P. G., Radhamani, T. R., and Prakesh, K. S. 1988. Induced genetic variability in amphidiploids generation of mungbean and ricebean crosses.Genome.30: Supplement 1,466; in Genetics and the unity of Biology. (Abstract of paper presented at the inter XVI International Congress of Genetics, Toronto to Canada 20-27 August.

Senthilkumar, N and Chinna, S .K. 2012. Stability for seed yield in black gram (*Vigna mungo* L. Hepper). *International Journal of Recent Scientific Research*. **(3).** PP 336 – 339.

Shukla, G. P., Melkania, N. P., Singh, K., Rajpali, S. K., Arya, O. N. 2003. Genotype x location environment interaction in rice bean [*Vigna umbellata* (Thunb.) Ohwi and Ohashi] with special reference to acidic soil. *Forage Research.* **28**(4): 194-200.

Sharma, B. K., Singh, M and Pattanayak, A. 1991. Evaluation of rice bean *(Vigna umbellata)* germplasm in upland terraces of Meghalaya. *Indian Journal Agricultural Sciences*. **61**(3):182-184.

Sharma, B .D and Hore, D .K. 1994. Association of yield attributes in ricebean (*Vigna umbellata*). *Legume Research* .**17**(2):135-137.

Sinha, B. B., Pujari, M. M. and Tiwari, V. 2000. Stability analysis for pod yield in cowpea (*Vigna unguiculata* (L.) walp). *Journal of Applied Biological sciences.* **10** (1): 26-31

Singh, M. and Sohu, H. K. 1995. Stability analysis of multiline and their components in groundnut. *Crop Improvement.* **22** (1): 87 -90.

Singh, J., Bhardwaj, B.L., Singh, P.2007.Genetic diversity analysis in grain cowpea over environments. *Crop improvement*. **34**:175-178.

Singh, G., Singh, S. P. and Chaudhary, B. S. 1997. Genetic divergence analysis in rice bean. *www.Indian Journals*.com. **58** (1):210-112.

Singh, G .and Dhiman, K. R. 1991. Genetic variability, correlation and path analysis in rice bean.Proc.of Golden jubilee Symposium of Indian Society of Genetics, held at IARI, New Delhi, Vol. **3**(1): 338.

Singh, G. and Singh, M. 1994. Association among quantitative traits in ricebean germplasm. *Journal of Hill Research*, **7**(1):59-60.

Singh, G., Singh, M. and Dhiman, K .R. 1992. Correlation and path analysis in rice bean under mid altitude conditions. *Crop improvement* .**19**(2): 152-154.

Singh, G., Singh, S. P. and Chaudhary, B. S. 1998. Genetic divergence analysis in rice bean. *Indian Journal of Genetics*. **58** (1): 101-105.

Singh, P. K., Ojah, H., Singh, J. K., Alpana, D., Pattanayak, A., Verma, M. R. 2006. Genetic variability and characters association in rice bean (*Vigna umbellata*) genotypes of north east India. *Environment and Ecology* .**24:** 923-926.

Singh, R. K. and Chaudhuary, B .D. Biometrical methods in Quantitative Genetic Analysis.

Singh, A., Singh, S.K., Sirohi, A. and Yadav, R. 2009. Genetic variability and correlation studies in green gram (*Vigna radiata* (L.)Wilczek). *Progressive Agriculture*. **9**(1): 59-62.

Singh, S. K., Singh, I. P., Singh, B .B., Onkar, Singh. 2009. Stability analysis in mungbean (*Vigna radiate* (l) wilczek).*Legume research*.pp 32.

Singh, S. P., Mishra, B. K. and Sikka, K. C. 1985. Studies on some nutritional aspects of rice bean (*Vigna umbellata*). *Journal of Food Science and Technology*. **22**: 180-185.

Singh, G., Brar, H. S. and Verma, M. M. 1991. Genotype x Environment interaction and phenotypic stability in chickpea. *Crop Improvement*. **18**(2): 135 – 141.

Singh, S. P., Misra, B. K., Chandel, K. P. S. and Pant, K. C. 1980. Major food constituents of rice bean. *Journal of Food Sciences and Technology* **17**: 238-240.

Singh, G., Sekon, H. S., Andhu, J. S. and Randhawa, A. S. 2003. Effect of location and seed rate on three genotypes of mungbean. *Tropical Science*. **43**: 116-120.

Singh, G., Kaur, H., Navneet, A., Hari, R., Gill, K. K .and Khanna, V. 2013. Symbiotic efficiency, thermal requirement and yield of black gram (*Vigna mungo* L. Hepper) genotypes as influenced by sowing time. *Indian Journal of Agricultural Sciences.* **83** (9): 953-8.

Sivasubramanian, S. and Menon. P. M.1973. Genotypic and phenotypic variability in rice. *Madras Agriculture Journal*. **60** (9-13): 1093-1096.

Sneller, C. H., Kilgore-Norquest, L. and D, Dombek. 1997. Repeatability of yield stability statistics in soyabean. *Crop Science*. **37**: 383-390.

Solanke, A.U., Navale, P.A. Genetic diversity studies in rice bean (*Vigna umbellata* (Thumb) Ohwi and Ohashi) 2001, M.P.K.V. Rahuri, (Maharashtra).

Sonene, A. H., Jadhav, S. J., Dahat, D .V. and Aher, R .P. (1999). Path analysis in rice bean (*Vigna umbellata*). *Legume Research* .**22**: 195-197.

Sowmini, K. and Jayamani, P. 2013. Genetic variability studies for yield and its component traits in RIL population of black gram (*Vigna mungo* (L.)

