COMPARATIVE ANALYSIS OF DIFFERENT STABILITY MODELS ON SUPERIOR CULTURES OF PADDY (*Oryza sativa*)

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by

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THESIS

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DECLARATION

I, hereby declare that this thesis entitled **"Comparative analysis of different stability models on superior cultures of paddy (*Oryza sativa*)"** is a bonafide record of research work done by me during the course of research and the thesis has not previously formed the basis for the award to me of any degree, diploma, associateship, fellowship or other similar title, of any other University or Society.

Place: Vellayani

Date: 25/08/2020

Adarsh V S

(2018-19-006)

CERTIFICATE

Certified that this thesis entitled **"Comparative analysis of different stability models on superior cultures of paddy (*Oryza sativa*)"** is a record of research work done independently by **Mr. Adarsh V S** under my guidance and supervision and that it has not previously formed the basis for the award of any degree, fellowship or associateship to him.

Place: Vellayani
Date: 25/08/2020

Dr. Brigit Joseph
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CERTIFICATE

We, the undersigned members of the advisory committee of **Mr. Adarsh V S**, a candidate for the degree of **Master of Science in Agriculture** with major in Agricultural Statistics, agree that the thesis entitled **"Comparative analysis of different stability models on superior cultures of paddy (*Oryza sativa*)"** may be submitted by **Mr. Adarsh V S**, in partial fulfilment of the requirement for the degree.

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"Words are failing short in expressing feelings"

When one writes, one pours one's soul out on paper. They say it takes courage to do that. They also say that courage comes only when one knows that many stands with him, I'd like to acknowledge those who stand with me: Who gives me courage: Who make me realize that I am not alone.

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"Words provide the wings to our ideas but
Sometimes it is very difficult to express the feelings in words and languages"

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ADARSH V S

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LIST OF ABBREVIATIONS AND SYMBOLS USED

AMMI	Additive Main effect and Multiplicative Interaction
ANOVA	Analysis of variance
cm	centimeter
Cul	Culture
d.f	degrees of freedom
et al.	Co-workers
etc	et cetera
Fig.	Figure
g	gram
GxE	Genotype X Environment
i.e.	that is
kg ha^{-1}	Kilogram per hectare
No.	Number
PC	Principal component
PCA	Principal Component Analysis
RBD	Randomized Block Design
SPSS	Statistical Package for Social Sciences
t ha^{-1}	Tonnes per hectare
UPGMA	Unweighted Pair Group Average Method
WPGMA	Weighted Pair Group Average Method
%	Percent

Introduction

1. INTRODUCTION

Rice ***(****Oryza sativa* L.) from the *Poaceae* (Graminae) family is one of the most important food crops in the world which originated in India. It acts as a source of food for over 80 percent of Asian population. In the crop year 2018-2019, about 486.62 million metric tonnes of rice was consumed worldwide. India had the largest harvest area under rice (43.79 million hectares) in the 2017-2018 year, and it plays the important role for food security and sovereignty in the country (Shahbandeh, 2020). Further it is being considered as an integral part of the human tradition used in rituals and ceremonies connected with birth, marriages and funerals from ancient times. It is an essential constituent of daily diet of people in the southern and eastern parts of India to provide 20 per cent calories (Chaudhary *et al.*, 2001). As per the United States Department of Agriculture (USDA) nutrient database, on consumption of 100g of rice, would provide an energy of 365 Kcal thus becoming an important source of energy. It also provides vitamins like Thiamine (Vit.B_1), Riboflavin (Vit.B_2), Niacin (Vit.B_3), Pantothenic acid (Vit.B_5) and minerals like Calcium, Magnesium, Iron, Phosphorus, Zinc etc. to the world population. Rice, being primarily composed of carbohydrates (79 g), with higher amount of dietary fibre (1.3 mg) and almost negligible amount of fats (500 mg) per 100g.

Rice is grown extensively in tropical and subtropical regions of the world. It is cultivated as a monocrop during *Kharif* season under rainfed conditions in two different topographical locations *viz.*, uplands and lowlands. It normally grows in temperature between 20°C to 35°C and the height of the plant normally varied from 0.3 to 0.4 m for dwarf mutants and more than 7 m in some of the floating varieties. However, majority of the commercial varieties have a height of 1 to 2 m (Tzu and Eliseo, 1965).

Conventionally, the rice cultivation has occupied a pride place in the agrarian economy of Kerala and is the staple food for the people of the state. One of the most appealing features of Kerala's landscape is the lush green paddy fields. The area under rice cultivation was 2.02 lakh ha with a production of 5.78 lakh tonnes and productivity of 2850 kg ha^{-1} respectively during the year 2018-2019. Paddy fields are

a vital part of Kerala's environment and ecological systems and it provides natural drainage paths for flood waters conserve groundwater and are crucial for the preservation of a rich variety of flora and fauna. Paddy cultivation is carried out in such a way in several regions of Kerala so that the cultivation enriches their specific geographical and ecological features. For instance, *kaipad* fields in Kattampally, Kannur district where the paddy is traditionally grown in fields filled with saline water. Farmers are practicing alternate cultivation like prawn production in the *pokkali* fields in the Ernakulam district. A similar type of alternate cultivation is following in the *kole* fields in Thrissur and Ponnani, paddy fields in Meppayar in Kozhikode and Kabani in Wayanad.

Though many rice varieties have been released as national varieties, only few of them are showing stable performance and continue to be under cultivation even after several years of their release. Therefore, performance trials, multi-location trials and seasonal trials need to be done frequently before the release of a promising rice genotype as national variety to recommend them to the farmers as the end users.

The rice varieties developed through several crop improvement methods will eventually be planted in farmers' fields in different environments in the same season as well as in different seasons to check their stability. The results of these trials often reflect differences in grain yield in each season and the highest yield of a genotype in one season often showing its inconsistency in other seasons also (Chen *et al.,* 2019) This is because of the interaction between genotypes and environment, making it hard for plant breeders in choosing the best genotype. So, analysis is usually performed to recommend stable genotypes for specific environments as well as for different environments.

Some varieties of the crops are broadly adapted while others are not. An adapted genotype is one which survives the pressure of selection by revealing an improved performance. Adaptability is the capacity for genetic response to select and depends upon the provision of inconsistency (Mather, 1943). Plant breeding is the present stage of evolution in which the breeders attempt to develop progressively well adapted populations to the existing or altered environments.

Allard and Bradshaw (1964) classified the environments into predictable and unpredictable environments. The predictable environment comprises the eternal structures of environments such as climate, soil type and day length. It also includes all the controllable variables. While an unpredictable environment comprises weather variations such as alterations between seasons in terms of the quantity and distribution of rainfall and the prevailing temperature. For the uncontrollable variables, a low level of interaction would be desirable between the variables so as to have the maximum homogeneity of performance over a number of seasons.

The various parametric methods for estimating the stability of genotypes over environments are given by Yates and Cochran (1938), Plaisted and Peterson (1959), Wricks (1962), Finlay and Wilkinson (1963), Eberhart and Russell (1966), Perkins and Jinks (1968) and Freeman and Perkins (1971). A non-parametric approach was proposed by Huehn (1990) based on the rank of the genotypes in each environment. This method helps in easy computation of data than the classical methods.

In various research programmes, it is quite common to carry out the same experiment at a number of different locations, on several seasons or years. In agricultural and animal husbandry experimentation, many projects are being undertaken by keeping a view that their results can be applied in actual field condition. A single experiment will precisely furnish information about only one place or one season in which the experiment is conducted. So repeated experiments need to be conducted at different places or over a number of years to obtain the valid outcomes. In such cases of repeated experiments appropriate statistical procedures like combined analysis of the data would have to be followed. In pooled analysis, the main points of interest would be to estimate the average response of varieties and to test the consistency of the responses from place to place or occasions to occasions.

The enactment of genotypes is examined by statistical models developed to describe and interpret the genotype x environment interaction. These analyses should provide an estimate for parameters that indicate both how well the genotypes will perform on an average across the environmental range and how well they perform to specific environmental conditions, over the years and over the seasons.

In this context the present the study on ‘Comparative analysis of different stability models on superior cultures of paddy (*Oryza sativa*)’ was undertaken with the following specific objectives.

1. To compare various linear and nonlinear stability models to identify stable superior cultures of paddy.

2. To study the clustering pattern of cultures over the years.

In response to fulfil the objectives of the study, secondary data from the yield evaluation trails of thirteen cultures of paddy was collected from Regional Agricultural Research Station (RARS), Pattambi. The main five characters *viz.,* plant height (cm), number of panicles per plant, straw yield (t ha^{-1}), grain yield (t ha^{-1}) and 100 grain weight (g) were chosen for the study. The four stability models were used for the comparative analysis (Eberhart and Russell’s model, Perkins and Jinks model, Freeman and Perkins model and AMMI model). The cluster analysis was done by hierarchical clustering techniques with Euclidean distance as the measure of similarity.

1.1 SCOPE OF THE STUDY

This study predominantly aims at a comparative analysis of different stability models used in plant breeding programmes. In most of the cases only the Eberhart and Russell model is used to identify the stable genotypes while other models are rarely adopted. So, by this comparative study we will be able to compare the results obtained from each model in relation to the stable genotypes and any variations in the stability of the crop. Moreover, a comparison of results based on the recently developed AMMI models is also made.

1.2 LIMITATIONS OF THE STUDY

Owing to paucity of time, funding and resource availability, the study was limited to the investigation on 13 cultures of paddy only. These cultures were used in yield evaluation trials by RARS, Pattambi during 2015-18. Also, the secondary data utilised for this study may be prone to possible errors owing to errors at primary

recording stage. However, adequate care has been taken to clean the data for suitability for statistical treatment and earnest efforts has been carried out to bring out reliable results.

1.3 PRESENTATION OF THE THESIS

The present study contains five chapters namely, introduction, review of literature, materials and methods, results and discussion and summary. In the first chapter introduction, the importance, objectives, scope, limitations and future aspects of the present study are included. Review of the past works related to the current study is included in the second chapter. Third chapter describes various statistical methods and techniques used to analyse the data. The inferences drawn from the analysis are explained in the fourth chapter on results and discussion. Summary of the entire research is presented in the last chapter followed by references and abstract.

1.4 FUTURE PROSPECTS

The present study is focussed on the comparison of stability models based on only one character (grain yield). This can further be extended to other characteristics. The experiment emphasizes the advantages of field experiments and research trials in all agricultural and allied subjects. Similar studies should also be taken for other crops as well as for different varieties (cultures) along with varying environmental conditions to give a complete picture about the best stable genotypes.

Review of literature

2. REVIEW OF LITERATURE

In this chapter, an inclusive review of published literature has been presented so as to comprehend the concepts considered and technique followed in past studies. This would support the researchers to navigate the study in the correct direction, collect the appropriate data and to draw eloquent results out of it. This will also visualize addressing the gap in literature. Taking into consideration the objectives of the study, the reviews are presented chronologically and under the following headings.

2.1 Stability models

2.2 Cluster analysis

2.1 STABILITY MODELS

Finlay and Wilkinson (1963) defined and represented the environment, measure in terms of 'site-mean'. This study composed of 227 varieties of barley, grown in seven environments and concluded that the component of genotype x environment interaction was linearly related to environmental effects and suggested two parameters of stability of genotypes: (a) means performance and (b) the regression coefficients (linear response) associated with each genotype. Under this method an ideal variety was inferred as the one which on account of regression coefficient and its value should be one, combining maximum potential in the most favourable environment with low Genotype x Environment interaction through consistency of high performance over environments.

Eberhart and Russell (1966) updated the Finlay and Wilkinson's model and suggested three stability parameters *viz.,* means, regression coefficient (linear sensitivity) and deviation from linearity (nonlinear sensitivity) to describe varietal performance over time and space and suggested that both linear and nonlinear functions should be considered while judging the phenotypic stability of genotype.

The Perkins and Jinks (1968) approach is based on fitting a model which specify the contributions of genetic, environmental and G x E interactions to the general means and variances allowing for the contribution of additive, dominance and

epistatic gene effects to the genetic and interaction components. The stable variety rendering to this method is one which has high mean, regression coefficient and least mean square deviation from regression.

Freeman and Perkins (1971) put forward a method involving traditional analysis of variance based on basic biometrical model and joint regression analysis to understand the relative involvement of linear and nonlinear components to G x E interactions. This method also gave correct partitioning of sum of squares. A variety with, regression coefficient around unity, least mean square deviation from regression (around zero) and high mean was measured as a stable one in this method.

Gabriel (1971) was the first to develop the concept of biplot with the application of principal component analysis. The biplot being a useful tool of data analysis allows the visual assessment of the structure of large data matrix. It shows inter unit distances and indicating clustering of units as well as displays the variances and correlations of the variables.

Arora *et al.* (1982) conducted different evaluation trials on tomato varieties during summer season. The results of the analysis concluded that HS-102 gives early fruit set along with highest early and total yield during all three seasons.

Gauch and Zobel (1988) analysed the performance of AMMI analysis using ANOVA and regression approach regression approach and it was clear from the study that, if there is a specific regression model, then the regression could detect significant interaction component, whereas ANOVA could not.

If changes in environment lead to a variation in differences between a number of genotypes, then genotype x environment interaction said to exist. It is decisive from the existence of this interaction that, it is not possible to select a genotype from single environment. Instead evaluation at different environments are required (Ceccarelli, 1989).

Yield stability of 14 medium advanced lines of rice was done by Ali *et al.* (1992). Values of regression coefficients for average yield on the environmental index varied from -0.17 to 2.06, whereas that of coefficient of determination was 0.02 to

0.95. From the study it was evident that, PK 3717-9, PK 3717-12 and PK 3849-18 showed yield stability over the 3 environments, whereas PK 3727-2 and PK 3727-5 were unstable for yield.

An assessment of grain yield stability in pearl millet using 45 genotypes was done by Mahalakshmi *et al.* (1992). These genotypes which include pollinators and topcrosses were grown at three locations (ICRISAT, Anantpur and Fatehpur) during 1988, 1989 and at Hisar in 1989. It was concluded that in improved environmental conditions, top crosses were more responsive compared to their pollinators using Eberhart and Russell model.

Prajapathi (1994) compared some stability models using nine genotypes of pearl millet. They were screened under four weed management methods like no weeding, hand weeding and herbicide at two levels. The features like grain yield, dry fodder yield, plant stand, plant height, ear head length and weed counts at the time of harvest were recorded and analysed. Eberhart and Russell and Perkins and Jinks models showed similar ranking pattern of genotypes based on stability parameters, whereas a different pattern was noticed in Freeman and Perkins model. Precision and computation convenience were found to be good in Eberhart and Russell model. The environment-wise analysis showed variable response of genotypes to weed control treatments. For no weeding and hand weeding environments, GHB 229 was found to be the high yielding and stable genotype, whereas in herbicide application for weed control conditions, it was MH 179. But sensitivity to the environment and the relative mean performance should be evaluated for breeding purpose.

Twenty-eight rainfed rice genotypes were studied by Vivekanandan and Subramanian (1994) for understanding their adaptability and stability. It was found that there are significant mean differences due to genotypes and genotype-environment interactions which indicate that genotype differ in their stability and adaptability. The pooled deviations were also significant for all the characters studied, indicating that the genotypes differed in their deviation from linearity.

Gauch and Zobel (1996) proposed AMMI (Additive Main Effects and Multiplicative Interaction) as a statistical method to understand genotype –

environment interaction and to gain accuracy and improve selections of stable genotypes for the trials repeated over locations (or years or both).

Kumar (1997) studied thirty-four genotypes in rice over three seasons *i.e.,* dry, wet and winter using Eberhart and Russell model. There observed a G x E interaction for all the characters studied and were attributed by both non-linear and linear components. Genotype KBCP 1 was observed to be suitable for all environments, whereas Jaya, HP 10 and IR 54R were found to be suitable for dry and wet environments. The genotypes Mukti and IR 54R were found to be stable but their performance was unpredictable.

Abamu *et al.* (1998) evaluated 25 rice genotypes across six locations using AMMI analysis to identify genotypes resistant to rice blast and reported that four improved upland varieties (IRAT 13, LAC 23, ITA 257 and ITA 235) and three improved lowland plant types (ITA 116, ITA 118 and ITA 120) showed high and stable resistance to blast.

Phenotypically stable genotypes are of great importance, because the environmental condition varies from year to year/region to region. Although a number of varieties have been recommended for the cultivation, the information on the stability is lacking for the agro-climatic conditions. So, there is a necessity to evaluate and screen the potential genotype giving consistent performance over different years and to select the genotypes on the basis of stability parameters for important yield and maturity attributes (Kalloo *et al.,* 1998).

Nine genotypes of grain Amaranthus were evaluated for stability of ten characters (Waghmode *et al.,* 1998). The three regression models were used for estimating stability parameters. Genotype, Environment and Genotype X Environment interaction variances were significant almost for all the characters. Similar results were shown by Eberhart and Russell and Perkin and Jinks analysis. Eberhart and Russell model was reliable and easy for handling and analysis of data. Even if Freeman and Perkins model was more precise, yet it has the disadvantage of being more laborious and complex. Eberhart and Russell and Perkins and Jinks models were more effective for selection of stable genotypes of Amaranthus.

Seven rice genotypes for the evaluation of stability of yield and its components for growing in wet season was studied over four years during 1993-96 at Igatpuri, Maharashtra. Both the component of G x E interaction was significant, but the linear component was prime for number of panicles per square meter, grains per panicle and panicle length. The linear component for grain yield was significant in only one genotype, while the non-linear component was significant in three genotypes, indicating the preponderance of nonlinear G x E interaction for this trait (Chaudhari *et al.*, 2002)

Kumar (2003) evaluated the stability of 44 rice genotypes across five environments by using AMMI model. The analysis of the study observed that the genotypes *viz.*, R3270-300, IR42342, R574-11, Mahamaya and IR-36 showed stable performance for high yield in almost all the environments, while CT9897-55-2-M-3 performed well only at one site. The genotypes, Safri 17 and NSG19 were found adapted to environments with rapid onset of late drought condition.

Swamy and Kumar (2003) found that variance due to genotypes, environment and genotype x environmental interactions were significant for most of the characters studied. A linear relationship between mean performance and environment index was observed. An ample portion of genotype x environmental interaction (linear) was significant for all the characters except days to 50 per cent flowering, 100- grain weight and yield per hectare. Considering all the stability parameters, PSP-87, PSP -14-2-3 and Arkavathi among the selections and IR-20, Java, Mandya Vani and Mandya Vijaya had better stability over the environment. Among genotypes PSP -4-2-3, PSP-87 and IR- 20 are stable for yield. Based on the stability parameters and overall mean PSP-87, PSP 4-2-3, Arkavathi, IR-20, Java, Mandya Vani and Mandya Vijaya were identified as elite genotypes in this study.

Alberts (2004) analysed nine late maturing maize hybrids and fourteen hybrids with ultra-short to medium maturity under dry land conditions across forty two environments for Genotype X Environment interaction (GEI) and yield stability. AMMI model was used to explain Genotype X Environment Interaction (GEI) and adaptation to certain environments. A significant difference between hybrids and

environments was observed *via*., AMMI model2 combined analysis of variance. 68% of the total G x E interaction was accounted by IPCA 1 whereas, IPCA 2 accounted for 32 percent of the interaction. From the study it was found that AMMI model 2 was the best fit for the data. DKC 80-10 and CRN 4760 were adapted to higher yielding and lower yielding environments respectively. A specific adaptation to certain environments was observed in CRN 3505.

Kumar *et al.* (2004) studied fifteen characters of twenty-five genotypes of rice under four environments for genotype X environment interaction. They observed significant genotype x environment interaction for plant height at sixty five days after sowing, plant height at harvest, days to 50 percent flowering, test weight, gram yield, biomass, harvest index, kernel L B ratio, hulling percent and milling percent and non-significant G X E interaction for productive tillers per plant, gram elongation ratio and protein content. The genotypes PR106, NLR 145 and JGL 3S4 were found to be stable for biomass and MTU-7029 and MTU-2716 were stable for grain yield.

