Original Research Article

ANALYSIS OF YIELD STABILITY IN DIVERSE RICE GENOTYPES

ABSTRACT

Aims/ objectives: This study aims to improve stable and sustainable rice varieties adaptable to changing climatic conditions.It involves assessing genetic variability and Genotype X Environment interaction (G x E) among 186 diverse rice genotypes. The goal is to select genotypes with high breeding value, contributing to the development of rice varieties well-suited to varying climatic conditions.

Study Design: The study employed an augmented design in a Randomized Complete Block Design (RCBD~~)~~). Swarna, Madhuraj-55, Safri-17, Improved Samba Mahsuri, Thavalkannan, and IR64 checks were replicated across environments.

Place and Duration of Study: The study took place in College of Agriculture, Raipur, IGKV, under diverse environmentsover two years (wet season-2020 and 2021).

Methodology: Analysis of genetic variability and G X E interaction among 186 rice genotypes.Execution of the experiment in an augmented design with a randomized complete block design.Replication of standard rice checks across different environments.Assessment of yield-attributing traits such as plant height, number of effective tillers, panicle length, number of grains per panicle, biological yield per plot, and grain yield.Evaluation of stability was done using univariate (Shukla stability variance, Wricke'secovalence, Kang stability statistic) and multivariate (AMMI yield stability index and GGE biplot) stability parameters.Selection of stable genotypes with high yield based on stability analyses.

Results: Significant phenotypic variation was observed in yield-attributing traits across seasons.Genetic variability and G x E interaction effect demonstrated by variable genotype performance across environments.Univariate and multivariate stability parameters (S^2i, W^2i, KSi, AMMI stability value, GGE biplot) were used for stability analyses.Identification of stable genotypes with high yield across environments, including IR13f167, ARC13156, IR93354, F50, Ngalongyi, Giza 178, Arc 10159, Sadajira 19-317, Arith, IR 57920-Ac 25-2-B, Pesagro 102, Mekenzie small, Nasaenge, Kula Karuppan, Vary Gony, MR 69, Kanu Dam, IRRI 123, Sativa IRGC17083-1, Kalia, and Swarna.

Conclusion: The study concludes that stability in genotype performance across diverse environments is crucial for the development of sustainable rice varieties.Genotypes with high stability and yield, as identified through stability analyses, hold potential breeding value for developing rice varieties adaptive to

Comment [MMAA1]: ????????????????????????????

Formatted: Underline, Highlight

Formatted: Underline, Highlight

Formatted: Superscript

Formatted: Superscript

climate change.The stable genotypes listed, including IR13f167, ARC13156, IR93354, and others, are recommended for further breeding and development efforts to enhance rice productivity and adaptability.

Keywords: Rice; stability; Genotype X environment Interaction;GGE biplot, high yield.

1. INTRODUCTION

Rice is cultivated under different agro-climatic conditions therefore it exhibits varying phenotypic expressions in response to climate and annual fluctuations. Breeders frequently utilize phenotypic expression along with yield performance for screening and selection of suitable varieties in different test environments. Previously, plant breeding programs have relied on several techniques to enhance crop potential and generate high-yielding cultivars however, current trends in breeding rapidly shift in focus to prioritizing stability and adaptability of cultivar performance. ~~[13,22].~~