Hepper). *Electronic Journal Plant Breeding and Genetics.* **4**(1): 1050-1055.

Sonone, A. H., Saste, S .V. 2004. Genetic diversity and path analysis in rice bean (*Vigna umbellata* (Thumb) Ohwi and Ohashi.

Sunayana, R. S., Somveer, N., Mor, V .S. and Pinki. 2018. Impact of genotype × environment interaction and stability for seed cotton yield and its component traits in Asiatic cotton (*Gossypium arboreum* L.) .*Journal of Cotton Research and Development.* **32** (1): 23-29.

Srivastava, G. P. and Srivastava, V. C. 2003. Effect of row spacing on yield of rice bean (*Vigna umbellata*) varieties. *Journal of Research, Birsa Agricultural University* **15**(1): 95-96.

Tehlan, R. S. 1973. Unpublished M.Sc. Thesis, Haryana Agricultural University, Hissar.

Temesgen, T., Keneni, G., Sefera, T. and Jarso, M. 2015.Yield stability and relationships among stability parameters in Fababean (*Vicia faba* L.) genotypes. *The Crop Journal*. **3**: 258-268.

Tiwari, A., Mishra, A. K. and Nag, S. K. 2014. Correlation and path coefficient analysis for seed yield and its components in Mungbean (*Vigna radiata* (L.)Wilczek). *Trends Bioscience.* **7**(1): 42-45.

Thakur, S. and Bhardwaj, N. 2017. Correlation and path analysis of yield and its components plant traits in Rice bean [*Vigna umbellata* (Thunb.) Ohwi

and Ohashi]. *International Journal of Current Microbiol and Applied Science*. **6** (12): 3272-3278

Thanki, H. P. and Sawargaonkar, S. L. 2010. Path coefficient analysis in pigeonpea [*Cajanus Cajan* (L) Millsp.]. *Electronic Journal of Plant Breeding*. **1**(4): 936-939.

Thomas, T. A., Dabas, B. S., Patel, D. P. and Joshi, B. D. 1983. Ricebean. A new pulse for North-Western Himalayas. *Indian Farming*. **33**: 17-19.

Thaware, B. L., Birari, S. P., Dhonukshe, B. L. and Jamadagni, B. M. (2000). Correlation between yield and yield attributes under different environments in rice bean. *Indian Journal of Agricultural Research*. **34 (1):** 47-50.

Thaware, B. L., Birari, S. P., Dhonukshe, B. L. and Jamadagni, B. M. 1998. Stability analysis for grain yield in rice bean. *Indian Journal of Agricultural Research*. **32(1)**: 17-20.

Thaware, B. L., Bendale, V. W. and Toro, V. A. 2005. Konkan rice bean-1 (RB-10), a new fodder rice bean variety for Konkan Region of Maharashtra. *Journal of Maharashtra Agricultural Universities.* **30**: 295-298.

Thorat, A. and Gadewar, R. D. 2013. Variability and Correlation studies in cowpea (Vigna unguiculata). *International Journal for Environmental Rehabilitation and Conservation*. **4**(1): 44 – 49.

Tolessa, T. T., Keneni, G., Sefera, T., Jarso, M. and Beele, Y. 2013. Genotype x Environment interaction and performance stability for grain yield in

Field pea (*pisum sativum*. L) Genotypes. *International Journal of Plant Breeding*.**7** (2):116-123.

Tony, N., Ashraf, M., Meseka, S. 2013. Soybean (*Glysine max L*). Genotype and Environment interaction Effect on yield and other related Traits. *American Journal of Experimental Agriculture*.**3** (4): 977-987.

Tomooka, N. C., Lairungreang, P., Nakeeraks,Y, Y., Egawaand and Thavarasook, C.1991. Mungbean and genetic resources, the subgenus Ceratotropics, *Tropical Agricultural Research Center*, Japan.

Vargas, M., Crossa, I., Eeuwijk, F. V., Sayre, K. D. and Reynolds, M. P. 2001. Interpreting treatment x environment interaction in agronomy trials. *Agronomy Journal*. **93**: 949-960.

Wilson, R. F. 2004. Soyabean; Improvement, Production and Uses.3rd Edition, ASA, CSSA and SSSA, Madison, WI. pp. 621-668.

Wilcox, J. R., Cavins, J. F. 1995. Backcrossing high seed protein to a soybean cultivar. *Crop Science*. **35**: 1036– 1041.

Wilmar, F. L., Jose, F. F., Carlos, A. A. and Marcelo, F. D. 2000. Stability of soybean yield through different sowing periods. *Pesquisa Agropecuária Brasileira*, Brasília. **35**: 2181-2189.

Wright, S. 1921. Correlation and causation . *Journal of Agricultural Research*. **20**: 557-587.

Wu, R. L. and O'Malley, D. M. 1998. Nonlinear genotypic response to macro- and microenvironments. *Theoretical and Applied Genetics.* **96**: 669-675.

Yadav, N. K., Ghimire, S. K., Sarker, A., Shrestha, S. M., Sah, S. K. 2016. Genotype x environment interaction and stability analysis in lentil (lens *culinaris* Medik.). *International Journal of Environment, Agriculture and Biotechnology*. **1**: 354-361.

Zali, H. E., Farshadfar, Sabaghpour, S. H. and Kariizadeh, R. 2012. Evaluation of genotype X environment interaction in chickpea using measures of stability from AMMI model. *Annals of Biological Research*. **3**: 3126-3136.

Zobel, R. W., Wright, M. S. and Gauch, H. G. 1988. Statistical analysis of a yield trial. *Agronomy Journal*. **80**: 388-393.