Venugopalan and Gowda (2005) described the statistical considerations in different approaches used for developing stability models in vegetable crops where they used three years (2001-03) of yield and yield related biometrical characters data on eleven promising genotypes of onion grown at the experimental plot of Bangalore. Efforts have been made to develop suitable stability models with a view to identify stable genotypes suitable for commercial exploitation in wide range of environment The study concluded that Freeman-Perkins model was significantly efficient and helps the breeders to minimize the information loss on ideal lines to the extent of 40 percent as compared to the routine Eberhart and Russell method for estimated bulb yield per hectare.

Francis *et al.* (2005) observed G X E interaction for grain yield and other yield attributes in seven rice cultures and two local checks under three different ecological situations of Kerala. Significant G X E interaction were observed for many traits. Among the linear and non- linear components of G X E interaction, linear component was predominant for days to 50 percent flowering, volume expansion ratio and head rice recovery suggesting variation in the performance of different cultures grown over

environments could be predicted. Based on stability parameters, culture C 26T (b) was identified as the stable culture for grain yield in three different ecological situations of Kerala.

Gauch (2006) conclude that relatively new additive main effects and multiplicative interaction (AMMI) model has helped to obtain accurate yield estimates, reliable selections and efficient designs, and helped in the understanding or modeling of complex data sets. AMMI yield estimates are routinely as accurate as raw means based on 2 to 4 times as many replications and are applicable to all crops in all environments.

Mahalingam *et al.* (2006) tested six short duration rice genotypes over fifteen environments in different blocks of Ramanathuram district of Tamil Nadu. AMMI analysis indicated a significant genotype x environment interaction that influenced the relative ranking of the varieties across the environments. As per the AMMI model, three genotypes RM96019, AD00119 and AD99111 were identified as having general adaptability.

Kumar and Shadadshari (2007) evaluated fifteen rice mutants of P. U. Belliyappa local for the stability of yield and yield components in *Kharif* season during 2002 to 2004 using Eberhart and Russell model. Both the components of genotypes x environments interaction were significant, representing that the major portion of interaction was linear in nature and forecast over the environment was possible. Significant pooled deviations observed for all the traits, advocated that there is a sizable genotypic difference. Based on the stability parameters, rice mutant PUBM-8 exhibited higher mean gram yield, regression coefficient near unity and deviation from regression was low. PUBM- 24 had higher mean gram yield with reduced plant height, and it is profound to environments.

Shanthi *et al.* (2007) evaluated twenty black gram genotypes over three seasons from *Rabi* 2001 and 2003 and *Kharif* 2002. Out of nine entries four were having higher yield per plant and lower CV values. Out of these VBG 89, VBN (Bg) and VBG 62 have recorded higher mean yield per plant, average responsiveness to season and stability.

A combined analysis of genotype x environment interaction and seven AMMI stability statistics was undertaken for stability analysis and to identify stable genotypes of eleven lentil genotypes across twenty environments (Sabaghnia *et al.,* 2008). Differential responses of the genotypes were obtained from the combined analysis of variance for environments (E), genotypes (G) and G X E interaction was highly significant ($P < 0.01$) which calls for the stability analysis. According to them the stable genotypes were ILL6037 and FLIP 82-1L under parametric stability measures of environmental variance and priority index measure respectively. The first two PC axes cumulatively accounted for 71 percent of the total G X E interaction in the significant first seven principal component (PC) axes ($P<0.01$). While genotype FLIP 92-12L was found to be the more stable genotype having high mean performance when considering the AMMI stability value.

Statistical models for stability analysis in watermelon was developed Venugopalan and Pitchaimuthu (2009). Freeman and Perkins (FP) and Eberhart and Russell (ER) model were utilized for carrying out stability analysis research. They came to a conclusion that breeders may exploit the use of Freeman-Perkins approach for performing stability research.

Hassanpanah and Azimi (2010) conducted studies with the objective to determine the yield performance and to assess the yield stability of the twelve cultivars of potato in spring cultivation and after barley harvest cultivation by using the AMMI statistical model applied to the data from a two years study. The analysis of variance for the AMMI model of tuber yield showed that type cultivation, cultivars and their interaction and AMMI component were significant.

Pabale and Pandya (2010) were made use of twenty-four genotypes of pearl millets to compare the stability models namely, Eberhart and Russell, Perkins and Jinks and Freeman and Perkins. The study was conducted in *Kharif* 2007 using Randomized Block Design (RBD) with three replications. For the study the parameters like, grain yield, fodder yield, days to 50 percent flowering, days to maturity, final plant stand, plant height, number of effective tillers per plant, ear head weight, ear head length and 1000 seed weight were considered. AMMI analysis was

used for the identification of stable and adaptable genotypes as well as for estimating the magnitude of G X E interaction. The genotypes GHB-788, GHB-832 and GHB-840 were identified as the adapted ones. Among the models, Eberhart and Russell model was considered as better one. It was also observed that, Eberhart and Russell and Perkins and Jinks models were similar in ranking pattern of genotypes based on stability parameters like, regression coefficients and deviations from regression. Whereas Freeman and Perkins model showed a distinct pattern.

To assess the stability and yield performance of advanced finger millet genotypes Lule *et al.* (2014) evaluated thirty finger millet genotypes along with two standard checks (Gute and Taddese) across four locations (Arsi Negele, Assosa, Bako and Gute) in 2012 and 2013 main cropping seasons. The trial was arranged in a Randomized Complete Block Design (RCBD) replicated three times. AMMI, Genotype and Genotype by Environment interaction (GGE) biplot analysis and Eberhart and Russell model were used in the study. The results revealed that Acc. 203544 is stable high yielding with yield advantage of 13.7 percent over the best standard check, Gute and thus should be recommended for possible release with wider environmental adaptability. Whereas, Acc. 242111, Acc. BKFM0051 and Acc.229738 were the second to fourth high yielding respectively showed narrow stability.

Swarup and Singh (2014) carried out experiments in rabi season for consecutive three years *viz.,* 2007-08, 2008-09 and 2009-10 with twenty-eight genotypes of safflower. The observations were recorded on days to 50 percent flowering, days to maturity, plant height, branches per plant, capitula per plant, seeds per capitulum, hull content, 100 seed weight, seed yield per plant and harvest index. Analysis of variance revealed highly significant differences among genotypes for all the characters during all the three years. Non-significance of chi-square value suggested that the error variances were homogenous for all the traits under study. Pooled analysis indicated that the genotypes and environments differed among themselves and the genotypes showed differential performance over varying environments i.e., years per locations. The stability analysis as per the Eberhart and Russell model suggested the existence variability in the experimental materials and all the three environments differed significantly among themselves. Stable performance

was exhibited by the genotypes JSI-124 and JSI-135 for seed yield per plant and JSI 134 for earliness in maturity.

Stability of five elite chickpea genotypes and three check varieties were studied by Balapure *et al*. (2016). RBD with three replications was adopted in the study. The AMMI analysis of variance for seed yield indicated a broad range of diversity among genotypes. Significant value of G X E mean sum of square indicated that the genotypes performance was different over the environments. Three genotypes *viz.*, Phule G-07102, Phule G-09103 and Digvijay showed stable performance over all environment (non-interacting) for seed yield kg per plot. It was also noticed that all genotypes produced stable seed yield in three environments namely, E3 (sowing date 1/11/2011), E4 (sowing date 16/11/2011) and E5 (sowing date 1/12/2011).

Stability of the twenty genotypes of pigeon pea was evaluated in the three year trial was conducted in Kalaburagi, Karnataka under rainfed condition (Ramesh *et al.*, 2017). Highly significant differences among varieties were observed for all the characters except for pod bearing length (cm), number of pods per plant and seed yield. Significant variance was observed for the characters like number of seeds per pod and pod length in the case of Genotype X Environmental interaction. There were no significant differences for 100 seed weight in different environment. There was no marked difference for traits like primary branches, pod length and number of seeds per pod while high significance in the variance due to pooled deviation for all other characters. ICP-13270 were found to be a stable genotype for pod length and ICP 9691 and ICP 12654 were on par with check for seed yield across the environments for rainfed conditions.

Mean performance and stability of cultivars were evaluated by Jain *et al.* (2018) using twenty-two basmati rice genotypes using AMMI and GGE stability models under four different environments *viz.*, direct seeded (wet and dry), indirect seeding transplanted rice and system of rice intensification (SRI). Under SRI, genotypes like Pusa Basmati 6, Pusa Sugandh 3, Haryana Basmati-1 and Pusa RH 10 were identified stable for days to 50 percent flowering. Whereas, CSR-30 under DSR

(dry) and DSR (wet) and HKR 98–476, Pusa Sugandh 2 and Pusa Sugandh 5 under TPR conditions.

Highland adapted rice genotypes stability was studied by Rahayu (2020). The AMMI analysis found that ICN10-111, ICN-20-124 and RB-10-98 mutant lines were the most stable genotypes across environments evaluated. Specifically, the mutant lines like C430-21, RB-10-95 and ICN- 20-127, and ICK-10-249, in 700 and 900 m above sea level area respectively. In the rainy season, mutant line PK-20-133 showed high stability in 1200 m above sea level while OS-30-199 and Sarinah for dry season with low temperatures stress.

2.2 CLUSTER ANALYSIS

Clustering technique which is a multivariate procedure has shown rapid improvement only after 1950's. A number of algorithms have been developed in order to classify a group of objects into smaller groups of objects of similar character (Singh *et al.,* 2002).

Sneath and Sokal (1973) characterized the clustering methods into hierarchical or non-hierarchical, divisive or agglomerative and polythetic or monothetic.

Hardle and Simar (2007) stated that cluster analysis as a set of tools for building groups from multivariate data and it is divided into two fundamental steps, which include choice of proximity measures and the choice of group building algorithm.

2.2.1 Proximity measures

Cluster analysis attempts to identity the observation vectors that are similar and group them into clusters, many techniques use an index of similarity or proximity between each pair of observations. A convenient measure of proximity is the distance between two observations. Therefore, similarity measure is defined as the measure of distance between various data points of objects. Distance between two units increases

as they become further apart. Similarity represents the strength of relationship between items or objects.

Jaccard (1901) introduced a similarity coefficient for binary data often referred as Jaccard's coefficient in which all terms have equal weight.

Mahalanobis (1936) introduced a statistical measure for group distance based on multiple characters called D^2 distance. It is a relative measure of a data point's distance from a common point. It is mostly used for quantitative data and they are unitless in nature.

Dice (1945) developed another method for qualitative data which do not consider negative matches and gives double weight to unmatches, commonly used in the case of binary data sets.

Euclidean distance is the ordinary straight-line distance between two points (Anton and Howard, 1994). It gives greater weight on the objects that are farther apart. The Euclidean distance between two points is the length of line segment connecting them.

Minkowski distance can be used for variables that are both ordinal and quantitative in nature (Prasad, 2007). It is also known as the generalized distance metric.

Hair *et al.* (2015) listed four different distance or dissimilarity measures such as Euclidean distance, Squared Euclidean, City block distance and Mahalanobis for continuous variables.

2.2.2 Clustering techniques

Clustering techniques are used to generate different clusters. The commonly used clustering techniques fall into two general categories, Hierarchical clustering and Non-hierarchical clustering (Davidson, 2002).

Hierarchical clustering works to divide or merge a particular dataset into a sequence of nested partitions or clusters. The hierarchy of these nested partitions can be of two types, viz., agglomerative hierarchical clustering or divisive hierarchical clustering (Johnson and Wichern, 2006).

Non-hierarchical clustering technique assigns data points to a cluster such that the sum of the squared distance between the data points and the cluster's centroid is at the minimum. It allows the reallocation of items to clusters that is not available in the hierarchical clustering methods (Cambridge, 2009).

2.2.3 Clustering methods

Complete linkage method proposed by Sorensen (1948) is an agglomeration which involves fusion of two clusters depending on the most distant pair of objects. This method is also known as farthest neighbour clustering.

Rao (1952) advanced a method which is extensively used in clustering quantitative data based on their distances calculated as D^2 values using Mahalanobis distance. This method is mainly based on the average D^2 values between the objects or data points.

Single linkage method proposed by Sneath (1957) is a clustering method opposite to that of complete linkage. The fusion of two objects depends on the minimum distance (nearest neighbour).

Ward (1963) proposed a clustering method which is related to the centroid method. It uses analysis of variance approach to evaluate the distance between the clusters based on minimizing the loss of information from joining two groups. This method is also called the incremental sum of squares method.

Sneath and Sokal (1973) developed four different clustering methods which rely on average similarities among objects and on centroids of clusters. Unweighted Pair Group Average clustering (UPGMA) and Weighted Pair Group Average clustering (WPGMA) depends on the arithmetic average while Unweighted pair group

centroid clustering and Weighted pair group centroid clustering depends on the centroid.

Hartigan (1975) found that the k-means algorithm produces a clustering which is only locally optimum. The within-cluster sum of squares may not be decreased by transferring an object from one cluster to another, but different partitions may have the same or smaller within cluster sum of squares. Usually less than 10 iterations are required to attain local optimality.

2.2.4 Application of cluster analysis in agricultural studies

Lin and Thompson (1975) attempted cluster analysis when there was G X E interaction analysis and showed that this approach obviously depends on the efficiency of linear regression in modelling genotypic response.

In maize hybrids for studying the stability, Johnson (1977) used cluster analysis with the weighted Euclidean distance as measure of similarity.

Vanangamudi *et al*. (1988) classified eighty-five rice varieties using cluster analysis based on colour of hulled grain, vitreous characters, length, shape, profile value (width), 100 grain weight, presence or absence of pearl spots and shape of pearl spots.

Mahalanobis D^2 statistic was applied on fifty rice genotypes based on nine quantitative characters (Bharadwaj *et al*., 2001). Mean of five randomly selected rice plants of each genotypes were used for the analysis. Metroglyph analysis was also conducted and pen circles were used for Indian genotypes and solid clusters were used for foreign genotypes in order to distinguish between them. Tocher's method was followed to obtain clusters. ANOVA indicated that there was significant difference among the clusters. Cluster 1 had twenty-seven genotypes which was maximum when compared to other clusters.

Guler *et al*. (2002) compared different multivariate methods like K- mean clustering, PCA, hierarchical clustering etc. for the classification of water chemistry

samples into different groups. A total of 118 samples and eleven chemical variables was subjected to the analysis after the removal of unimportant variables and outliers. Ward's method along with Euclidean distance was used to group the samples into homogeneous sets. Dendrogram classified 118 samples into three clusters. Results of HCA showed that cluster 1 samples had high TDS which was significantly different from all other clusters.

Misra *et al.* (2004) studied genetic divergence of 116 germplasm lines of semi-dry water ecology of rice. Based on the results, nine clusters were obtained for the genotypes. Among the clusters I and III observed to have more genotypes i.e. 48 and 36 respectively. A single genotype was included in cluster VI, VII and VIII. Greater divergence was noticed in cluster IV, VI, VII and VIII. Parents for intra population improvement were selected from cluster IV, VIII and VII.

Mahalanobis D^2 statistics was used by Chand *et al.* (2005) to study their genetic divergence using nineteen genotypes of *Aman* rice. Among the six clusters obtained, Cluster I included eight genotypes followed by cluster II with four genotypes. Highest inter cluster distance was observed between these groups.

Chaturvedi and Mourya (2005) made use of Mahalanobis D^2 to analyse the nature and magnitude of genetic divergence in 35 rice genotypes and groped them into eight clusters. It was identified that the genotypes in cluster VII can be used as a parent in hybridization program.

Senapati and Sarkar (2005) studied genetic divergence of forty tall *Indica* rice genotypes and were grouped into five clusters. Cluster I included 30 genotypes. There occurred maximum genetic distance between cluster IV and cluster V. Genetic divergence was highly contributed by panicle length and 1000 grain weight.

Luthra *et al.* (2009) evaluated thirty-four potato genotypes for tuber yield and its components at two harvesting dates in early and main crops during two succeeding crop seasons for detecting stable genotypes. In early crop *K. Surya* and in the main crop *K. Arun*, *K. Satlaj* and *MS/97-621* were found responsive for total tuber yield. The genotypes *CP 3359*, *MS/93-1344*, *MS/94-899* and *MS/98-6955* were found

preferably stable for tuber yield over the environments. *CP 3359* was an ideally stables genotype for tuber yield components across the environments.

Praveen *et al.* (2012) studied genetic divergence of thirty aromatic rice accessions which included fifteen improved varieties depending on their nature and magnitude of diversity. Tocher's canonical (vector) and Euclidian methods were adopted for divergence analysis and it found the presence of appreciable amount of genetic diversity in the material. Using these methods, genotypes were grouped into six clusters. JGL 15336 × Taroari Basmati for effective tillers per plant, Badsabhog × Rajendra Kasturi for filled grain per panicle, JGL 15336 × Birsamati for grain weight per panicle and Gandhasala × Pusa Sugandha-3 for leaf area index were identified as the most diverse parent combinations for grain yield by 3D diagram of PCA scores and Euclidean distance matrix. These genotypes also proposed as potential donor for breeding programs.

Genetic divergence of 470 genotypes based on nineteen characters was assessed by Prasad *et al.* (2013). The method of Euclidean squared distances grouped the genotypes into eight clusters. It was noticed that most of the genotypes of one cluster were adapted to only one region. Closeness between the clusters were revealed from the clustering pattern and it also indicated the geographical adaptation of the genotypes.

A study was conducted for the performance assessment of 49 flax varieties based on their thirteen agronomic parameters using clustering technique. Assessing the variability of a large no. of varieties was also possible by means of clustering. Dissimilarity measure used as Euclidean distance. Four clusters were obtained in which 1st cluster had high oil and seed yield and hence good for seed production (Bakry *et al*., 2015).

Clustering quality has been influenced by different distance measures used for grouping the objects. Average measure and Euclidean distance were found to be the best methods among the similarity measures. Performance of similarity measures varies for low and high dimension data set (Shirkhorshidi *et al*., 2015).

Devi (2018) studied genetic divergence of twenty rice genotypes using fifteen characters. Presence of sufficient genetic variability in the material was revealed from the ANOVA itself. Same was also depicted by the D^2 analysis. Out of the five clusters, maximum number of genotypes was present in cluster I (9) followed by cluster II (6) and cluster IV (3). Clusters III and V were solitary clusters. It was also noticed that inter cluster D^2 values were greater than intra cluster D^2 values. The maximum inter cluster D^2 values was observed between cluster II and V (444.87) followed by cluster I and V (267.50). Based on the characters studied, hybrid S-8001 was found as the superior one.

2.2.5 Comparison of clustering methods and cluster validation

A comparison of seven hierarchical clustering methods based on the association between the inlet dissimilarity values and equivalent distance values attained from the ultimate clustering pyramid (Cunningham and Ogilvie, 1972).

The evaluation of clustering algorithms using an internal evaluation scheme is the Dunn index (DI), where the result is based on the clustered data itself. It helps to identify sets of clusters that are compact, with a small variance between members of the cluster, and well separated, where the means of different clusters are sufficiently far apart, as compared to the within cluster variance. The clustering efficiency increases when the DI value rises. (Dunn, 1974).

Six hierarchical clustering procedures (single linkage, complete linkage, median, average linkage, centroid and Ward's method) were analysed for multivariate normal data. In their study with unequal cluster size, centroid and average linkage method evolved the best and with equal cluster sizes Ward's method and complete linkage method were found to be the best respectively (Kuiper and Fisher, 1975).

The comparative study on four types of hierarchical clustering methods (single linkage, complete linkage, average linkage and Ward's method) by Blashfield (1976) reported that Ward's method performed significantly better than the other clustering procedures and average linkage gave moderately poor results.