Initiating a multi-environment study is essential to identifying the complex relationships between genotype and environment in rice cultivation and to provide a comprehensive assessment of stability and adaptation across locations and years. Inmulti-environment analysis,genotypes were analyzed in different locations and years and estimated changes in yield due to their response to various environmental factors such as soil fertility, temperature, presence of pathogenic diseases, etc. [16]. Genotype × environmental interaction has a significant effect on the phenotypic variation of genotypes under different seasons and locations,[18]. The stability and adaptability of the genotypes have been analyzed using various statistical tools such as analysis of variance (ANOVA), joint regression analysis, additive main effects and multiplicative interaction (AMMI), and genotype main effect plus genotype-by-environment interaction (GGE) biplot, and non-parametric stability statistics. Analysis of variance (ANOVA) is frequently employed in the analysis of multi-environmental yield trials to determine if a G × E interaction exists. ANOVA tests the significance of genotype by environment interaction and only evaluates the component of variation present among random and fixed factors (e.g. genotype, replication, site, year, etc.). ANOVA has limitations in differentiating the genotypes in non-additive terms known as G × E [36]. Numerous statistical techniques have been designed to evaluate genotype stability, representing several GEI aspects that may be utilized to identify genotypes that function consistently in various contexts. The most prominent method for evaluated stability analysis is Shukla's stability variance (S2i), which is a linear combination of Wricke'secovalance(W2i), which is the percentage of each genotype's contribution to the variance in the environment caused by genotype. Low W2i and S2i genotypes are thought to be stable [15]. Genotypes with low W2iand S2iare regarded to stable [14]. Kang's stability statistic (KSi) is a non-parametric stability approach introduced by [17]. It employs both the mean (M) andS2i, giving each equal weight. The genotype with the highest yield and lower S2i is assigned a rank of 1. Then, the ranks of yield and stability variance are added for each genotype and Genotypes with a lowest rank sum (KSi) are the most stable.

Comment [MMAA2]: 1,2

Formatted: Strikethrough, Highlight

Formatted: Strikethrough, Highlight

Formatted: Strikethrough

Comment [MMAA3]: 3

Formatted: Highlight

Formatted: Highlight

Comment [MMAA4]: 4

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

Multiplicative models having the additive main effect and multiplicative interaction (AMMI) model is used in the analysis [11]. The AMMI model evaluates the performance of genotypes in various settings by fitting the sum of many multiplicative terms as opposed to only one multiplicative term [4]. AMMI analysis is used to determine the stability of the genotypes across locations using the AMMI stability value (ASV) and PCA (principal component axis) scores[12]. The interaction main components axes 1 and 2, respectively, IPCA1 and IPCA2 scores for each genotype in the AMMI model form the basis of the ASV[26]. Widely adapted genotypes are the ones with the least ASV. Stability does not give much information about the level of yield so Farshadfar[9]and Tumuhimbise[30].used the yield stability index (YSi) which combined high-yield performance with stability. The YSi is based on the sum of the yield or performance ranking and ranking according to ASV scores. Lower YSi values indicate genotypes having high yield or performance with stability. GGE biplot analysis is a useful method that is extensively being employed to evaluate yearly MET data. The GGE biplot presents these interactions in a two-dimensional graphical format and explains how environments differentiate across genotypes and how genotypes react to various environments[33].

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

This study involved the assessment of yield-related traits and grain yield performance in 186 rice genotypes cultivated over two years. Furthermore, it investigates the correlation between grain yield and other yield contributing parameters. The objective of is present study to understand and identify stable genotypes across different seasons, accounting for their responses to environmental conditions using Multi-Environment Analysis (MEA). These findings can offer valuable insights for effective guidance in future breeding programs aimed at the development of climate resilient varieties

2. MATERIALS AND METHODS.

2.1 Plant materials, locations, and cultural practices

186 diverse rice genotypes, including checks, were utilized to determine the grain yield and its correlation with other characteristics. The study was carried out at the research farm of the College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur (21^0 16' N and 81^0 36' E at an altitude of 289 meters above sea level),during the Wet Season seasons 2020 and 2021. All 186 diverse genotypes including checks were transplanted and each genotype covered a one m^{2}area. In augmented design (RCBD), 3 blocks including 6 checks were used for the field experiment and checks were repeated in each block. (genotype name list in supplementary table) during the Wet Season 2020 and Wet season 2021. Normal management practices and measures to protect plants were taken during crop growth.

Formatted: Superscript

2.2 Data Collection

At various phenological stages, the phenotypic data of yield and yield-related traits were recorded. Observationswere taken on five randomly tagged plants of each genotype and data was recorded on quantitative characters, it included days to 50% flowering (DFF), plant height (PH), panicle length (PL), effective number of tillers/plant (ETN), Total number of grains/panicle (NGP), Biological Yield(gm)/plot (BY) and Grain yield(gm)/plot (GY). The grain yield was measured by weighing the plot yield (1 m^2 each) at a 13% moisture level.