An internal evaluation scheme for evaluating clustering algorithms is Davies–Bouldin (DB) index (Davies and Bouldin, 1979), where the validation of how well the clustering has been done is made using quantities and features inherent to the dataset. The clustering efficiency increases when the DB index value decreases.

Halkidi *et al*. (2002) listed out several cluster validity measures and mentioned that evaluating the clustering algorithm is an important aspect as it is an unsupervised process. As there are no predefined classes it is difficult to find out the appropriate method for clustering of objects.

Cluster validation gives the quantitative evaluation of the result of clustering algorithm. The validation techniques are categorized into internal, external and relative cluster validation techniques. Internal validation measures rely on the compactness, the connectedness and the separation of the cluster while the external validation compares the clusters to an external reference (Theodoridis and Koutroumbas, 2003).

Being unsupervised process cluster analysis need an evaluation of the results of clustering procedures. Cluster validity is meant by identifying the clusters that best fit the data. Davies- Bouldin index is a measure whose value should be minimum for optimum clusters (Legany *et al.*, 2006).

Tarpey (2007) studied several clustering methods which focused on k-means clustering and analysed the effects on the clustering outcomes based on how the observed data were smoothed. From the results it was understood that there is a relation between clustering on functional data and how well the smooth curves fit the raw data. Best smoothing method was determined by true mean curve of each cluster.

Performance of various hierarchical methods like single linkage, complete linkage, average linkage and Ward's method for clustering the data was studied by Ferreira and Hitchcock (2009) using Rand index. The study found Ward's method as the best one, whereas average linkage is also good in some special situations especially when the number of clusters were over detailed.

Comparison of proximity measures viz., Jaccard, Dice, Simple matching coefficient and classification methods for binary data was performed by Ojurongbe (2012). Clustering with single linkage, complete linkage, UPGMA, WPGMA method were used in the study. The result showed that Jaccard and Dice measure gave similar results under different method. It also indicated that the single linkage method is not an appropriate one since it has low consensus for index value. It was suggested that UPGMA method gives consistent result with respect to grouping irrespective of the similarity measure based on the cophenetic correlation value.

Materials and Methods

3. MATERIALS AND METHODS

This chapter provides the details about important procedures used in the current research. The present investigation on "Comparative analysis of different stability models on superior cultures of paddy" was undertaken from the data collected during kharif season of 2015 – 2018 at RARS, Pattambi. The various procedures adopted for the present research work are explained in the following subheadings.

3.1 Details of the experiment and variables of measurement

3.2 Statistical methods to measure stability

3.3 Stability models

3.4 Comparison of Stability models

3.5 Cluster analysis

3.1 DETAILS OF THE EXPERIMENT AND THE IMPORTANT CHARACTERS

The data used in the study was taken from the evaluation trial conducted at RARS, Pattambi during 2015 to 2018. The experiment was laid out in Randomized Block Design (RBD) with two replications. Thirteen superior cultures including two checks *viz.*, Cul 1, Cul 2, Cul 3, Cul 5, Cul 6, Cul 9, Cul 10, Cul 13, Cul 14, Cul 15, Cul 17, Jyothi and Uma. In each year the varieties (cultures) were sown during the kharif season. Details of data on both growth parameters and yield parameters were taken for the study.

3.1.1 Growth parameters

Various growth parameters such as plant height and number of tillers were taken at monthly intervals from each basic unit separately.

3.1.1.1 Plant height

The plant height of paddy was taken at monthly intervals in centimetres. The height is measured by holding the meter stick from the soil surface close to the till to the tip of the plant.

3.1.1.2 Number of panicles per plant

It was documented by adding the number of ears bearing per plant.

3.1.2 Yield parameters

Yield attributes on paddy was taken at the time of harvest from each basic unit separately.

3.1.2.1 Hundred grain weight

Hundred grains were selected randomly from each basic unit and weight is recorded with the help of electronic balance. The hundred grain weight was expressed in gram.

3.1.2.2 Grain yield

The weight of grain from each basic unit was recorded separately and expressed in t ha^{-1}.

3.1.2.3 Straw yield

The straw obtained from each basic unit was sun dried for 3 to 4 days and weighed and expressed in t ha^{-1}.

3.2 STATISTICAL METHODS TO MEASURE STABILITY

The most desirable properties for selection or recommendation of a specific genotype in plant breeding programme is the stability in performance. To achieve this aim, multilocational trials over number of years are conducted. Sometimes the uni-location trials are also used for testing stability of genotypes by generating artificial environments *viz.*, different dates of sowing, various spacing levels, different doses of fertilizers and irrigation levels etc (Luthra and Singh, 1974). The data of such trials are subjected first to ANOVA technique and thereafter to stability analysis. In the current study, the methods suggested by Eberhart and Russell (1966), Perkins and Jinks (1968), Freeman and Perkins (1971) and AMMI models (Gauch and Zobel, 1988) were compared with a view to identify suitable culture applicable to the paddy.

3.2.1 Analysis of variance for individual location

Panse and Sukhatme (1986) methodology of analysis of variance was used in the analysis of the experimental data collected from solitary locations (Table 1). The model for RBD is structured as

$$Y_{ij} = \mu + R_i + G_j + \epsilon_{ij} \qquad 3.1$$

Where,

Y_{ij}= Yield performance of j^{th} genotype in i^{th} replication

(i = 1, 2,…,r and j = 1, 2,…,g)

μ = General mean,

R_i = Effect of i^{th} replication,

G_j = Effect of j^{th} genotype

$\in_{ij}$ = Error associated with individual plot $\in_{ij}$ was assumed to be normally distributed with zero mean and common variance σ_e^2.

Table 1 ANOVA for individual location

Sources of variation	**Degree of freedom**	**Sum of squares**	**Mean sum of squares**	**F calculated**
Replication	(r-1)	$\sum_i \frac{Y_{i.}^2}{g} - \frac{Y_{..}^2}{rg}$	MS_{Rep}	MS_{Rep}/ MS_{Er}
Genotypes	(g-1)	$\sum_j \frac{Y_{.j}^2}{r} - \frac{Y_{..}^2}{rg}$	MS_{Ge}	MS_{Ge}/ MS_{Er}
Error	(r-1) (g-1)	Total SS- SSR - SSG	MS_{Er}	
Total	(rg-1)	$\sum_i \sum_j Y_{ij}^2 - \frac{Y_{..}^2}{rg}$		

3.2.2 Pooled analysis of variances over years

The individual sites pertaining to the experimental data were also subjected to the pooled analysis of variances (Table 2) using following statistical model,

$$Y_{ijk} = \mu + R_{i(j)} + E_j + G_k + (EG)_{jk} + \epsilon_{ijk} \qquad 3.2$$

Where,

Y_{ijk} = response of k^{th} genotype in i^{th} replication of j^{th} environment

(i = 1, 2,...r; j = 1,2,....e; k = 1, 2,....g)

μ = the general mean

$R_{i(j)}$ = effect of i^{th} replication in j^{th} environment

E_j = effect of j^{th} environment

G_k = effect of k[th] genotype

EG_{jk} = interaction effect of k[th] genotype in j[th] environment

$\in_{ijk}$ = error term

The random component $\in_{ijk}$ is assumed to be independently and normally distributed with zero mean and variance σ_e^2.

Table 2 ANOVA for pooled analysis of variance over years

Sources of variation	**Degree of freedom**	**Sum of squares**	**Mean sum of squares**	**F calculated**
Replication within environment	e(r-1)	$\sum_i \frac{Y_{ij.}^2}{g} - \frac{Y_{..}^2}{rge}$	MS_{Re}	MS_{Re}/ MS_{er}
Environments	e-1	$\sum_j \frac{Y_{.j.}^2}{rg} - \frac{Y_{..}^2}{rge}$	MS_{En}	MS_{En} / MS_{er}
Genotypes	g-1	$\sum_j \frac{Y_{..k}^2}{rk} - \frac{Y_{..}^2}{rge}$	MS_{Gp}	MS_{Gp} / MS_{er}
G × E Interaction	(g-1) (e-1)	$\sum_j \sum_k \frac{Y_{ijk}^2}{r} - \frac{Y_{..}^2}{rge}$	$MS_{(GE)}$	$MS_{(GE)} / MS_{er}$
Pooled error	e (g-1) (r-1)	TSS-SSR-SSE-SSG-SS(GE)	MS_{er}	
Total	rge-1	$\sum_i \sum_j \sum_k Y_{ijk}^2 - \frac{Y_{..}^2}{rge}$		

3.3 STABILITY MODELS

3.3.1 Eberhart-Russell model

The model for stability proposed by Eberhart and Russell (1966) partitioned the genotype x environment interaction of individual variety into two parts, *viz.*, (1) slope of the regression line and (2) deviation from the regression line. In this model, the total variance is first divided into two components, *i.e.*, (1) genotypes and (2) environment plus interaction (E+ G×E). The second component (E+ G×E) is further sub divided into three components, *viz.*, (a) environment linear, (b) genotype x environment (linear) and (c) pooled deviations (Table 3).The sum of squares due to pooled deviations are further divided into sum of squares due to individual genotype.

The following model was used for evaluating three stability parameters viz., mean ($\bar{Y}_i$), regression coefficient (b^{Ei}) and mean square deviation $S^2_{di}(E)$ for each genotype and the model is

$$Y_{ij} = \mu_i + \beta_i I_j + \delta_{ij} + \overline{e_{ij}} \qquad 3.3$$

This model defines stability parameters that may be used to describe the performance of a variety over a series of environments.

Y_{ij} is the variety mean of the i^{th} variety at the j^{th} environment, μ_i is the i^{th} variety mean over all environments, β_i is the regression coefficient that measures the response of the i^{th} variety to varying environments, δ_{ij} is the deviation from regression of the i^{th} variety at the j^{th} environment, I_j is the environmental index and $\overline{e_{ij}}$ is the random error component.

The regression component b^{Ei} and mean square deviation $S^2_{di}(E)$ were obtained using the following formulae for each genotype.

$$b^{Ei} = \frac{\sum_j Y_{ij} I_j}{\sum_j I_j^2} \qquad 3.4$$

$$I_j = \sum_j \left(\frac{Y_{ij}}{g}\right) - \sum_i \sum_j \left(\frac{Y_{ij}}{ge}\right) \quad 3.5$$

$$S^2_{di}(E) = \left[\sum_j \frac{\delta^2_{ij}}{e-2}\right] - (\sigma^2_e) \quad 3.6$$

$$\sum \delta^2_{ij} = \left[\sum_j Y^2_{ij} - \frac{Y^2_{i.}}{g}\right] - \frac{\left[\sum_j Y_{ij} I_j\right]^2}{\sum_j I^2_j} \quad 3.7$$

= Genotype SS- Regression SS

G = number of genotypes

e = number of environments

r = number of replications

I_j = Environmental index

σ^2_e = pooled error mean square

Table 3 ANOVA for Eberhart-Russell model

Sources of variation	**Degree of freedom**	**Sum of Square**	**Mean Square**	**F calculated**
Genotype	g-1	$\frac{1}{e}\sum_i Y_{i.}^2 - C.F$	MS_G	MS_G/ MS_e
Environments	e-1	$\frac{1}{g}\sum_i Y_{.j}^2 - C.F$		
G× E Interaction	(e-1) (g-1)	$\sum_i\sum_j Y_{ij}^2 - \left(\sum_e Yi.^2\right) - \sum_g Yi.^2 + CF$		
Environment (linear)	1	$\frac{1}{g}\left(\frac{(\sum Y_{ij}I_j)^2}{\sum_j I_j^2}\right)$	MS_E	MS_E/ MS_e
G× E Interaction (linear)	g-1	$\sum_j\left[\frac{(\sum Y_{ij}I_j)^2}{\sum_j I_j^2}\right] - Environment\ (linear)SS$		
Pooled deviation	g(e-2)	$\sum_i\sum_j \delta_{ij}^2$	MS_d	MS_d /MS_e
Pooled deviation due to i^{th} genotype	e-2	$\left[\sum_j Y_{ij}^2 - \left(\sum_i \frac{Y_{i.}^2}{e}\right)\right] - \left(\frac{(\sum Y_{ij}I_j)^2}{\sum_j I_j^2}\right)$		
Pooled error	e(g-1)(r-1)	$\sum_i\sum_j e_{ij}^2$	MS_e	

Test of significance for the following hypotheses was carried out.

To test the significance differences among the variety means *i.e.* H_0: $\mu_1=\mu_2=\ldots=\mu_g$ against H_1: $\mu_1\neq \mu_2\neq\ldots\neq \mu_g$, the appropriate 'F' test is defined as

$$F=MS_G/MS_d \qquad 3.8$$

To test the varieties do not differ for their regression on the environmental index, *i.e.* H_0: $b^{E1}=b^{E2}=\ldots=b^{Eg}$ against H_1: $b^{E1}\neq b^{E2}\neq\ldots\neq b^{Eg}$

$$F=\frac{MS_E}{MS_e} \qquad 3.9$$

To test H_0: $B_i=1$ against H_1: $B_i\neq1$

$$F=\frac{(b^E-1)^2\sum_j e_j^2}{\sum_j \delta_{ij}^2/(e-2)} \qquad 3.10$$

Individual deviation from linear regression is tested as follows:

$$F=\frac{(\sum_j \delta_{ij}^2)/(e-2)}{MS_e/r} \qquad 3.11$$

This significance is in turn used for testing the deviations of individual variety from its regression. According to this model a stable variety as one with a regression coefficient of unity (b^{Ei}=1) and a minimum deviation from the regression line ($S_{di}^2(E)$=0).

3.3.2 Perkins and Jinks model

A distinct stability analysis model was given by Perkins and Jinks (1968). This model divides the total variance into three components, *viz*., (1) genotypes, (2) environment, and (3) genotypes × environment. The G×E variance is subdivided into (a) heterogeneity due to regression and (b) sum of square due to remainder. The sum of square due to remainder is further divided into sum of square due to individual genotype (Table 4).

The model involves three stability parameters viz., mean, regression coefficient (b_i) and deviation from regression (S_{di}). They were estimated using the above methodology in which a regression of G x E interaction on environmental index is obtained rather than regression on mean performance. The joint regression analysis for a set of genotypes over a range of environments (Table 4) was based on the model,

$$Y_{ij} = \mu + d_i + E_j + g_{ij} + \overline{e_{ij}} \qquad 3.12$$

Defining interaction effect $g_{ij} = B_i E_j + \delta_{ij}$ and substituting this in above model, the ensuing model is

$$Y_{ij} = \mu + d_i + E_j(1 + B_i) + \delta_{ij} + \overline{e_{ij}} \qquad 3.13$$

Where,

d_i = Additive confribution of genotype i

μ = General mean

B_i= Linear regression coefficient

δ_{ij}= Deviation from regression in j^{th} environment of i^{th} genotype

$\overline{e_{ij}}$= Random error component

In comparison to Eberhart and Russell's model, the regression co-efficient in this model is different in the sense that Perkins and Jinks proposed to calculate the regression of genotype× environment interaction value on the environmental index. In terms of this model, the earlier model of Eberhart and Russell is thus regression of

$E_j + g_{ij}$ on E_j. The regression of E_j on $E_j$being one, and regression of g_{ij} on E_j being B_i, and b^{Ei} value of Eberhart and Russell is thus: b^{Ei}=1+ B_i, S_{di}^2 and remains the same.

Table 4 ANOVA for Perkins and Jinks model

Sources of variation	**Degree of freedom**	**Sum of square**	**Mean sum of square**	**F calculated**
Replication within Environment	e(r-1)	$\frac{1}{r}\sum_{k}\left(\frac{Y_{jk}^2}{g}\right)-\left(\frac{Y_{j.}^2}{gr}\right)$	MS1	MS1/MS7
Genotype (G)	(g-1)	$\frac{1}{e}\sum_{i} Y_{i.}^2 - C.F$	MS2	MS2/MS7
Environment (E)	(e-1)	$\frac{1}{g}\sum_{i} Y_{.j}^2 - C.F$	MS3	MS3/MS7
Int. G x E	(g-1) (e-1)	By subtraction	MS4	MS4/MS7
Heterogeneity between regression	(g-1)	$\sum_{i} B_i^2 \sum_{i} e_j^2$	MS5	MS5/MS7
Residual	(g-1) (e-2)	$\sum_{i}\sum_{j} \delta_{ij}^2$	MS6	MS6/MS7
Pooled error	e(r-l)	Pooled over environment	MS7	

Test of significance for the following hypotheses was carried out.

The hypothesis H_0: $B_i = 0$ against H_1: $B_i \neq 0$ was tested by F test as

$$F = \frac{B_i^2 \sum_j e_j^2}{\sum_j \delta_{ij}^2 / e - 2} \qquad 3.13$$

3.3.3 Freeman and Perkins Model

Freeman and Perkins (1971) proposed an improved way for partitioning of sum of squares in stability analysis. In this model the total variance is first divided into three components, *viz.*, (1) genotypes, (2) environment, and (3) interactions (G×E). The environmental sum of squares is subdivided into two components, namely (a) combined regression and (b) residual 1. The interaction variance is also subdivided into two parts, *viz*., (a) homogeneity of regression and (b) residual 2. The two residuals sum of squares from the pooled deviations in this model.

For describing Y_{ijk}, *i.e.*, performance in k^{th} replicate of i^{th} genotype in the j^{th} environment, Freeman and Perkins proposed the model:

$$Y_{ijk} = \mu + b_i + b_i Z_j + \delta_j + b_{di} Z_j + \delta_{dij} + e_{ijk} \qquad 3.14$$

where,

μ = general mean

Z_j = environmental index

b_i = regression coefficient for i^{th} genotype

δ_j = deviation of i^{th} genotype from its linear regression on j^{th} environment

e_j = additive environmental effect

δ_{dij} = the deviation of the ith genotype from each linear regression on Z_j

e_{ijk} = the random error component.

Analysis of variance: Variance due to environment is divided into combined regression and environmental residual. If the former is significant in comparison to the latter, that gives the true measure of environment (Table 5).

Table 5 ANOVA for Freeman and Perkins model

Source of variation	**d.f**	**Sum of square**	**Mean square**	**F calculated**
Genotypes(G)	g-1	(1/rs) ($\sum_i Y^2_{i.}$) - (1/rst) ($Y^2_{..}$)	MS1	MS1/MS8
Environments(E)	e-1	(1/rt) ($\sum_i Y^2_{j.}$) - (1/rst) ($Y^2_{..}$)	MS2	MS2/MS8
Combined regression	1	$\frac{\sum_j (Y_{.j} Z_j)^2}{rt \sum_j Z_j^2}$	MS3	MS3/MS8
Residual (1)	(e-2)	By subtraction from Environment S.S.	MS4	MS4/MS8
Interaction(G×E)	(g-1)(e-1)	(1/r) ($\sum_i \sum_j Y_{ij}^2$) $- (1/rs)$	MS5	MS5/MS8
Heterogeneity in regressions	g-1	S.S due to regression - S.S due combined regression	MS6	MS6/MS8
Residual (2)	(g-1)(e-2)	$\sum_i \sum_j \delta_{ij}^2$ $- Residual\ Env.S.S$	MS7	MS7/MS8
Error (between replications)	ge(r-1)	$\sum_i \sum_j \sum_k Y_{ijk}^2$ $- (1/r)(\sum_i \sum_j Y_{ij}^2)$	MS8	

In this model Freeman and Perkins proposed independent estimation mean performance and environmental index. The replications are divided into two groups. One group is used to measure the mean performance of genotypes in different environments, while the other group is used for the estimation of environmental index. Sometimes, one or more genotypes are used as checks to assess the environment.