Formatted: Superscript

2.3 Data analysis

Phenotypic data were used for statistical phenotypic data analyses. Analysis of variance (ANOVA) augmented design RCBD was estimated using the R studio package version (augmentedRCBD)[5,28].Stability ~~Analysis~~ analysis for grain yield was computed using the Shukla stability variance (S2i), Wricke'secovalance(W2i), Kang's stability statistic (KSi), AMMI Yield stability index and GGE biplot[5,28]. Stability analysis was computed using R studio, a simplified version of R statistical. Metan package is used for GGE biplot while stability packages were used to compute Shukal's variance, Wricke'ecovalence, Kang stability statistics, and AMMI yield stability index in R studio respectively[33]

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

3. RESULTS AND DISCUSSION

The rice grain yield is one of the most important aspects of crop improvement and is influenced by a variety of complex traits[22]. A phenotypic assessment of 186 genotypes was carried out in Wet Season-2020 and Wet Season-2021. The assessment revealed significant variations in all the traits related to grain yield (as shown in table 1). In the two wet seasons (2020 and 2021), a high magnitude of the coefficient of variation (more prominent than 10%) was seen across all genotypes for the accompanying characteristics: total grain yield per plot (22.69 % and 22.72 %) and total effective tillers per plant (27.46 % and 15.59 %), Biological yield (21.23% and 12.68%) and grain yield 22.69% and 22.72%)(Table1).Significant differences as revealed by ANOVA among the genotypes for all the characters in 2020 and 2021, treatment unadjusted and treatment adjusted, indicating the presence of high variability among the rice genotype, and effective tillers showed a nonsignificant result in 2020.(Table 2 and Table 3).

Formatted: Highlight

Table 1. Mean Performance of rice genotypes in Wet Season-2020 and Wet Season-2021

Traits	Season	Mean±SD	Range	SE	CV%	CD
DFF	2020	98.58±11.86	67.22-126.56	0.87	2.33	0.12
	2021	105.31±14.48	60.22-138.22	1.06	2.02	0.14
PH	2020	117.67±25.23	58.84-170.61	1.85	9	0.21
	2021	144.52±26.99	79.35-191.37	1.98	13.66	0.19
PL	2020	24.8±2.97	17.35-35.71	0.22	4.03	0.12
	2021	25.58±2.6	19.02-32.4	0.19	8.11	0.11
ENT	2020	8.43±2.35	3.48-17.68	0.17	27.46	0.27
	2021	7.51±1.87	4.02-12.86	0.14	15.59	0.25
NGP	2020	130.04±46.32	46.67-274.8	3.4	18.32	0.36
	2021	135.95±48.02	46.24-281.74	3.52	20.5	0.35

BY	2020	1013.6±516.2	63.8-2488.8	37.8	21.23	0.51
	2021	1475.6±648.3	248.8-3325.0	47.5	12.68	0.43
GY	2020	287.0±202.4	9.4-1291.3	14.8	22.69	0.72
	2021	360.8±157.2	38.1-760	11.5	22.72	0.44

DFF- Days To 50% Flowering, PH- Plant Height, PL- Panicle Length, ENT- Effective Number of Tillers per plant, NGP-Number of grains /Panicle, BY- Biological Yield (g/sq. m.), GY- Grain Yield (g/sq. m.)

Table 2.Analysis of variance (ANOVA) for yield and yield-related traits in 186 rice genotypes during Wet Season 2020

Source	Df	DFF	PH	PL	ENT	NGP	BY	GY
Block unadjusted	2	332.23 **	5509.26 **	59.29 **	0.54 ns	39501.11 **	10294998.38 **	2259296.29 **
Treatment unadjusted	185	146.34 **	727.24 **	9.43 **	5.64 ns	2324.52 **	704129.76 **	107270.27 **
Block adjusted	2	7.39 ns	405.39 ns	0.69 ns	0.35 ns	738.3 ns	5101.39 ns	10040.72 ns
Treatment adjusted	185	142.82 **	672.07 **	8.8 **	5.64 ns	1905.46 *	592887.63 **	82953.99 **
Treatment: Check	5	293.56 **	1543.66 **	7.11 **	6.86 ns	3326.81 **	653545.29 *	109419.69 **
Treatment: Test	179	139.09 **	653.52 **	8.95 **	5.57 ns	2244.23 **	690787.21 **	106563 **
Treatment: Test vs. Check	1	706.81 **	9840.77 **	108.15 **	11.66 ns	11683.44 **	3345367.42 **	223124.12 **
Treatment: Test and Test vs. Check	180	138.64 **	647.85 **	8.85 **	5.61 ns	1865.98 *	591202.69 **	82218.83 **
Residuals	10	5.26	109.53	0.99	5.42	554.01	118123.12	10597.26