Estimation of environmental index:

$$Z_j = Y_{.j} - \bar{Y} \qquad 3.15$$

Z_j= environmental index

$Y_{.j}$= The total overall of varieties under j^{th} environment and

$\bar{Y} = \sum_i \sum_j Y_{ij}$/total number of observations. *3.16*

The stability parameters b_{Fi} and $\bar{S}^2_{di(F)}$ are estimated as:

$$b_{Fi} = \frac{\sum_j \sum_k Y_{ij} Z_j}{\sum_j Z_j^2} \qquad 3.17$$

$$\bar{S}^2_{di(F)} = \left[\frac{\sum_j \delta_{ij}^2}{(e-2)}\right] - \left(\frac{S_e^2}{r}\right) \qquad 3.18$$

$$\sum_j \delta_{ij}^2 = \sigma_{Vi}^2 - b \sum_j Y_{ij} Z_j \qquad 3.19$$

$$\sigma_{Vi}^2 = \sum_i Y_{ij}^2 \qquad 3.20$$

F test: If environment residual S.S is significant, environmental index is adequately the index of additive environmental effect. If b_{Fi} is not significantly differ from unity, then independent environmental values adequately estimate additive environment component and the Freeman and Perkins model reduces to Perkins and Jinks model.

3.3.4 AMMI Model

The Additive Main effect and Multiplicative Interaction (AMMI) method proposed by Gauch (1988) is a statistical tool which leads to identification of stable genotypes with their adaptation behaviour in an easy manner. The necessary statistical background for AMMI models was made available in 1918 after development of the two components PCA by Pearson (1908) and ANOVA by Fisher (1918). This model associates regular analysis of variance (ANOVA) for additive main effects with principal components analysis (PCA) for multiplicative structure within the interaction. When both the main effects and interaction are important, the statistical method of choice is AMMI model.

The main purpose of employing the AMMI models are as follows:

(1) Understanding GE interaction, including identifying mega-environments.

(2) Enhancing the precision of yield estimates, which increases the probability of effectively selecting genotypes with the highest yields.

(3) Attributing the missing data.

(4) Increasing the flexibility and efficiency of experimental designs.

The AMMI model for t genotypes and s environment can be stated as

$$\overline{Y_{ij}}. = \mu + G_i + E_j + \left(\sum_{n=1}^{n'} \lambda_n \alpha_{in} \gamma_{jn}\right) + \overline{e_{ij.}} \qquad 3.21$$

$e_{ij} \sim N(0,\sigma^2)$; i = 1,2,…t; j =1,2,…,s.

Where,

$\overline{Y_{ij}}.$ = observed mean yield of the i^{th} genotype in j^{th} environment

μ = general mean

G_i = effects of the genotype

E_j = effects of the environment

λ_n = eigen value of PCA axis n

α_{in} = eigenvector of the i^{th} genotype for the n^{th} axis

γ_{jn} = eigenvector of the j^{th} environment for the n^{th} axis

n = number of PCA axes retained in the model

$\overline{e_{ij.}}$ = average of the corresponding random errors

The number of n is judged on the basis of empirical consideration of F test of significance (Gauch, 1988).

AMMI consists, quite simply, of fitting an additive ANOVA model in the usual manner (producing a grand mean, row means, and column means), and then for the interaction (that is, the non-additive residual from this additive model) fitting a multiplicative PCA (Table 6). The first principal component (PC1) represents responses of the genotypes that are proportional to the environments, which are associated with the GxE interaction. The second principal component (PC2) provides information about cultivation locations that are not proportional to the environments, indicating that those are responsible of the GxE crossover interaction. It computes a genotype score and an environment score whose product estimates yield for that genotype in that environment.

Table 6 ANOVA for AMMI model

Source of Variation	**Degree of Freedom**	**Sum of squares**	**Mean squares**
Treatment	ge-1		
Replication	r-1	Environment pooled over	M_R
Genotype (G)	g-1	$\frac{1}{e}\sum_i Y_{i.}^2 - CF$	M_G
Environment (E)	e-1	$\frac{1}{g}\sum_j Y_{.j}^2 - CF$	M_E
Genotype X Environment Interaction (GE) IPCA 1 IPCA 2 Residual	(g-1)(e-1)	$\sum_{ij} Y_{ij}^2 - \frac{1}{e}\sum_i Y_{i.}^2$	M_{GE}
Total	ger-1	$\frac{1}{r}\sum_i Y_{ij}^2 - CF$	
Error	b(v-1)(n-1)	pooled	M_e

Graphical representation of interaction using AMMI interaction parameters is known as biplot. Till date, the stability conclusions made from AMMI model are based on biplots which limits the scope of its use. Biplot formulation of interaction

will be successful only when significant of G x E interaction is concentrated in the first or first two PCA axes. There are two kinds of plotting *viz.*,

1. Biplot with first PCA axis

   a) First PCA scores of genotypes and environments are plotted against their respective means.
   b) Now the pattern of G x E interaction may be visualized from this plot. If the genotype or an environment has a PCA score of nearly zero, it will have smaller interaction effects.

2. Biplot with two PCA axis

   a) Here second PCA scores of genotypes and environments are plotted against their respective first PCA scores.
   b) For a better description of the interaction, both first and second PCA scores of genotypes and environments may be considered for plotting.

3.3.4.1 AMMI based Selection Index (ASTABi)

A new stability measure was proposed by Rao *et al*. (2004) incorporating it as a stability component of AMMI model. The interpretations strained from biplots are effective only when the first principal component axis (PC1) or the first two PCAs axis explain maximum interaction variation. Whenever, more than two axes are retained in AMMI model, the biplot formulation of interaction fails. When n' of N axes are retained in the AMMI model to explain GEI, then the stability measure of the ith genotype can be determined as the end points of the vector $\gamma_{1i}, \gamma_{2i}, \ldots, \gamma_{ni}$ from the origin 0_{nx1}. This is a squared Euclidean distance and calculated as

$$ASTABi = \gamma_{1i}^2 + \gamma_{2i}^2 + \cdots + \gamma_{n'i}^2 = \sum_{n=1}^{n'} \gamma_{ni}^2 = \sum_{n=1}^{n'} \lambda_n \gamma_{ni}^2 \qquad 3.22$$

Genotype is considered as highly stable, when the value of ASTABi is small or close to zero. This stability measure is used as stability component in other selection indices.

3.4 COMPARISON OF STABILITY MODELS

3.4.1 Correlation Coefficient

All methods of stability analysis described above were applied to evaluation trial data of paddy over the years. Simple correlation coefficient between stability parameters were calculated for studying association behaviour of the stability parameters (Snedecor and Cochran, 1967) and Kendall's coefficient of concordance to identify the similarity in ranking patterns of the four models.

3.4.1.1 Kendall's Coefficient of Concordance

The stability measures were ranked based on the grain yield characteristics of paddy. This is used to calculate the Kendall's W (Kendall's Coefficient of Concordance) given by Kendall and Smith (1939). It is a normalization of the statistic of the Friedman test, and can be used for assessing agreement among judges. Kendall's *W* ranges from 0 (no agreement) to 1 (complete agreement).

Suppose that genotype *i* is given the rank $r_{i,j}$ by judge number *j*, where there are in total *n* genotype and *m* judges. Then the total rank given to genotype *i* is

$$R_i = \sum_{j=1}^{m} r_{ij} \qquad 3.23$$

and the mean value of these total ranks is

$$\bar{R} = \frac{1}{n}\sum_{i=1}^{n} R_i \qquad 3.24$$

The sum of squared deviations, *S*, is defined as

$$S = \sum_{i=1}^{n} (R_i - \bar{R})^2 \qquad 3.25$$

and then Kendall's *W* is defined as

$$W = \frac{12S}{m^2(n^3 - n)} \qquad 3.26$$

If the test statistic *W* is 1, then all the judges or survey respondents have been unanimous, and each judge or respondent has assigned the same order to the list of objects or concerns. If *W* is 0, then there is no overall trend of agreement among the respondents, and their responses may be regarded as essentially at random. Intermediate values of *W* indicate a greater or lesser degree of unanimity among the various judges or respondents.

3.4.1.2 Spearman's rank correlation

Different stability measures were ranked taking into account of stability and yield performance. These ranks were used to calculate Spearman's rank correlation (Spearman,1904) among different methods as under.

$$r = 1 - \frac{6\sum d_i^2}{n(n^2-1)} \qquad 3.27$$

Where, d_i = difference of ranks between two methods, n = number of pairs

The value of rank correlation coefficient was tested as under for test of significance using 't' test

$$t = \frac{r\sqrt{(n-2)}}{\sqrt{1-r^2}} \qquad 3.28$$

The calculated value of 't' was compared with table value of t with (n-2) degrees of freedom at 0.05 and 0.01 level of probability. This helped to identify different methods of stability.

3.5 CLUSTER ANALYSIS

Cluster analysis is a multivariate technique used to classify objects or cases into homogenous groups called clusters (Singh *et al.,* 2002). The main objectives of cluster analysis include (Handl *et al*., 2005):

- Homogeneity in each cluster with respect to certain characteristics i.e., observations in each group are similar to each other.
- There should be heterogeneity in cluster from other groups with respect to the characteristics i.e., observations of one group should be different from the observations of other groups.

The various steps involved in the cluster analysis (Rokach, 2009) are as follows:

a) selection of similarity measures
b) selection of clustering techniques
c) selection of clustering method
d) no of clusters to be chosen
e) interpretation of results

3.5.1 Similarity measures

Cluster analysis attempts to identity the observation vectors that are similar and group them into clusters, many techniques use an index of similarity or proximity between each pair of observations. The distance between two observations is a convenient measure of proximity. Therefore, similarity measure is defined as the measure of distance between various data points of objects. Similarity represents the strength of relationship between items or objects (Hardle and Simar, 2007). Distance between two units increases as they become further apart.

3.5.1.1 Euclidean distance

It is the ordinary straight line distance between two points (Anton and Howard, 1994). It gives greater weight on the objects that are farther apart. The squared Euclidean distance measure between i^{th} and j^{th} individual is given as

$$E_{ij} = \sqrt{\sum_{k=1}^{p}(X_{ik} - X_{jk})^2} \qquad 3.29$$

Euclidean distance between two vectors X'= (x1, x2,…,.x_p) and Y'= (y1,y2,…..,y_p), defined as

$$D(X,Y) = \sqrt{(X-Y)'(X-Y)} \qquad 3.30$$

3.5.2 Clustering techniques

Clustering techniques are used to generate different clusters. The commonly used clustering techniques (Johnson and Wichern, 2006) divides into two classes, Hierarchical clustering and Non-hierarchical clustering.

3.5.2.1 Hierarchical Clustering Technique

Hierarchical clustering works to divide or merge a particular dataset into a sequence of nested partitions or clusters (Cambridge, 2009). The hierarchy of these nested partitions can be of two types, *viz.*, agglomerative hierarchical clustering or divisive hierarchical clustering.

3.5.2.1.1 Agglomerative Hierarchical Clustering

This technique begins with discrete objects. Thus, the number of clusters and objects will be same. The first grouping is done based on most similar objects and these initial groups merged according to the similarities between these groups. All subgroups get fused into a single cluster as the similarity increases.

Procedure for groups of K objects using agglomerative clustering (McQuitty, 1960).

i. Initially begins with K clusters, each comprising a single entity and symmetric matrix of distance or similarities of order K*K.
ii. Merge the most similar (nearest) pair of clusters using distance matrix. Let d_{AB} be the distance between nearest clusters A and B.
iii. After merging name, the newly molded cluster (AB). Reconstruct the values in the distance matrix by
iv. Removing rows and columns equivalent to clusters A and B.

v. Adding row and column giving distance between cluster (AB) and remaining clusters

vi. Repeat steps (ii) and (iii) upto K-1 times.

3.5.2.1.2 Divisive Hierarchical Clustering

It works in the opposite direction of agglomerative method. Single group of objects in the initial stage is divided into two sub groups such that the objects in one subgroup are more dissimilar than the objects in the other. These subgroups are further divided into more dissimilar subgroup. This process continues until each object form a group.

3.5.3 Dendrogram

Tree is a family of clusters for which any two clusters are either disjoint or one includes the other (Hartigan, 1975). The hierarchical structure is often represented by a two dimensional diagram which is also known as tree diagram or hierarchical tree. The tree is often presented upside down so that the branches are at the bottom and the roots of the tree is at the top. We can illustrate the merges or divisions that have been made at successive levels using dendrogram.

3.5.4 Average linkage method

The similarity between two clusters depends on the average distance between the similar members (average distance). It is sub divided into two:

1. Unweighted Pair Group Method with Arithmetic mean (UPGMA)
2. Weighted Pair Group Method with Arithmetic mean (WPGMA)

3.5.4.1 UPGMA

It is a simple agglomerative hierarchical clustering method in which the distance between a cluster and an object is calculated as the average distance between all the objects in the cluster and the objects supposed to enter in to the cluster (Sokal and Michener, 1958). Thus, instead of taking only a distance between the closest or the farthest neighbour calculated based on the average of all pairs of objects along by

assigning weight to the clusters i.e., proportional averaging. The weight is assigned based on the size of the clusters.

Distance between AB and any other object D,

$$d_{(AB)D} = (d_{AD} + d_{BD}) / (n_{AB} * n_D) \quad 3.31$$

where, n_{AB} and n_D represents size of the respective clusters.

3.5.4.2 WPGMA

This is the modified form of unweighted pair group average method which do not use the weights as the number of objects in the cluster into which another object is sought to be included or excluded. In this method, similarity between two clusters equals the mean similarity of previously existing clusters when they are grouped and average always involves only two terms and does not weight clusters by their size. This method should be used when the cluster sizes are suspected to be greatly uneven.

R programming

R is a language and environment for statistical computing and graphics. R provides a wide variety of statistical (linear and nonlinear modelling, classical statistical tests, time-series analysis, classification, clustering etc) and graphical techniques, and is highly extensible (Das and Augustine, 2017). It is an open source software and to improve the user interface of R, it was further modified to Rstudio application.

The different R packages in Rstudio application used for the correlation and cluster analysis are as follows:

- Spearman's rank correlation- stats package (Marschner *et al.*, 2018).
- Kendall's Coefficient of Concordance- Desc tool package (Gamer, 2010).
- Correlogram- corrplot package (Friendly, 2010).
- Cluster analysis- fpc (Hennig, 2010) and factoextra (Kassambara and Mundt, 2017) packages.

Results and Discussions

4. RESULTS AND DISCUSSIONS

The results obtained by the application of suitable statistical techniques on the secondary data collected from the yield trial during the period 2015 to 2018 at Regional Agricultural Research Station (RARS), Pattambi, Palakkad on the study entitled “Comparative analysis of different stability models on superior cultures of paddy” are explained in this chapter. Thirteen cultures evaluated are included in the present study. The results of the study are given under the following subsections.

4.1 Preliminary statistical analysis

4.2 Pooled analysis of G X E interaction

4.3 Ranking of genotypes

4.4 Stability models

4.5 Comparison of different stability models

4.6 Cluster analysis

4.1 PRELIMINARY STATISTICAL ANALYSIS

Analysis of variance (ANOVA) was done to analyse the significant difference of thirteen cultures for each of the character under study in all the three years as shown in Table 7. The results showed that the difference in performance of cultures were significant for the characters plant height, straw yield and 100 grain weight in all the three years. However, grain yield was found to be significant only in first two years (2015 and 2016) except in the third year, and the number of panicles was significant only in the year 2016. The mean values of various characters corresponding to different cultures in three years are shown in the Table 8, Table 9 and Table 10 respectively.

Table 7 ANOVA for different characters over the years

Characters under study	**2015-16**	**2016-17**	**2017-18**
	Treatment MSS	Treatment MSS	Treatment MSS
Plant height (cm)	298.42**	207.77**	269.62**
No of panicles per plant	6.67^{NS}	9.26*	10.63^{NS}
Straw yield (t ha^{-1})	21.25**	7.86*	44.17*
Grain yield (t ha^{-1})	2.42**	0.22**	1.23^{NS}
100grain weight (g)	0.10**	0.06**	0.11**

** 1% level of significance, *5% level of significance, NS- Not Significant

As an initial step, in pooled analysis Bartlett's Chi square test was used for testing the homogeneity of the error variance over the years for all the characters (Table 11). Among the five characters studied only straw yield has shown significance in the test. This indicates the heterogeneity in error variance for the straw yield under study. Therefore, Aitken's transformation was carried out in the data of straw yield before the pooled analysis. For the rest of the characters Bartlett's Chi square test statistic was non-significant, suggesting homogeneity in the error variance to perform the pooled analysis for checking of G X E interactions.

Table 8 Average of biometrical and yield characters in the year 2015-16

2015-16					
Cultures	**Plant height(cm)**	**No of panicles**	**Straw yield (t ha^{-1})**	**Grain yield (t ha^{-1})**	**100 grain wt (g)**
Cul1	136.34	9.17	17.13	5.15	2.07
Cul2	133.67	7.34	13.85	6.51	1.98
Cul3	138.17	8.67	11.97	5.42	2.02
Cul5	136.17	11.00	10.93	7.04	2.43
Cul6	141.50	9.34	10.96	7.59	2.49
Cul9	134.17	8.00	8.11	6.79	2.47
Cul10	132.84	12.00	9.75	7.05	2.49
Cul13	121.84	10.83	7.28	5.81	2.55
Cul14	120.83	11.84	7.83	7.85	2.47
Cul15	120.34	10.33	7.20	6.44	2.42
Cul17	135.00	7.33	8.39	6.20	2.51
Jyothi	105.10	12.90	4.62	4.03	2.79
Uma	104.45	11.15	8.58	5.02	2.48
C.D	13.736	N/A	2.85	1.51	0.200
SE(d)	6.235	2.415	1.38	0.73	0.091

Table 9 Average biometrical and yield characters in the year 2016-17

2016-17					
Cultures	**Plant height (cm)**	**No of panicles**	**Straw yield (t ha^{-1})**	**Grain yield (t ha^{-1})**	**100 grain wt (g)**
Cul1	134.69	9.20	14.10	6.09	2.03
Cul2	136.57	9.10	12.01	6.18	2.05
Cul3	133.02	11.20	12.23	5.69	2.04
Cul5	117.60	12.60	11.14	6.45	2.45
Cul6	121.90	12.10	11.24	6.14	2.42
Cul9	117.60	11.40	7.84	5.44	2.43
Cul10	119.70	10.70	9.98	6.32	2.47
Cul13	111.90	10.50	8.29	5.26	2.41
Cul14	116.40	13.70	10.63	6.30	2.43
Cul15	114.30	12.40	7.52	6.23	2.51
Cul17	107.10	9.30	8.67	4.60	2.41
Jyothi	115.90	16.70	8.67	4.86	2.55
Uma	103.10	13.60	8.99	5.28	2.27
C.D	12.134	2.784	2.21	0.86	0.194
SE(d)	5.508	1.264	1.07	0.42	0.088

Table 10 Average of biometrical and yield characters in the year 2017-18

2017-18					
Cultures	**Plant height (cm)**	**No of panicles**	**Straw yield (t ha^{-1})**	**Grain yield (t ha^{-1})**	**100 grain wt (g)**
Cul1	134.60	10.90	12.49	6.08	2.09
Cul2	126.70	10.00	11.62	6.97	1.91
Cul3	135.90	11.40	12.61	6.50	1.96
Cul5	126.00	14.20	24.71	6.82	2.56
Cul6	115.20	12.10	17.17	5.57	2.44
Cul9	116.30	11.60	20.57	5.56	2.48
Cul10	117.50	12.40	17.47	5.21	2.46
Cul13	113.10	12.20	13.84	5.45	2.21
Cul14	107.10	7.70	13.46	5.38	2.31
Cul15	114.80	12.20	12.22	5.31	2.44
Cul17	119.10	9.90	8.89	4.77	2.35
Jyothi	98.00	16.67	7.66	4.18	2.67
Uma	100.00	8.67	17.22	5.69	2.59
C.D	11.904	N/A	7.00	N/A	0.298
SE(d)	5.404	2.239	3.40	0.80	0.135

Table 11 Result of Bartlett's Chi square test for all characters

Characters	**Chi square Value**	**Df**	**Significance**
Plant height (cm)	0.287	2	NS
No of panicles per plant	4.903	2	NS
Straw yield (t ha^{-1})	17.499	2	**
Grain yield (t ha^{-1})	4.813	2	NS
100grain weight (g)	2.844	2	NS

** 1% level of significance, NS- Not Significant

4.2 POOLED ANALYSIS FOR GxE INTERACTION

G X E interaction identified with the help of pooled analysis for all the characters under study are given in Table 12. The results presented in the table revealed a significant difference among the cultures for grain yield in each of the three environments suggesting the existence of GxE interaction. This further indicated that wide variability among the cultures included in the experiment. Moreover, significant differences due to environments was recorded for the characters straw yield and 100 grain weight, indicating wide variation among the environmental conditions used for the evaluation of different cultures of paddy including two released varieties Uma and Jyothi. GxE was also found to be significant for the biological character plant height which clearly provides an indication that the cultures differ in each environment. Since the characters like number of panicles per plant and 100 grain weight was found to be non-significant for GxE interaction, it was removed from further analysis done using different stability models. Parmar (2010) conducted a study on rice and found that broad range of diversity among the genotypes, locations (and or seasons) and inconsistent performance of genotypes to environmental stimuli suggesting the stability analysis to identify the stable and widely adaptable genotypes to environments.

Table 12 Pooled analysis of variance showing mean sum of squares for five characters over the years in paddy

Source	**df**	**Plant Height(cm)**	**No of panicles/plant**	**Straw Yield (t ha^{-1})**	**Grain Yield (t ha^{-1})**	**100 grain wt (g)**
Genotype	12	627.797**	17.395*	13.051*	2.554*	0.260*
Environment	2	805.165	23.603	169.469*	2.395	0.025*
GXE	24	74.010*	4.592^{NS}	4.339*	0.926*	0.015^{NS}
Pooled Error	36	32.806	4.147	1.000	0.449	0.011
CD (G)		10.767	2.471	0.755	0.487	0.033
CD (E)		13.493	3.361	3.267	1.509	0.189
CD (G x E)		15.559	5.532	2.716	1.821	0.291

** 1% level of significance, *5% level of significance, NS- Not Significant

4.3 RANKING OF GENOTYPES

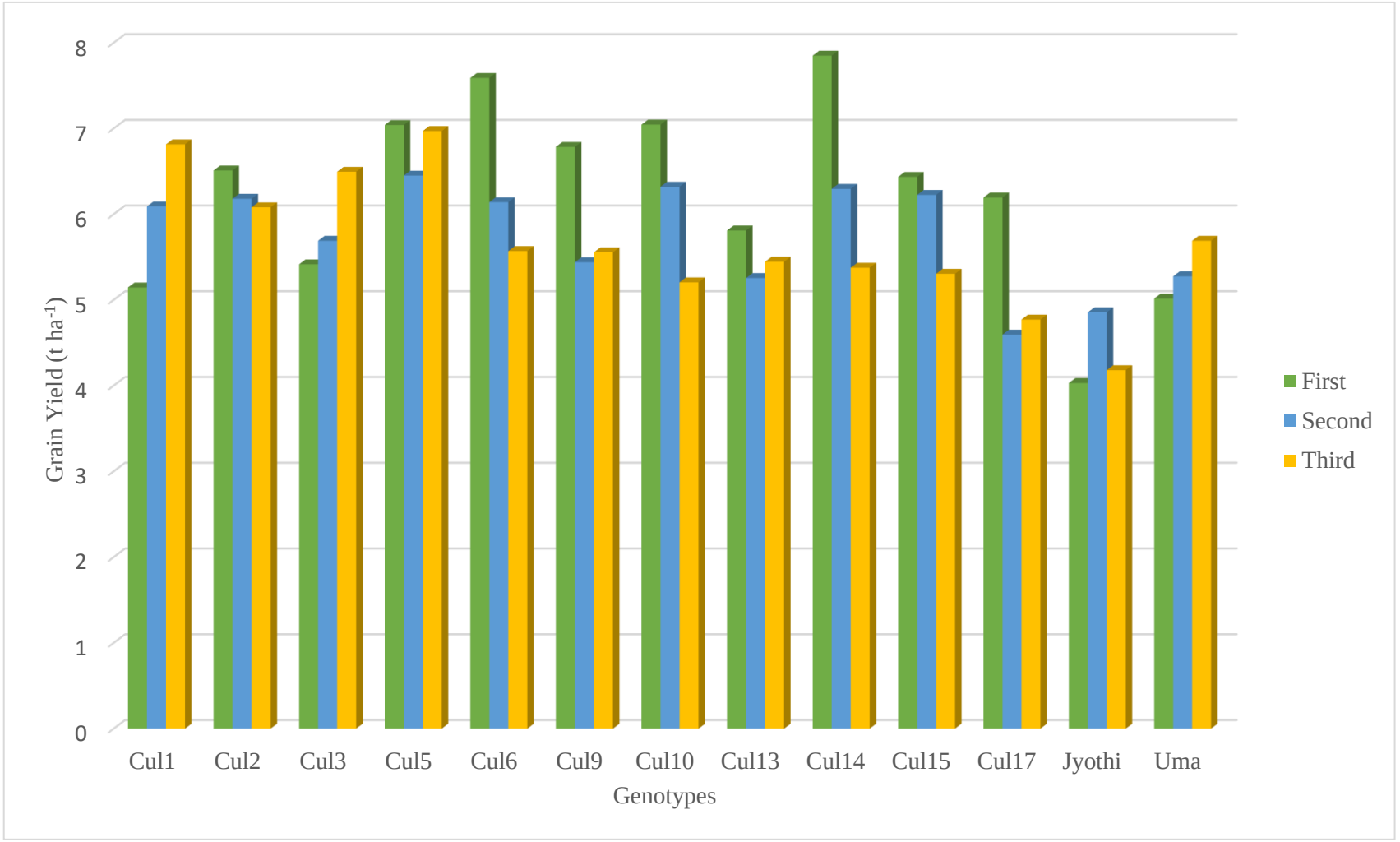
The G X E interaction was present in the mean performance of cultures. Ranking was done based on mean performance of grain yield of each genotype in each environment and the result is shown in Table 13. The details of the mean performance of genotypes over each environment have been summarized in Appendix I.

Table 13 Ranking of genotype under different environment for grain yield

Genotypes	**First(E1)**	**Second(E2)**	**Third(E3)**	**Mean(t ha^{-1})**
Cul1	11	7	4	6.02
Cul2	6	5	1	6.26
Cul3	10	8	3	5.87
Cul5	4	1	2	6.82
Cul6	2	6	6	6.43
Cul9	5	9	7	5.93
Cul10	3	2	11	6.19
Cul13	9	11	8	5.50
Cul14	1	3	9	6.51
Cul15	7	4	10	5.99
Cul17	8	13	12	5.19
Jyothi	13	12	13	4.36
Uma	12	10	5	5.33

The ranking of genotypes for grain yield in each environment showed that none of the genotypes had same rank in any of the environments. This also confirms the presence of G X E interactions for this character (grain yield). The genotypes Cul14, Cul5 and Cul2 ranked first in E1 (7.85 t ha^{-1}), E2 (6.45 t ha^{-1}) and E3 (6.9 t ha^{-1})

Fig 1 Performance of genotype under different environment for grain yield



respectively. Cul6 ranked second in E1 (7.5 t ha^{-1}), Cul10 in E2 (6.32 t ha^{-1}) and Cul5 in E3 (6.81t ha^{-1}). The lowest yield was produced by Jyothi in E1 (4.03 t ha^{-1}) and E3 (4.18 t ha^{-1}), whereas the lowest yield was recorded for Cul17 (4.59 t ha^{-1}) in E2 based on the Fig 1. Cul5 with average yield 6.82 t ha^{-1} ranked first based on the average performance based on three environments. The relative ranking of the genotypes varied from environment to environment, none of the genotype remain consistent in first position in all environment. The differential response of genotype to environment was once again confirmed from the above results. Therefore, it is necessary to carry out stability model analysis to determine the most stable genotypes in all environments. Similar findings were reported by Kana (2005) based on the study on the phenotypic stability in eighty genotypes of bread wheat in two different locations.

4.4 STABILITY MODELS

4.4.1 Eberhart and Russell Model

The result of stability analysis as per Eberhart and Russell model is given in Table 14. The results of ANOVA indicated that the Genotype, Environment and G X E interaction were significant for grain yield when tested against pooled deviation and pooled error. The (Env + Gen X Env) was also found to be significant in nature. The (Env + Gen X Env) component which was further divided into Env (linear), Gen X Env (linear) and pooled deviation and these were also found to be significant indicating that the prediction of variability is possible.

Eberhart and Russell proposed three stability parameters, *viz*. mean yield over locations or seasons ($\overline{Y_i}$), regression coefficient (b^{Ei}), and deviation from regression ($S^2_{di}(E)$) using an environmental index. The above mentioned three stability parameters for all the genotypes are given in Table 15. According to Eberhart and Russel model, a genotype is said to be stable if the genotype has a regression coefficient of unity (b^{Ei} =1) with a minimum deviation from the regression line ($S^2_{di}(E)$ = 0). In other words, we can say that genotypes with high regression coefficients indicate high yielding and with low regression coefficient indicating low yielding genotype. Moreover, genotypes with high deviation from regression are

Table 14 ANOVA for stability over three environments using Eberhart and Russells model

Source of Variation	df	Sum of Squares	Mean Squares	F-Calculated	Significance
Genotype (Gen)	12	15.322	1.277	2.757	**
Environment (Env)	2	2.395	1.198	2.586	*
Genotype X Environment	24	11.116	0.463	1.031	*
Env + Gen X Env	26	13.511	0.520		
Env (Linear)	1	2.395	2.395	16.800	*
Env X Gen (Linear)	12	9.262	0.772	5.414	**
Pooled Deviation	13	1.853	0.143	0.634	*
Pooled Error	36	16.179	0.449		
Total	38	28.833			

Pooled Error MSS for testing pooled deviations MSS = 0.225, ** 1% level of significance, *5% level of significance

considered as highly unstable and those with minimum $S_{di}^2(E)$ are considered as most stable ones. Several authors suggested that mean squared deviation from regression as the most appropriate criteria for stability and the regression coefficient as an indication of the type of response of a cultivar to varying environment rather than a measure of stability (Laghari *et al.,* 2003; Akcura *et al.,* 2005; and Bhakta and Das, 2008).

The result indicated that mean yield value $\overline{(Y_i)}$ over the three environments varied from 4.35 t ha^{-1} to 6.82 t ha^{-1} with an average of 5.88 t ha^{-1}. Among the thirteen genotypes eight genotypes had mean yield above the overall average of 5.88 t ha^{-1}. The highest yield was found out for the genotype Cul5 (6.82 t ha^{-1}) while lowest yield was recorded for Jyothi (4.35 t ha^{-1}). The estimated regression coefficient b^{Ei} of genotypes varied from -2.65 to 4.03. Cul1 (-2.65), Cul3 (-1.49), Cul14 (4.03), Cul6 (3.413) and Uma (-0.99) were found to have significant b^{Ei} values, which indicated that they are not suitable for varying environments. Cul9 (2.38), Cul10 (6.19), Cul17 (2.78) had high b^{Ei} values underline the suitability of these genotypes in favourable environments or rich environments. Cul5 (0.47) and Jyothi (-0.72) had low b^{Ei} values, shows the specific adaptation of these genotypes to poor environments. Cul2 (0.74), Cul13 (0.80) and Cul15 (1.51) had b^{Ei} values nearly equal to unity with least deviation from regression suggesting its adaptation ability to varying environments. $S_{di}^2(E)$ values range from -0.22 to 0.13 and all the $S_{di}^2(E)$ values were non-significant indicating the adaptability of all the genotypes to unfavourable environments. Further by combining the interpretation of three parametric criteria for stability the most stable genotypes identified were Cul2 followed by Cul5 and Cul15 which have a wider stability in varying environments.

Table 15 Stability Parameters for Eberhart and Russells Model

Genotypes	Mean $(\overline{Y_i})$	Reg Coefficient (b^{Ei})	d^2	Stability Parameter $S^2_{di}(E)$	Deviation (sd)
Cul1	6.017	-2.655**	0.104	-0.121 NS	0.562
Cul2	6.257	0.740	0.000	-0.224 NS	0.001
Cul3	5.867	-1.497*	0.217	-0.008 NS	1.178
Cul5	6.820	0.471	0.167	-0.058 NS	0.906
Cul6	6.433	3.413*	0.024	-0.201 NS	0.128
Cul9	5.927	2.380	0.068	-0.157 NS	0.369
Cul10	6.190	2.719	0.356	0.132 NS	1.934
Cul13	5.503	0.808	0.039	-0.186 NS	0.210
Cul14	6.507	4.036**	0.128	-0.096 NS	0.697
Cul15	5.988	1.516	0.299	0.074 NS	1.624
Cul17	5.187	2.785	0.112	-0.113 NS	0.605
Jyothi	4.355	-0.723	0.290	0.065 NS	1.574
Uma	5.327	-0.993*	0.050	-0.175 NS	0.271
Average	5.88	1.00			

** 1% level of significance, *5% level of significance, NS- Not Significant

4.4.2 Perkins and Jinks Model

The stability analysis of genotypes using Perkins and Jinks model is given in Table 16. The result of ANOVA showed that genotypes, environments and GxE interactions were found to be significant in nature for the grain yield when tested

against pooled error and the remainder. The G×E variance is further subdivided into heterogeneity due to regression and sum of square due to remainder and these were also found to be significant with respect to the pooled error indicating the performance of genotypes differently to different environments. The magnitude of mean square of heterogeneity between regressions was greater than the magnitude of mean square of remainder indicating the prediction of the performance of the character is possible. In this model, the sum of squares due to heterogeneity was the same as that of sum of squares due to G×E (linear) of Eberhart and Russell model, and sum of squares due to the remainder was equal to sum of squares due to pooled deviations in the Eberhart and Russell model.

This model also has three stability parameters, *viz*. mean yield over locations or seasons ($\overline{Y_i}$), regression coefficient(B_i), and deviation from the regression (S_{di}^2) and estimates of these three stability parameters for all the genotypes are given in Table 17. According to Perkins and Jinks model, a stable variety is one with high yield and having a regression coefficient of zero (B_i=0) with a minimum deviation from the regression line (S_{di}^2 = 0). The result presented in Table 17 indicated that mean yield $\overline{(Y_i)}$ ranges from 4.35 t ha^{-1} to 6.82 t ha^{-1} with an overall average of 5.88 t ha^{-1}. Among the thirteen genotypes eight genotypes showed above the average yield while others showed a below the average yield. The estimated B_i value varied from 3.66 to 3.03. The genotypes Cul1 (-3.65), Cul3 (-2.49), Cul6 (2.41), Cul14 (3.03) and Uma (-1.99) were found to have significant B_i values which is an indication of their low suitability to varying environments. Moreover, high B_i values are recorded for parameters requirement Cul9 (1.38), Cul10 (1.71) and Cul17 (1.78) emphasizing its suitability in favourable environments or rich environments. Low B_i values are noticed for Cul5 (-0.52) and Jyothi (-1.72) confirms its specific adaptation to poor environments. $B_i$value near to zero was seen in Cul2 (-0.26), Cul5 (-0.52) and Cul13 (-0.19), which shows their adaptation to varying environments. In general, S_{di}^2 values range from -0.22 to 0.13 and all the S_{di}^2 values were non-significant, indicating that all the

Table 16 ANOVA for stability over three environments using Perkins and Jinks model

Source of Variation	**df**	**Sum of Squares**	**Mean Squares**	**F-Calculated**	**Significance**
Genotype	12	15.322	1.277	8.29	**
Environment	2	2.395	1.198	7.77	**
Genotype X Environment	24	11.116	0.463	3.00	*
Heterogeneity bet Reg	12	9.262	0.772	5.01	**
Remainder	12	1.853	0.154		
Pooled Error	36	16.179	0.449		

** 1% level of significance, * 5% level of significance

genotypes are suitable to unfavourable environments. S^2_{di} estimates of this model is same as that of $S^2_{di}(E)$ in Eberhart and Russell model. Based on the interpretation of the three conditions or parameters of Perkins and Jinks model Cul2 and Cul5 were found to be the most stable genotypes among the thirteen genotypes, exhibiting their adaptability to varying environments.

Table 17 Stability Parameters for Perkins and Jinks model

Genotypes	**Mean**	**Reg Coefficient (B_i)**	**d^2**	**Stability Parameter (S^2_{di})**
Cul1	6.017	-3.655**	0.104	-0.121^{NS}
Cul2	6.257	-0.26	0.000	-0.224^{NS}
Cul3	5.867	-2.497**	0.217	-0.008^{NS}
Cul5	6.820	-0.529	0.167	-0.058^{NS}
Cul6	6.433	2.413**	0.024	-0.201^{NS}
Cul9	5.927	1.38	0.068	-0.157^{NS}
Cul10	6.190	1.719	0.356	0.132^{NS}
Cul13	5.503	-0.192	0.039	-0.186^{NS}
Cul14	6.507	3.036**	0.128	-0.096^{NS}
Cul15	5.988	0.516	0.299	0.074^{NS}
Cul17	5.187	1.785	0.112	-0.113^{NS}
Jyothi	4.355	-1.723	0.290	0.065^{NS}
Uma	5.327	-1.993*	0.050	-0.175^{NS}
Average	5.88	0		

** 1% level of significance, *5% level of significance, NS- Not Significant

4.4.3 Freeman and Perkins Model

The stability analysis using Freeman and Perkins model determines independent estimation of mean performance and environmental index. For this purpose, the replications were divided into two groups. One group is used to measure the mean performance of genotypes in different environments, while the other group is used for the estimation of environmental index. The stability parameter used in this model were mean yield over locations ($\overline{Y_i}$), regression coefficient (b_{Fi}) and deviation from regression ($\bar{S}^2_{di(F)}$) using environmental index. The present study has only two replications restrain the computation of environmental index and the deviation from regression based on this index. So, the partition of the replication resulted only in determining two stability parameters of this model *i.e.*, mean yield ($\overline{Y_i}$) and regression coefficient (b_{Fi}) and the estimated values are presented in Table 18.

The stability criteria for a genotype in this model are the genotype with high yield, regression coefficient equal to one ($b_{Fi} = 1$), and minimum deviation from regression ($\bar{S}^2_{di(F)} = 0$). The result specified that mean yield value $\overline{(Y_i)}$ ranges from 4.35 t ha^{-1} to 6.82 t ha^{-1} with an average 5.88 t ha^{-1}. Among the thirteen genotypes eight genotypes *viz.*, (Cul1, Cul2, Cul5, Cul6, Cul9, cul10, Cul14 and Cul15) showed above average yield while Cul3, Cul13, Cul17, Jyothi and Uma had a mean yield below the average yield. The estimated b_{Fi} values varied from -3.50 to 6.17. Cul1 (-3.508), Cul3 (-2.475), Cul14 (6.173), Cul17 (3.460) and Jyothi (-1.285) had significant b_{Fi} values specifying their instability in the adaptation of varying environments. Cul9 (0.17), Cul5 (-0.25) and Uma (-0.68) had low b_{Fi} values establishing the adaptive nature of these genotypes to unfavorable environments. Cul6 (2.59) and Cul15 (2.35) had high b_{Fi} values confirming its suitability in rich environments. Cul2 (-0.57), Cul10 (0.71) and Cul13 (0.89) had regression coefficients (b_{Fi}) nearly equal to unity indicating their stability as compared to other genotypes. By combining the two parametric conditions for the stability of genotypes in this model, Cul10 was found to be the most stable genotype for a given environment followed by Cul2 and Cul5.