*ns P > 0.05; * P <= 0.05; ** P <= 0.01*

Table 3. Analysis of variance (ANOVA) for yield and yield-related traits in 186 rice genotypes during Wet Season 2021

Source	Df	DFF	PH	PL	ENT	NGP	BY	GY
Block unadjusted	2	2504.02 **	1709.2 *	4.39 ns	6.89 *	33257.24 **	10206567.7 **	115697.28 *
Treatment unadjusted	185	213.36 **	778.83 ns	6.92 ns	3.56 *	2367.52 *	1089297.68 **	64611.7 *
Block adjusted	2	2.72 ns	13.68 ns	2.99 ns	2.07 ns	974.28 ns	68678.72 ns	2570.67 ns
Treatment adjusted	185	186.31 **	760.5 ns	6.9 ns	3.51 *	2018.51 *	979698.88 **	63388.71 *
Treatment: Check	5	319.82 **	2709.56 **	16.01 *	3.58 ns	3591.79 *	433884.49 *	73091.07 *
Treatment: Test	179	204.94 **	708.25 ns	6.7 ns	3.58 *	2276.33 *	1105077.47 **	64731.12 *
Treatment: Test vs. Check	1	1186.91 **	3758.74 *	0.06 ns	0.62 ns	12567.95 **	1541781.95 **	838.5 ns
Treatment: Test and Test vs. Check	180	182.61 **	706.36 ns	6.65 ns	3.51 ns	1974.81 *	994860.4 **	63119.2 *
Residuals	10	4.59	384.9	4.3	1.37	758.13	88236.79	17175.13

*ns P > 0.05; * P <= 0.05; ** P <= 0.01*

DFF- Days To 50% Flowering, PH- Plant Height, PL- Panicle Length, ENT- Effective Number of Tillers per plant, NGP-Number of grains /Panicle, BY- Biological Yield (g/sq. m.), GY- Grain Yield (g/sq. m.)

In the present study, genotype performance has changed across the environment due to genotype-environment interaction. The presence of GEI in multi-environment trials is expressed in different genotypes (genetic makeup of individuals) that can respond differently to various environments. Stability analysis was computed for grain yield using different statistical approaches. The first approach is univariate analysis, Univariate stability methods according to Mekbib [23], univariate stability Shukla stability variance (S2i),Wricke'secovalence(W2i) and Kang stability statistic (KSi). Multivariate analysis is AMMI Stability Value, yield stability index (YSi), and GGE biplot [21]

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

3.1 Wricke'secovalence (W^2i) and Shukla's stability variance (S^2i)

According to Wricke[30] and Shukla [28], if a genotype's performance with respect to the environment is parallel to the mean performance of all genotypes in the trial, it is considered to be stable.Wricke's equivalence (W2i) defined the contribution of each genotype to the G × E interaction sum of squares while Shukla stability variance (S2i) is a measure of stability rather than mean performance. a genotype is considered to be stable according to these concepts, if it's having lowW2i and S2i. As per this study, the genotypes having the lowest stability variance are regarded as the most stable ones and they are ranked top. For grain yield there are 82 genotypes that have low W2i and S2i moreover here top ranked genotypes which has the lowest W2i and S2i with high mean yield are Kalia>BR-51>Kalukaruppam>kanudam> War72-2-1-1>Eanouna>MR 69> Makenzie small>Dhaneburwa>Sadajira 19-317> Vary Gony. According to Becker and Leon[3],the level of interaction in response of genotypes across environments is determined by the range of variables. Genotypes having the lowest interaction variance are more stable or they are less responsive to the environment while the ones with larger variances are having more environmental influences Nevertheless, it was very challenging to find the same pattern of response to support this hypothesis, which may complicate selection when taking into account various stability analyses on genotypes because variations in genotype ranking variance show that some genotypes are less sensitive to environmental influences than others.