Table 18 Stability Parameters for Freeman and Perkins model

Genotypes	**Mean** $(\overline{Y_i})$	**Var of Mean**	**Reg Coefficient (b_{Fi})**
Cul1	6.017	1.403	-3.508**
Cul2	6.257	0.101	-0.578
Cul3	5.867	0.630	-2.475**
Cul5	6.820	0.208	-0.256
Cul6	6.433	2.169	2.590
Cul9	5.927	1.112	0.178
Cul10	6.190	1.718	0.716
Cul13	5.503	0.159	0.898
Cul14	6.507	3.130	6.173**
Cul15	5.988	0.722	2.350
Cul17	5.187	1.540	3.460**
Jyothi	4.355	0.386	-1.285*
Uma	5.327	0.232	-0.682
Average	5.88		1.00

** 1% level of significance, *5% level of significance

4.4.4 AMMI Model

AMMI model was also used to determine the stable genotype under three environments based on grain yield. AMMI model first partitioned the variation into main effects, Genotype (GEN), Environment (ENV) and Genotype X Environment (GEN x ENV) and then it applies Principal Components Analysis (PCA) to (GEN x

ENV) interaction. The results of AMMI ANOVA are presented in Table 19 and it indicated a significant difference between genotypes, environments at 1 percent level of significance and GEN x ENV interaction at 5 percent level of significance. This insisted that broad range of diversity existed among the genotypes and environment and also the performance of genotypes was not consistent over the environments. Out of the total treatment variation (total SS), the proportion of variance due to differences in genotypes was the largest (31.51per cent) followed by the variance due to G x E interaction (22.84 per cent). These results gave evidence regarding genotypes, environments and G x E interaction exerted a significant effect or not. These results confirmed to the observations made by Zobel *et al.* (1988). In general ANOVA didn't provide any insight into the particular pattern of genotypes or environments that give rise to interactions but explained the main effects effectively.

ANOVA model was combined with PCA model to further analyse the residuals. The GEN x ENV interaction was further divided into two principal axes (IPCA). PC1 explained 86.6 percent of GEN x ENV interaction variance while PC2 explained 13.4 percent of the variance.

The AMMI analysis provides a graphical representation or biplot to summarize the information on main effect (mean yield) based on PC1 and PC2 for both genotypes and environment simultaneously. The AMMI1 biplot provided a visual expression of the relationships between the interaction of first principal component axis (PC1) and mean of genotypes and environments (Fig 2). The first principal component axis (PC1) was significant and it explained the interaction pattern better than another axis.

Genotypes or environments located on the same parallel line, relative to the ordinate, have similar yield, while those located on the right side of the midpoint of the axis has higher yield than those on the left-hand side. The result of AMMI 1 biplot classified the genotypes mainly into four group *viz.*,

(i) Uma to low yielding and unstable.

(ii) Jyothi, Cul3 and Cul17 to low yielding and moderately stable.

Table 19 ANOVA for stability over three environments using AMMI model

Source of Variation	df	Sum Squares	Mean Sum square	F value	Significance	Explained sum square (%)	Explained variance (%)
ENV	2	4.783	2.392	5.710	**	4.90	
REP(ENV)	3	1.257	0.419	0.933	NS	1.29	
GEN	12	30.703	2.559	5.700	**	31.51	
GEN X ENV	24	22.257	0.927	2.066	*	22.84	
PC1	13	19.274	1.483	3.3	**	19.78	86.6
PC2	11	2.983	0.271	0.6	NS	3.06	13.4
Residuals	36	16.159	0.449			16.58	
Total	77	97.416					

** 1% level of significance, *5% level of significance, NS- Not Significant

Fig 2 AMMI 1 Biplot PC1 scores (Y axis) with mean grain yield (X axis)

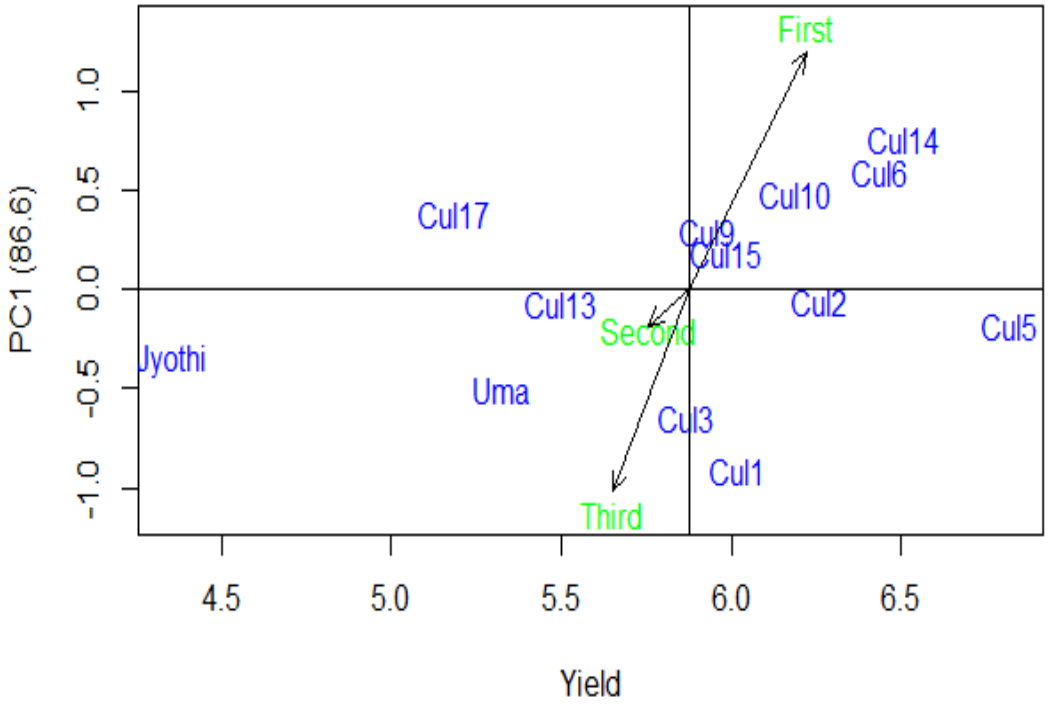
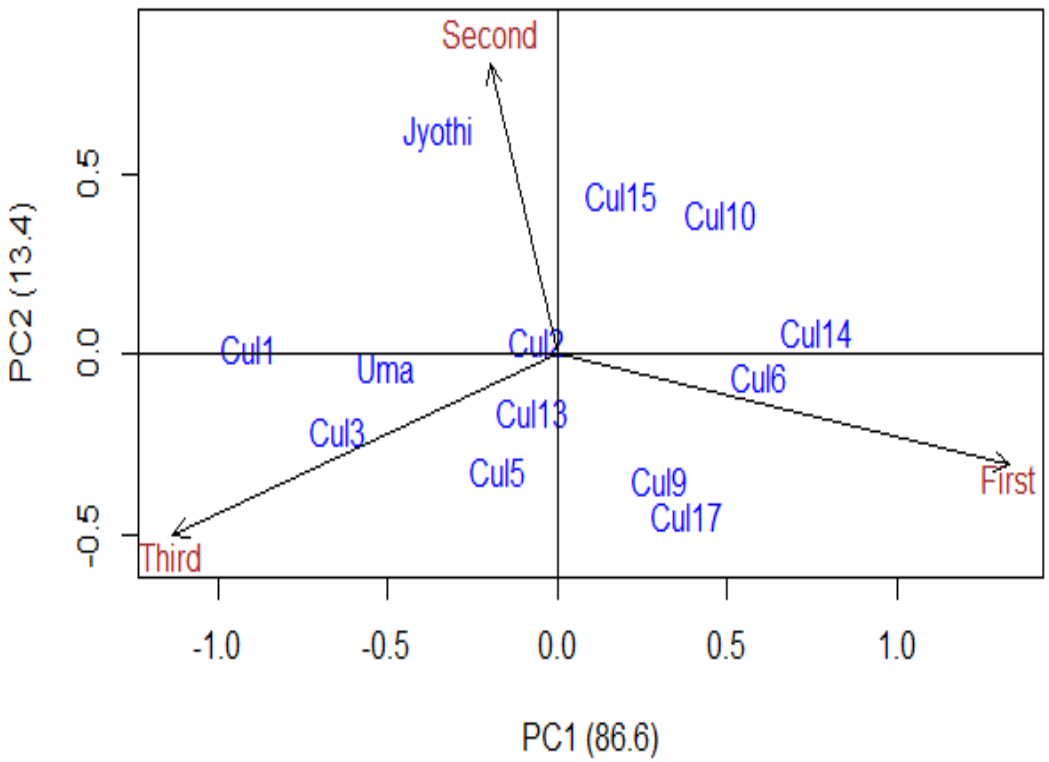


Fig 3 Interaction Biplot for AMMI 2 model, PC1 score (X axis) and PC2 score (Y axis)



(iii) Cul1, Cul14 and Cul6 to high yielding and specifically adaptable to favourable environments.

(iv) Cul2, Cul5, Cul15 and Cul9 to high yielding and highly stable across different environments, while Cul13 was poorly adapted to all environments.

Genotypes with PC1 scores near to zero had little interaction across the enviroments while genotypes with very high PC1 scores have considerable interaction with the environments (Table 20). Morever, when a genotype and an environment has the same sign on the PCA axis, their interaction is positive, if different, their interaction is negative.The AMMI 1 biplot (Fig 2) clearly indicated that all the 13 genotypes studied were differed from each other not only for the mean yield but also for their interaction effects. However, the environments studied were differed only for their interaction effects and they exhibited less difference for the main effect. The genotypes Cul2, Cul5, Cul15 and Cul9 had negligible interactions characterized by low PCA scores and these genotypes were considered to be the relatively stable genotypes showing its broad adaptation across environments. The PCA scores was high for the genotypes Jyothi, Uma, Cul10, Cul6 and Cul3, showing high interactions with low stability across different environments. The reason for the observed interaction can be based on both genetic difference between these genotypes and different environments. Similar sign of PC1 score for both genotypes and environments imply positive interaction and thus it attributed to higher yield of genotype at particular environment (Anandan *et al.,* 2009).

The AMMI 2 biplot in which PC1 and PC2 score are plotted in X and Y axis (Fig 3), the environmental scores are joined to the origin by straight lines. Environments with short spokes in figure exert weak interaction; those with long spokes exert strong interaction. The environment E2 had short spokes and they do not exert any strong interactive forces. The genotypes closed together in the plot will tend to have similar yields in all the environments. The genotypes near to the origin are non-sensitive to environmental interaction and those away from the origin are sensitive and have large interaction. In the present study Cul1, Cul3, Jyothi, Cul17 and

Cul14 showed more sensitive interaction to environmental forces since they are away from the origin while Cul2, Cul5, Cul15, Cul9 and Cul13 showed less interaction since they are close to the origin of the biplot. Correspondingly, the environments close together exert similar pattern of interaction. E1 and E2 showed opposite characteristics since they are in the opposite quadrants of the biplot and others had no similar interaction pattern.

Finally, the AMMI analysis reported that Cul2, Cul5, Cul15 and Cul9 had broad adaptation and they are hardly affected by G x E interaction and thus may perform well across the wide range of environments. Moreover, Env 2 was comparatively most stable among all three environments but it provides a low yield. The results are in agreement with those reported by Shinde *et al.* (2002), they also identified stable genotypes and idle environment for pearl millet genotypes.

Table 20 AMMI Mean Yield and PC Scores

Genotypes	**Mean Yield**	**PC1**	**PC2**
Cul1	6.017	-0.911	0.017
Cul2	6.257	-0.059	0.037
Cul3	5.867	-0.648	-0.208
Cul5	6.820	-0.175	-0.318
Cul6	6.434	0.592	-0.060
Cul9	5.927	0.300	-0.345
Cul10	6.190	0.481	0.390
Cul13	5.501	-0.070	-0.158
Cul14	6.508	0.766	0.067
Cul15	5.985	0.188	0.442
Cul17	5.184	0.384	-0.443
Jyothi	4.355	-0.348	0.615
Uma	5.327	-0.502	-0.035
Environments			
First (E1)	6.220	1.334	-0.339
Second (E2)	5.650	-0.199	0.894
Third (E3)	5.755	-1.134	-0.555

4.4.4.1 AMMI based Selection Index (ASTABi)

The biplots and PC scores in AMMI models are very much limited to provide a numerical measure for stability, a quantitative measure of stability known as ASTABi was calculated. This stability measure (squared Euclidean distance) was calculated by using the retained 'm' axis out of total ‘M’ axis and the estimated indices are presented in Table 21. This stability measure can be considered as a measure of

stability component of the genotypes. A genotype is considered to be highly stable, when the value of ASTABi is small or near to zero. It is evident from table that Cul2 (0.005) had lowest ASTABi value and it was ranked first followed by Cul13 (0.463) and Cul5 (0.132), specifying their stability in adapting a wide range of environments.

Table 21 AMMI based Selection Index (ASTABi) stability parameter

Genotypes	**ASTABi**	**Rank (ASTABi)**	**Yield**	**Rank (Yield)**
Cul1	0.830	13	6.017	6
Cul2	0.005	1	6.257	4
Cul3	0.463	10	5.867	9
Cul5	0.132	3	6.820	1
Cul6	0.355	8	6.434	3
Cul9	0.209	4	5.927	8
Cul10	0.384	9	6.190	5
Cul13	0.030	2	5.501	10
Cul14	0.591	12	6.508	2
Cul15	0.231	5	5.985	7
Cul17	0.344	7	5.184	12
Jyothi	0.499	11	4.355	13
Uma	0.254	6	5.327	11

The highest ASTABi value was for the genotype Cul1 (0.83) indicating its instability in the response to different environments. But based on grain yield Cul5 ranked first followed by Cul14 and Cul6 and the low yielding genotypes as Uma, Jyothi and Cul17.

4.5 COMPARISON OF DIFFERENT STABILITY MODELS

The analysis based on different stability models *viz.*, Eberhart and Russel model, Perkins and Jinks model, Freeman and Perkins model and AMMI model are compared for their efficiency and similarity empirically, so that an efficient method could be recommended for the stability analysis based on the grain yield. The comparison between the models was done by ranking the stability parameters of various genotypes under each method and Spearman's rank correlation coefficient was calculated based on the ranks under any two models to analyse the agreement of ranking of genotypes between any two models. The estimated Spearman's rank correlation coefficients are presented in Table 22 which in turn used for the comparative study of the stability models. The correlogram was also used for diagrammatic representation of the comparison of four models to suggest the best model along with the best genotype for the varying environments.

4.5.1 Kendall's Coefficient of Concordance

The different stability parameters of the four models of the thirteen cultures were ranked initially and these ranks are used to obtain the Kendall's coefficient of concordance value. It represents the ratio of the variability of the total ranks for the ranked entities to the maximum possible variability of the total ranks. The value obtained was W = 0.37. Since the value is very small and near to zero, indicating that there is not much similarity between the rankings of the parameters of four stability models. Also, there is no overall trend of agreement among the cultures, and their responses may be regarded as essentially at random. Hence, Spearman's rank correlation coefficient was calculated to get an idea about the similarity based on pairwise comparison of the parameters of the models.

4.5.2 Spearman's Rank Correlation

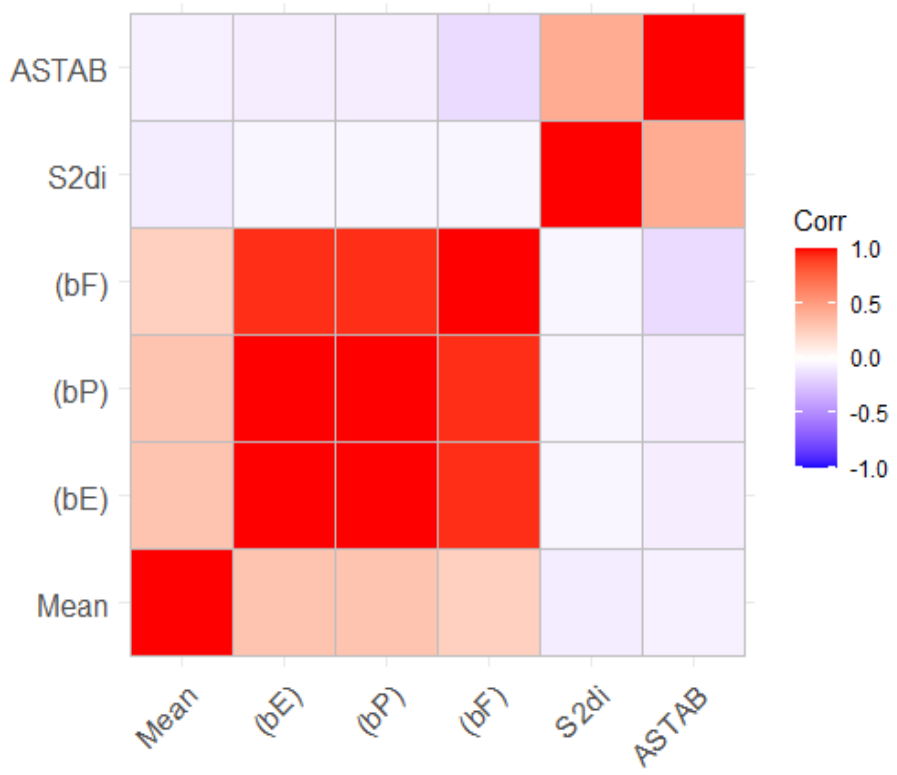
The genotypes are ranked based on the stability parameters of four stability models and the Spearman's correlation was used for the comparative study and the resultant correlation matrix is shown in Table 22. The rank correlation between b^{Ei} and B_i was found to be unity (r = 1) indicating the strong agreement between the

ranking of parameters in Eberhart and Russell (ER) and Perkins and Jinks (PJ) models even though the maximum and minimum values of the stability parameters differs. Fikere *et al.* (2009) also reported the same result. Similarly, there was a strong significant rank correlation between the ranking of b^{Ei} and b_{Fi} (0.94) and B_i and b_{Fi} (0.94) indicating an almost similar type of ranking. The ranking pattern of Freeman and Perkins (FP) model were different from that of the other two regression models. The Cul2 was found to be most stable in the case of ER model and PJ model, while Cul10 was found to be the most stable by FP model. However, the rank correlation between ASTABi and other three models are almost nearly equal to zero suggesting no agreement between the rankings of these genotypes with AMMI model. The correlogram based on this result is shown in Fig 4. Most of the other parameters had negative correlation especially in the case of ASTABi with the regression parameters indicating ranking pattern of genotypes was entirely different.

Table 22 Correlation Matrix of Spearman's rank correlation method

	ER (b^{Ei})	**PJ** (B_i)	**FP** (b_{Fi})	**AMMI** (ASTABi)
ER(b^{Ei})	1.000			
PJ (B_i)	1.000**	1.000		
FP (b_{Fi})	0.940**	0.940**	1.000	
AMMI (ASTABi)	-0.066	-0.066	-0.154	1.000

Fig 4 Correlogram using Spearman's rank correlation method



4.5.3 Adaptive genotype and appropriate model

On the basis of grain yield performance and the stability parameters of the different models used in the present study Cul2, Cul5, Cul9 and Cul15 were found to be the adaptive genotypes across the different environments. Among the four, Cul2 was the most stable and high yielding genotypes adaptable to the varying environmental conditions.

On the basis of stability parameters of the three regression models in the present study concluded that the deviation detected between ranking patterns of genotypes in FP model with other two models was mainly due to the fact that FP model used only a portion of the experimental data in contrary to the use of full set of data as in ER and PJ models. FP model did not reflect what actually existing in the full set of data. Theoretically FP model is good but practically ER and PJ are preferred. This study also discloses the same observational relationship between the models.

The ordinary ANOVA model is additive and effectively describes the main additive effects, while interaction (residuals from the additive model) is non-additive and it requires other techniques, such as PCA to identify the interaction pattern. For the estimation of performance of genotypes in an environment the cell means (averaged over replication) is considered. So, the averaging of few replications may not be good enough to get accurate estimate for performance, hence, computer intensive statistical methods like AMMI analysis can be used which provides a better estimate than estimates based on traditional three models. AMMI partitions GEI and summarizes the patterns and relationships of G and E with more accuracy in yield estimates (Zobel *et al.,* 1988; Crossa *et al.,* 1990). So, AMMI model was chosen as the best model from among the four models included in the study.

4.6 CLUSTER ANALYSIS

Stability analysis was used to identify the best stable genotype which is adaptable to the differential environments; however, cluster analysis provides homogenous groups of genotypes which in turn used for the comparison between the genotypes.

4.6.1 Comparison of cluster analysis with stability model

The hierarchical cluster analysis was performed for the genotypes based on the grain yield from 2015 to 2018. The Euclidean distance was adopted as the distance measure for cluster analysis and the dissimilarity matrix is given in Table 23. The agglomerative hierarchical clustering technique was adopted to determine the number of clusters and cluster members. The clustering method used was UPGMA clustering method. Initially clusters are formed by combining the objects having smallest distance and cluster distance was taken as the average distance between the objects in the clusters. Clustering was done using R studio statistical package and the resultant dendrogram is shown in Fig 5. The number of clusters was chosen by gap statistics method which established three clusters and they are given in Table 24. Cluster II had the maximum number of genotypes (seven) while the cluster III had the least (one).

The genotypes included in the cluster II are Cul2, Cul5, Cul6, Cul9, Cul10, Cul14 and Cul15 these were the genotypes found as the stable across various environments using four different stability models. The genotypes in cluster I (Jyothi) was the least stable genotype found out in the stability analysis. So, the comparison of cluster analysis results with the stability model analysis provides a similar result. The comparative analysis concludes that Cul2, Cul5, Cul9 and Cul15 are the stable accessions didn't differ very much and they can widely be used across the different environments. The least stable genotype was grouped separately indicating its less adaptability over the environments. This genotype also reported to has minimum stability across the varying environmental conditions in the stability model analysis. The intra cluster distance (Table 25) for cluster II (1.43) was relatively high representing wider diverse for the accessions in these clusters. This also shows its application of these accessions for further crop improvement programmes.

Table 23 Dissimilarity matrix of Euclidean distance

Genotypes	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**
1	0.000												
2	1.558	0.000											
3	0.587	1.267	0.000										
4	1.937	1.071	1.854	0.000									
5	2.747	1.193	2.401	1.535	0.000								
6	2.176	0.950	1.679	1.759	1.066	0.000							
7	2.506	1.035	2.170	1.772	0.682	0.985	0.000						
8	1.742	1.327	1.200	2.299	1.996	1.005	1.653	0.000					
9	3.075	1.518	2.744	1.795	0.360	1.377	0.826	2.296	0.000				
10	1.994	0.783	1.652	1.791	1.192	0.898	0.629	1.162	1.424	0.000			
11	2.748	2.085	2.185	3.004	2.237	1.301	1.979	1.021	2.456	1.733	0.000		
12	3.117	3.395	2.822	4.404	4.034	3.137	3.507	2.216	4.258	2.984	2.257	0.000	
13	1.397	1.793	0.988	2.669	2.721	1.788	2.337	0.832	3.033	1.749	1.645	1.850	0.000

Fig 5 Cluster dendrogram of grain yield (2015-2018)

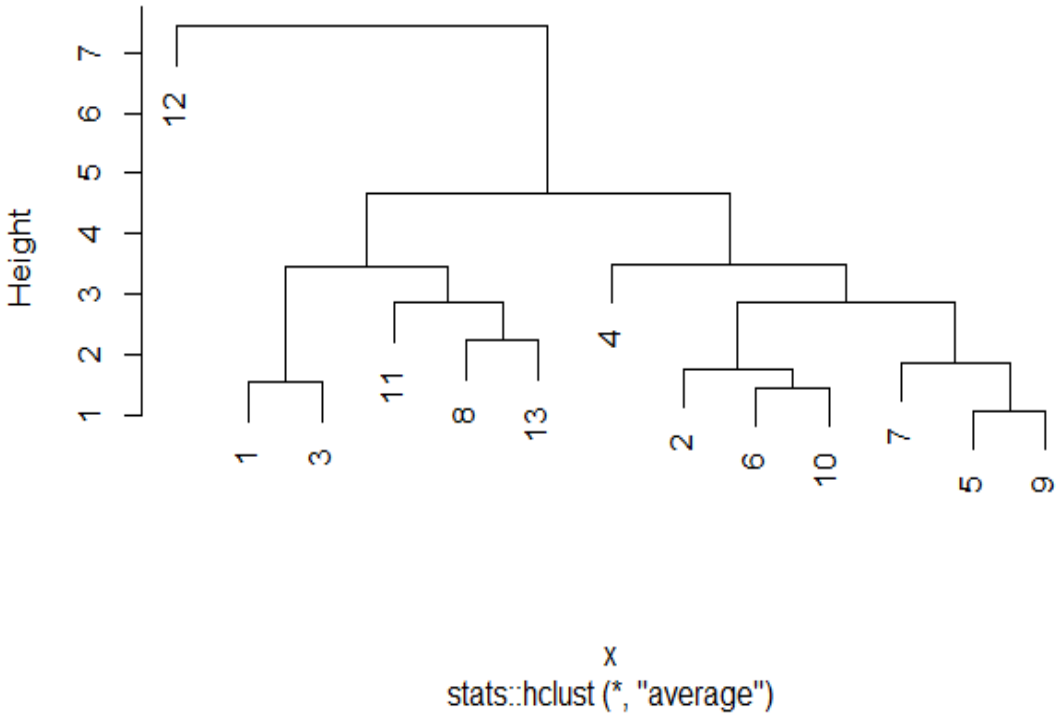


Table 24 Cluster membership of grain yield (2015-2018)

Cluster	**Genotypes**	**No of Genotypes**
I	Cul1, Cul3, Cul17, Uma, Cul13	5
II	Cul2, Cul5, Cul6, Cul9, Cul10, Cul14, Cul15	7
III	Jyothi	1

Table 25 Intra and Inter cluster distance between clusters for grain yield (2015-18)

	I	II	III
I	**1.43**	2.07	2.45
II		**1.17**	3.67
III			**0**

Note: Diagonal (**Bold**) values are intra cluster distances and off diagonal values are inter cluster distances

4.6.2 Clustering pattern of accessions over the years

The cluster analysis using hierarchical clustering technique was performed to comprehend the clustering pattern of the accessions over the years. The distance measure used for the study is Euclidean distance and the dissimilarity matrix for each year is represented in Appendix III, Appendix IV and Appendix V respectively. The clustering method adopted was UPGMA method and distance between clusters was taken as the average distance between objects. All the five characteristics were used for the clustering process. The number of clusters was chosen by using gap statistics method and the classification of classifying the accessions into four different clusters for every three years is shown in Table 26. Fig 6, Fig 7 and Fig 8 represents the dendrogram for the three years respectively.

In the year 2015-16 cluster II had the highest number of accessions i.e., six (Cul2, Cul3, Cul5, Cul9, Cul10, Cul17). In the year 2016-17 also cluster II had the maximum no of accessions i.e., six (Cul5, Cul9, Cul13, Cul14, Cul15, Jyothi) but the cluster members are different from that of the first year. The total clustering pattern was entirely different from that of the year 2015-16. In the case of 2017-18 clustering

pattern was virtually found same as that of first year (2015-16) with maximum no of accession in cluster II with the same genotypes (Cul2, Cul5, Cul9, Cul10, Cul17). The second environment (year 2016-17) is distinct from the other two environments as mentioned in the AMMI analysis and due to this reason, the clustering pattern also varied. The environmental behaviour in the first (year 2015-16) and third (year 2017-18) was nearly same which may be resulted in the similar clustering pattern.

The average intra and inter cluster distance values were calculated for each year and it is given in Table 27. In the year 2015-16, intra cluster distances ranged from 2.16 to 8.42. The highest distance was recorded for cluster II (8.42), showing its divergence as compared to other clusters. The accessions in this cluster can be further used for the hybridization purposes. High inter cluster distance was seen between Cluster I and Cluster IV (35.38) showed the peak genetic divergence followed by Cluster II and Cluster IV (30.38). In the year 2016-17, intra cluster distances varied from 2.90 to 5.92.

Table 26 Clustering pattern of genotypes (2015-2018)

Cluster	**2015-16**	**2016-17**	**2017-18**
I	Cul1, Cul6	Cul1, Cul2, Cul5	Cul1, Cul3
II	Cul2, Cul3, Cul5, Cul9, Cul10, Cul17	Cul9, Cul13, Cul14, Cul15, Jyothi	Cul2, Cul5, Cul9, Cul10, Cul17
III	Cul13, Cul14, Cul15	Cul6, Cul10, Cul3	Cul6, Cul13, Cul14, Cul15
IV	Jyothi, Uma	Cul17, Uma	Jyothi, Uma

The highest value was for the cluster I (5.92), indicating its genetic adaptability over the environments. High inter cluster distance was seen between Cluster I and Cluster IV (30.09) shows its peak genetic divergence followed by Cluster I and Cluster II (19.94). In the year 2017-18, intra cluster distances ranged from 1.44 to 13.80. The highest intra cluster was recorded for cluster II (13.8). The accessions in this cluster were almost similar to that of cluster II in 2015-16 which also had highest intra cluster distance. High inter cluster distance was seen between Cluster I and Cluster IV (36.86) followed by Cluster II and Cluster IV (29.44). The cross combinations involving the parents belonging to most divergent clusters will display maximum amount of heterosis. The greater the distance between two clusters, the wider the genetic diversity between the accessions. By accessing the above outcomes, it is advisable to use the accessions Cul2, Cul5, Cul9 and Cul15 in any of the further genetic improvement programmes.

Table 27 Intra and Inter cluster distance between the different clusters (2015-2018)

2015-16				
	I	II	III	IV
I	**4.92**	7.30	19.63	35.38
II		**8.42**	14.77	30.89
III			**2.16**	16.62
IV				**4.50**
2016-17				
	I	II	III	IV
I	**5.92**	19.94	14.31	30.09
II		**4.73**	6.27	11.19
III			**2.90**	16.04
IV				**3.40**
2017-18				
	I	II	III	IV
I	**1.44**	12.15	21.10	36.86
II		**13.80**	14.49	29.44
III			**7.47**	17.58
IV				**12.71**

Note: Diagonal (**Bold**) values are intra cluster distances and off diagonal values are inter cluster distances

Fig 6 Dendrogram of accessions in the year 2015-16

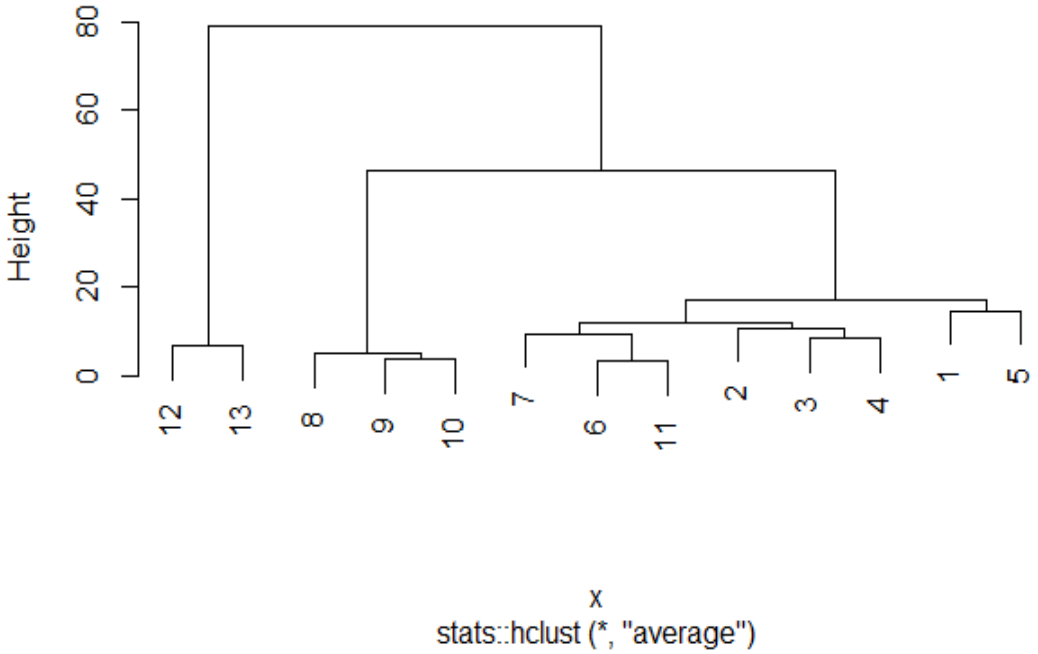


Fig 7 Dendrogram of accessions in the year 2016-17

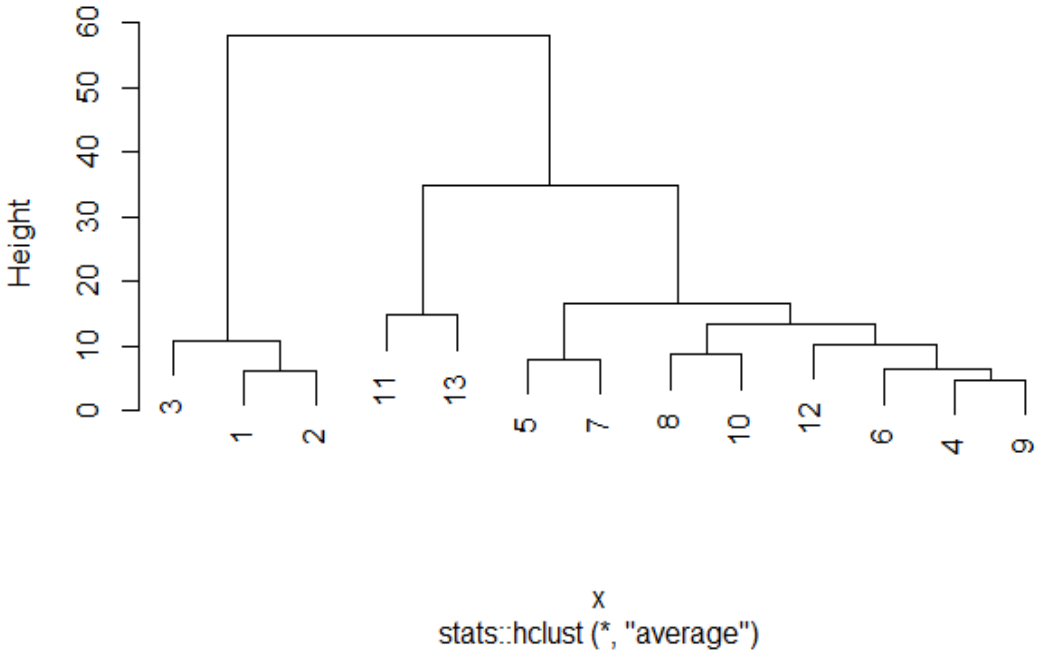
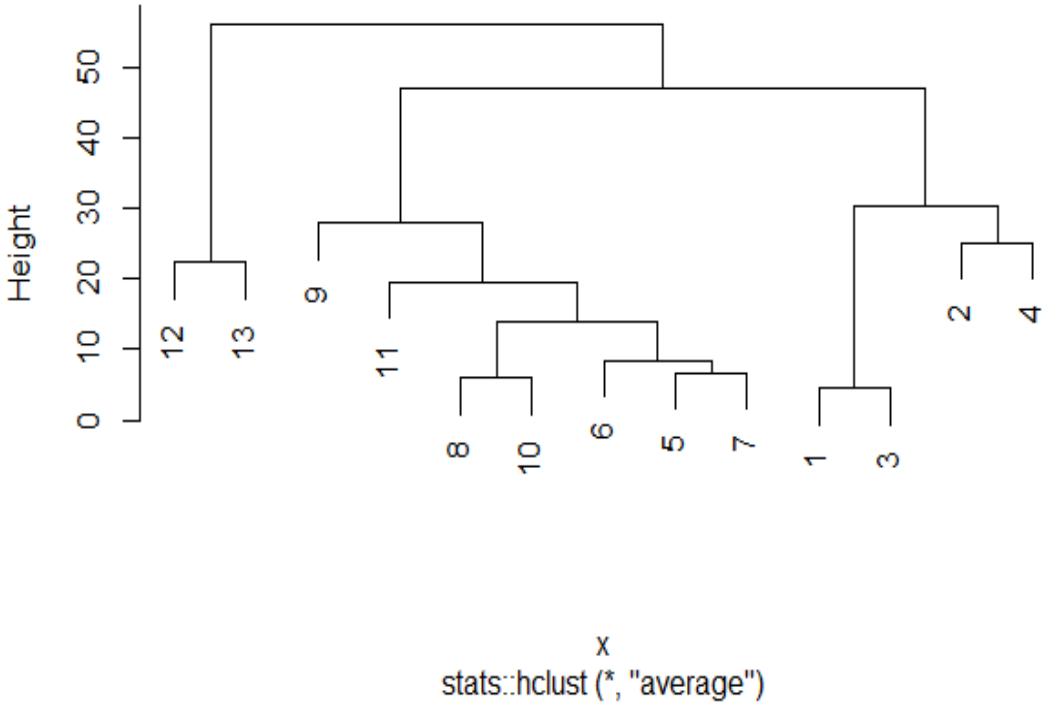


Fig 8 Dendrogram of accessions in the year 2017-18



4.6.3 Cluster mean values of characters

The cluster mean for each of the five characters over three years is given in Table 28. There was an extensive difference which existed for all the traits studied. The plant height (cm) varied from 104.33cm (Cluster IV) to 132.37cm (Cluster I), number of panicles per plant varied from 10.45 (Cluster I) to 13.28 (Cluster IV), straw yield (t ha^{-1}) ranges from 9.29 (Cluster IV) to 13.32 (Cluster II), grain yield (t ha^{-1}) ranges from 4.84 (Cluster IV) to 6.30 (Cluster II) and the 100 grain wt (g) varied from 2.17 (Cluster I) to 2.56 (Cluster II). The cluster mean value showed a wide range among the cultures studied, which indicates that genetic differences among the clusters were also reproduced in the cluster means.

It is observed that cluster II had recorded highest mean for most of the character (straw yield (t ha^{-1}), grain yield (t ha^{-1}) and 100 grain wt (g)). Cluster I exhibited highest mean for the character plant height (cm) and cluster IV for number of panicle trait. Therefore, hybridization between the selected genotypes from the divergent clusters is essential to judicously combine all the targeted traits.

The lowest cluster mean was seen in cluster IV for plant height (cm), straw yield (t ha^{-1}) and grain yield (t ha^{-1}). Cluster I had lowest cluster mean for the triats on number of panicles per plant and 100 grain wt (g). The cultures in these clusters have given less importance in the crop improvemnet programmes.

Table 28 Cluster mean values of five characters

Clusters	**Plant height(cm)**	**No of panicles**	**Straw yield (t ha^{-1})**	**Grain yield (t ha^{-1})**	**100 grain wt (g)**
I	132.37	10.45	13.16	6.11	2.17
II	126.23	10.86	13.32	6.30	2.56
III	116.82	10.69	9.52	5.79	2.42
IV	104.43	13.28	9.29	4.84	2.35

FUTURE LINE OF WORK

The present study focussed only on the comparison of stability models based on one character (grain yield (t ha^{-1})). This analysis can further be extended to adding other characteristics. The experiment emphasizes the advantages of field experiments and research trials in all agricultural and allied subjects. Similar studies should also be taken in other crops as well as for different varieties (cultures) along with varying environmental conditions to give a complete picture about the best stable genotype.

Summary

5. SUMMARY

Genes showing intra- and inter-allelic interactions are known to interact with external agencies of the organism, collectively called the environment, in producing their effects. This type of interaction is known as genotype x environment interaction which means that in dissimilar environments varieties executes differently. A quantified difference in environment may produce differential effects on genotypes. This interplay of genetic and non-genetic effects causes differential relative performance of different genotypes in different environments (Jain, 1982). In multi environment trials, genotype x environment interaction plays an important role in identifying the stable genotypes. Numerous researchers have designed statistical methods to examine such experimental data to study the stability of genotypes through subdividing of G x E interaction. However, studies on the comparison of stability analysis models are very meagre.

The research work entitled 'Comparative analysis of different stability models on superior cultures of paddy (*Oryza sativa*)' was carried out at College of Agriculture, Vellayani during 2018-2020. The objective was to compare the various linear and non-linear stability models to identify stable superior cultures of paddy and to study the clustering pattern of cultures over the years. The secondary data from the yield evaluation trail of thirteen cultures of paddy collected from RARS, Pattambi was used in the analysis. The five characters chosen are plant height (cm), number of panicles per plant, straw yield (t ha^{-1}), grain yield (t ha^{-1}) and 100 grain weight (g). Statistical analysis was carried out with the help of statistical packages including SPSS, OPSTAT and R studio.

A preliminary statistical analysis (ANOVA) was done for all the characters under study in all the three years to analyse the significant difference among the cultures. The results of the analysis confirm the significant difference in the performance of cultures for the characters plant height, straw yield and 100 grain weight in all the three years. As a first step of pooled analysis, test for the homogeneity of the error variance was done using Bartlett's Chi square test. Among the characters studied heterogeneity was observed only for straw yield.

To determine the presence of G x E interaction pooled analysis of thirteen cultures over the years was carried out for all the characters. A significant difference between the cultures and three environments was observed for the grain yield suggesting the presence of G x E interaction based on grain yield. This further indicated that there was variability among the genotypes and hence stability analysis was performed to identify the stable genotypes included in the present study.

The different stability models that are suitable for multi environmental trials are also used in the present study. These include Eberhart and Russell's model, Perkins and Jinks model, Freeman and Perkins model and AMMI models, for identifying the stable genotype. Model descriptions along with ANOVA tables for each model were presented and model wise stability parameters were estimated.

The results of ER model specified that the genotype (G), environment (E) and G X E interaction were significant for the grain yield when tested against pooled deviation and pooled error. The (Env + Gen X Env) was also found to be significant in nature. The three stability parameters *viz*. mean yield over locations or seasons ($\overline{Y_i}$), regression coefficient (b^{Ei}), and deviation from regression ($S^2_{di}(E)$) were also estimated. The result indicated that mean yield $\overline{(Y_i)}$ over the three environments varied from 4.35 t ha^{-1} to 6.82 t ha^{-1} with an average of 5.88 t ha^{-1}. The highest yield was observed for the Cul5 (6.82 t ha^{-1}) while lowest yield was recorded for Jyothi (4.35 t ha^{-1}). The estimated regression coefficient b^{Ei} of the genotypes varied from -2.65 to 4.03. Cul2 (0.74), Cul13 (0.80) and Cul 15 (1.51) had b^{Ei} values nearly equal to unity and having least deviation from regression underline its capability of adaptation to varying environments. The deviation from regression ie., $S^2_{di}(E)$ values were non-significant, and it varied from -0.22 to 0.13 indicating the adaptability of all the genotypes to unfavourable environments. Cul2 followed by Cul5 and Cul15 was identified as the stable genotypes in this method.

The stability analysis of genotypes using Perkins and Jinks model resulted in significant difference between genotypes, environments and G X E interaction for grain yield when tested against pooled error and the remainder. The three stability parameters *viz*., mean yield over the locations or seasons $\overline{(Y_i)}$, regression coefficient

(B_i) and deviation from regression (S^2_{di}) were also estimated using this model. The mean yield $\overline{(Y_i)}$ of the thirteen cultures was within the range of 4.35 t ha^{-1} to 6.82 tha^{-1} with an average of 5.88 t ha^{-1}. The estimated regression coefficients B_i varied from 3.66 to 3.03. B_i value near to zero was recorded for Cul2 (-0.26), Cul5 (-0.52) and Cul13 (-0.19), which shows their adaptation ability to varying environments. S^2_{di} estimate of this model is exactly same as that of $S^2_{di}(E)$ in ER model. Cul2 and Cul5 were found to be the most stable genotypes based on the regression estimates and deviation from regression in this model.

Freeman and Perkins model determined an independent estimation of mean performance and environmental index. The stability parameter used in this model were mean yield over locations $\overline{(Y_i)}$, regression coefficient (b_{Fi}), and deviation from regression ($\bar{S}^2_{di(F)}$). It is already observed that the mean yield $\overline{(Y_i)}$ varied from 4.35 t ha^{-1} to 6.82 t ha^{-1} with an average of 5.88 t ha^{-1}. The estimated regression coefficients b_{Fi} in this model varied from -3.50 to 6.17 with Cul2 (-0.57), Cul10 (0.71) and Cul13 (0.89) had regression coefficients (b_{Fi}) nearly equal to unity indicating their stability as compared to other genotypes. By combining the two parametric conditions for the stability of genotypes Cul10 was found to be the most stable genotype for a given environment followed by Cul2 and Cul5.

The AMMI model associates a normal ANOVA for additive main effects with PCA for multiplicative structure within the interaction. The AMMI ANOVA results indicated a significant difference between genotypes, environments at 1 percent level of significance and GEN x ENV interaction at 5 percent level of significance. The GEN x ENV interaction was further divided into two principal axes (IPCA). PC1 explained 86.6 percent of GEN x ENV interaction variance while PC2 explained 13.4 percent of the variation. The AMMI 1 biplot provided a visual view of the relationships between the interaction on the first principal component axis (PC1) and the mean of genotypes and environments. Based on this biplot the genotypes are mainly grouped into four group *viz.*, Uma to low yielding and unstable, Jyothi, Cul3 and Cul17 to low yielding and moderately stable, Cul1, Cul14 and Cul6 to high yielding and specifically adapted to favourable environments and Cul2, Cul5, Cul15 and Cul9 to the high yielding and highly stable across different environments. The

genotypes Cul2, Cul5, Cul15 and Cul9 had negligible interactions characterized by low PCA scores were considered as the relatively stable genotypes, showing broad adaptation across different environments. The PCA scores were high for the genotypes Jyothi, Uma, Cul10, Cul6 and Cul3, showing high interactions with low stability across different environments. It is evident from AMMI 2 biplot that Cul1, Cul3, Jyothi, Cul17 and Cul14 showed more sensitive interaction to environmental forces since they are away from the origin while Cul2, Cul5, Cul15, Cul9 and Cul13 showed less interaction as they are very close to the origin of the biplot. The environments E1 and E2 showed opposite characteristics since they were in the opposite quadrants of the biplot and others had no such similar interaction pattern. The AMMI analysis concluded that Cul2, Cul5, Cul15 and Cul9 had broad adaptation spectrum and were found to be highly stable.

A quantitative measure of stability known as ASTABi was calculated in the AMMI 2 model analysis. This stability measure can be considered as a measure of stability component of the genotypes. A genotype is considered to be highly stable, when the value of ASTABi is small or near to zero. Cul2 (0.005) had lowest ASTABi value and was ranked first specifying its stability in adapting a wide range of environments and highest ASTABi value was noticed for the genotype Cul1 (0.83).

The comparison between the stability models was done by ranking the stability parameters of various genotypes under each method. In order to get an idea about the agreement of ranking of four methods and Kendall's coefficient of concordance was estimated. The estimated Kendall's coefficient of concordance was W = 0.37 which is near to zero, indicating there is not much similarity between the ranking of four stability models. Hence, Spearman's rank correlation coefficient was calculated for pair wise comparison between the models. The Spearman's rank correlation between b^{Ei} and B_i was found to be unity (r = 1) indicating the strong agreement between the ranking of Eberhart and Russell and Perkins and Jinks models. Similarly, there was a strong significant rank correlation between the ranking of b^{Ei} and b_{Fi} (0.94) and B_i and b_{Fi} (0.94) indicating an almost similar type of ranking. The ranking pattern of Freeman and Perkins (FP) model were different from that of the other two regression models.

Cul2, Cul5, Cul9 and Cul15 were found to be the adaptive genotypes across the different environments on the basis of grain yield performance and the stability parameters of the different models. Cul2 was the most stable and high yielding genotype adaptable to the varying environmental conditions. However, the results of the FP model showed a deviation from the results of other two (ER and PJ) models. AMMI analysis provides better estimates than the estimates based on traditional three models. AMMI model partitions the Genotype Environment Interaction (GEI) and summarizes the patterns and relationships of G and E with more accuracy in yield estimates. So, the AMMI model was chosen as the best model from among the four models under study.

The cluster analysis was done by hierarchical clustering techniques with Euclidean distance as the measure of similarity and the genotypes were classified based on the average of the grain yield from 2015 to 2018. The clustering method used was the UPGMA clustering method and the number of clusters was chosen by a gap statistics method which established three clusters. The genotypes included in the cluster II were Cul2, Cul5, Cul6, Cul9, Cul10, Cul14 and Cul15, these are the genotypes found as the stable across various environments using four different stability models. The genotypes in cluster I was the least stable genotype found out in the stability analysis. So, the cluster analysis result when compared with the stability model analysis provides a similar result.

To visualize the clustering pattern of accessions over the years cluster analysis using hierarchical clustering techniques was done with UPGMA as the clustering method. All the five characteristics were used for the clustering process. The result depicted in classifying the accessions into four different clusters for every three years. In the year 2015-16 cluster II had the maximum number of accessions *i.e.,* six (Cul2, Cul3, Cul5, Cul9, Cul10, Cul17). In the year 2016-17 also cluster II had the maximum no of accessions *i.e.,* six (Cul5, Cul9, Cul13, Cul14, Cul15, Jyothi) but the cluster members are different from that of the first year. The clustering pattern was entirely different from that of the year 2015-16. In the case of 2017-18 clustering pattern was virtually found same as that of the first year (2015-16) with maximum no of accession in cluster II with the same genotypes (Cul2, Cul5, Cul9, Cul10, Cul17).

The average intra and inter cluster distance values were calculated for each year. In the year 2015-16, intra cluster distances ranged from 2.16 to 8.42. The highest distance was recorded for cluster II (8.42), showing its divergence as compared with other clusters. In the year 2016-17, intra cluster distances varied from 2.90 to 5.92. High inter cluster distance was seen between Cluster I and Cluster IV (30.09) shows its peak genetic divergence followed by Cluster I and Cluster II (19.94). In the year 2017-18, intra cluster distances ranged from 1.44 to 13.80. The highest intra cluster distance was recorded for the cluster II (13.8). The accessions in this cluster were almost similar to that of cluster II in 2015-16 which also had the highest intra cluster distance. It is desirable to use the accessions Cul2, Cul5, Cul9 and Cul15 in any of the further genetic improvement programmes. The cluster mean for the five characters showed extensive difference. Cluster II had recorded highest mean for most of the character (straw yield (t ha^{-1}), grain yield (t ha^{-1}) and 100 grain wt (g)). Therefore, hybridization between the selected genotypes from the divergent clusters is essential to judicously combine all the targeted traits.

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COMPARATIVE ANALYSIS OF DIFFERENT STABILITY MODELS ON SUPERIOR CULTURES OF PADDY (*Oryza sativa*)

by

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Abstract of thesis

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ABSTRACT

The research work entitled 'Comparative analysis of different stability models on superior cultures of paddy (*Oryza sativa*)' was carried out at College of Agriculture, Vellayani during 2018-2020. The objective was to compare various linear and nonlinear stability models to identify stable superior cultures of paddy and to study the clustering pattern of cultures over the years. Secondary data from various performance evaluation trials conducted on superior cultures of paddy (13 cultures) over the years (2015-2018) at RARS, Pattambi was used for the analysis. The five characters included in the study were plant height (cm), number of panicles per plant, straw yield (t ha^{-1}), grain yield (t ha^{-1}) and 100 grain weight (g).

Bartlett's Chi square test was used for testing the homogeneity of the error variance over the years for all the characters as an initial step. Among the five characters only straw yield has shown heterogeneity in error variance. Further, pooled analysis was done to test G X E interactions based on all the characters. The results of pooled analysis confirmed a significant G X E interaction for grain yield, straw yield and plant height revealing that genotypes responded differentially to environment.

The stability of 13 paddy cultures over the years was done using Eberhart and Russell's model, Perkins and Jinks model, Freeman and Perkins model and AMMI model. ANOVA and stability parameters viz regression coefficient and deviation from regression for each model was estimated. The stable genotypes identified in Eberhart and Russell's model based on regression coefficient (b^{Ei}) and deviation from regression ($S^2_{di}(E)$) were Cul2 followed by Cul5 and Cul15. In case of Perkins and Jinks model the stable genotypes determined on the basis of the regression coefficient (B_i) were Cul2 and Cul5. However, Cul10 followed by Cul2 and Cul5 were found to be the stable genotype under Freeman and Perkins model with respect to the stability parameter- regression coefficient (b_{Fi}). AMMI model incorporates Principal Components Analysis (PCA) for GEI and based on the results of this model cultures Cul2, Cul5, Cul15 and Cul9 were identified as the stable genotypes across different environments particularly in first and third environments. Env 1 and Env 2 showed opposite characteristics while Env 2 was comparatively more stable than other two but

was less yielding. One among the AMMI Model selection indices named as AMMI based Selection Index (ASTABi) was used to rank the genotypes to obtain the stable genotypes. This also resulted in obtaining the most stable genotypes as Cul2.

Comparison of the four stability models was carried out using Kendall's coefficient of concordance revealed no similarity among the ranking of parameters of these four models. Spearman's rank correlation coefficient was determined for the pair wise comparison of fur models. The correlation matrix and correlogram was also obtained. A perfect positive rank correlation was observed between the parameters of Eberhart and Russell model and Perkins and Jinks model suggesting the similarity of the parameters under these two models. Whereas the rank correlation between Eberhart and Russell and Freeman and Perkins with AMMI model were non-significant indicated the deviation of the results in AMMI model from other two models. However, AMMI model was found to be the best since complete enumeration, summarization, and pattern of GEI interaction was made possible only in this model. The most stable genotype based on the entire four models was Cul2 followed by Cul5, Cul9 and Cul15.

The hierarchical cluster analysis using euclidean distance as similarity measure and average linkage as clustering method was performed using the grain yield over the three years (2015-2018). This result of the study also emphasised that the highly stable genotypes identified under different stability models were clustered together in a single cluster (Cluster II). The intra cluster and inter cluster distance measure revealed that there was high genetic divergence between the clusters in which the stable genotypes are included. Cluster analysis was also performed for different years based on all the characters under study. The clustering pattern in the year 2015-16 and 2017-18 was found to be almost similar in nature since the genotypes enclosed in the clusters were nearly same. In the year 2016-17 the clustering pattern was found to be different from other two years. This shows the influence of environment in the performance of the genotype. The clusters in which high genetic divergence was found in the year 2015-16 which was similar to that of the clusters in 2017-18. The cluster mean for the five characters under study showed extensive difference. Cluster II had recorded highest mean for most of the character (straw yield (t ha^{-1}), grain yield

(t ha^{-1}) and 100 grain wt (g)). Therefore, hybridization between the selected genotypes from the divergent clusters is essential to judicously combine all the targeted traits.

Among the different stability models studied Eberhart and Russells and Perkins and Jinks models provided almost similar stable cultures which was highly related to the cultures selected on the basis of AMMI model. Moreover, the different stability cultures identified were put together in one cluster in cluster analysis further confirmed the superiority of the stable genotypes over the others.

Appendices

Appendix I

Mean grain yield performance of genotypes over each environment

Genotypes	**First**	**Second**	**Third**	**Mean**
Cul1	5.145	6.090	6.080	6.017
Cul2	6.510	6.180	6.970	6.257
Cul3	5.415	5.690	6.495	5.867
Cul5	7.040	6.450	6.815	6.820
Cul6	7.590	6.140	5.570	6.433
Cul9	6.785	5.440	5.555	5.927
Cul10	7.045	6.320	5.205	6.190
Cul13	5.810	5.255	5.445	5.503
Cul14	7.850	6.295	5.375	6.507
Cul15	6.435	6.225	5.305	5.988
Cul17	6.195	4.595	4.770	5.187
Jyothi	4.030	4.855	4.180	4.355
Uma	5.015	5.275	5.690	5.327
Mean	6.220	5.755	5.650	

Appendix II

Dissimilarity matrix of Euclidean distance (2015-16)

Genotypes	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**
1	0.00												
2	4.81	0.00											
3	5.50	5.17	0.00										
4	6.74	5.36	3.65	0.00									
5	8.42	8.67	4.19	5.62	0.00								
6	9.50	5.82	5.78	4.58	8.02	0.00							
7	8.86	6.31	6.88	3.68	9.16	4.53	0.00						
8	17.63	14.01	17.14	14.84	20.14	12.72	11.40	0.00					
9	18.47	14.94	18.27	15.69	21.05	13.92	12.18	2.55	0.00				
10	18.91	15.21	18.57	16.29	21.55	14.06	12.88	1.71	2.22	0.00			
11	9.10	5.65	5.05	4.69	7.40	1.25	5.39	13.67	14.97	15.02	0.00		
12	33.88	30.65	34.18	31.90	37.29	29.81	28.38	17.16	16.55	15.85	30.72	0.00	
13	33.07	29.97	33.98	31.87	37.26	29.94	28.49	17.45	16.66	16.03	30.81	4.50	0.00

Appendix III

Dissimilarity matrix of Euclidean distance (2016-17)

Genotypes	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**
1	0.00												
2	2.82	0.00											
3	3.23	4.16	0.00										
4	17.68	19.32	15.54	0.00									
5	13.42	15.00	11.21	4.34	0.00								
6	18.34	19.58	16.04	3.65	5.57	0.00							
7	15.62	17.07	13.53	3.06	2.90	3.20	0.00						
8	23.57	25.01	21.50	6.81	10.59	5.79	8.06	0.00					
9	19.15	20.74	16.89	1.71	5.76	3.90	4.51	6.09	0.00				
10	21.66	22.96	19.35	4.90	8.47	3.55	6.17	3.30	3.97	0.00			
11	28.16	29.70	26.25	11.43	15.36	10.77	12.86	5.01	10.61	8.09	0.00		
12	20.99	22.32	18.35	5.32	8.09	5.66	7.37	7.40	3.90	4.92	11.50	0.00	
13	32.31	33.92	30.19	14.74	19.01	14.71	16.91	9.36	13.44	11.40	5.92	13.18	0.00

Appendix IV

Dissimilarity matrix of Euclidean distance (2017-18)

Genotypes	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**
1	0.00												
2	8.03	0.00											
3	1.44	9.37	0.00										
4	15.30	13.80	15.90	0.00									
5	20.03	12.96	21.23	13.41	0.00								
6	20.06	13.83	21.18	10.95	3.61	0.00							
7	17.95	11.21	19.11	11.44	2.37	3.44	0.00						
8	21.63	13.97	22.87	17.05	3.95	7.48	5.72	0.00					
9	27.74	19.84	29.07	22.99	9.94	12.26	12.10	7.51	0.00				
10	19.91	12.15	21.16	16.97	4.97	8.50	5.90	2.36	9.01	0.00			
11	16.08	8.19	17.36	17.92	9.45	12.15	9.09	8.14	13.04	5.93	0.00		
12	37.46	29.80	38.66	32.99	20.23	23.00	22.26	16.97	14.09	18.01	22.20	0.00	
13	35.01	27.32	36.31	27.65	15.58	16.90	17.90	13.99	8.10	16.02	20.90	12.71	0.00