Formatted: Highlight

3.2 Kang stability statistic (KSi)

Even while the various stability statistics show high, midrange, and low stability performance, they are neither helpful or instructive in the selection process until they are combined with yielding capacity. Thus, attempts have been made to create a single selection criterion that incorporates yield and stability parameters (ecovalence and stability variance) [15]. kang-stability statistic (KSi) was developed by Kang ([17] which can be used as a selection criterion if the G × E interaction is significant and also to demonstrate the benefit of stability in their yield performance to the growers Therefore, genotypes with low KSi values with higher mean yield were considered stable genotypes [14]. According to this concept (KSi), the top ten genotypes with the highest mean yield of population and low KSi across are War 72-2-1-1>Kula Karuppan>EaNouan> IR13f167>Sadajira 19-317> IR93354> Kanu Dam> Mekenzie Small> Kalia.

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

3.3 Additive main effect and multiplicative interaction (AMMI) stability Value and

The AMMI model does not provide for a quantitative stability measure and it is required to quantify and rank genotypes according to yield stability [15,10]. Therefore, the AMMI stability value (ASV) was proposed by Purchase[26]) to quantify and rank genotypes according to their yield stability. Additive main effect and multiplicative interaction (AMMI) stability value (ASV) ranked the genotypes based on the lowest score Low scores of ASV represent the most stable genotypes and genotypesBucayab>ARC 18202>Sufaid 246> Tsao Sheng Li 1> ARC 13778>Qinognas>Leuang Lai Mae Prajan> Barik Kudi> Kalia> Br 51-115-4 have low ASV.

Formatted: Highlight

3.4 Yield stability index

Yield stability index (YSi) is another approach which is calculated by ranking the mean grain yield of genotypes across environments and ranking of AMMI stability value. Mean yield and stability are incorporated in YSI in a single criterion as follows. The yield stability index same as the ASV score, A Low score of YSi was a stable genotype and a high score of YSi is the least stable genotype. stable genotypes with high mean yield are the ones with low value of this parameter. The rice varieties which are suited to the various environmental conditions can be identified using these parameters. Stability per se should however not be the only selection parameter because the most stable genotypes would not necessarily give the best yield performance[24,25]. As a result, methods that combine mean yield and stability into a single index are required, which is why different authors have proposed diverse selection criteria for yield and stability selection at the same time. [7,17,6,2,27,8,1]. Since ASV considers both IPCA1 and IPCA2, the majority of the variation in the GE interaction is justified in this regard. As a result, the ranks of ASV and yield mean are summed to create the yield stability index (YSi), which is a single simultaneous selection index of yield and yield stability. The lowest rank of ASV is rank one, while the highest rank of yield mean is rank one. The lowest YSi is considered the most stable with a high grain yield. Based on the YSi, the most stable genotype was War 72-2-1-1, and genotype Toduli was ranked the least stable

Formatted: Highlight

Formatted: Highlight

because it had the highest YSi. A low ASV score and low YSi score are desirable since they combine high mean yield performance with stability. So as above statement, genotype War-72-2-H>Kalukaruppam>EaNouna>Sadajira, >IR13f167 >IR93354>Kanu Dam> F50 >Mekenzie Small> Giza 178 were most stable genotypes.

3.5 Genotype plus Genotype by Environmental Biplot (GGE biplot)

The GGE is the sum of genotype main effect (G) and the genotype by environment interaction (GE) effect. Genotype evaluation in multi-environment trials (MET) is done by considering G and GE which are the two main source of variation [34]. The GGE biplot result showed the existence of wide variations in grain yield performance across the testing environments [20]. Principal component 1(PC1) represents 63.14% variation among genotypes whereas Principal component 2 (PC2) has 36.86% variation among genotypes. The vector of the line extending from the origin represents Environment 1 (E1) and Environment 2 (E2) and the angle between that environment indicates the degree of correlation between the two environments [32,34,35]. (fig1) In the GGE biplot, genotypes were represented as a dot across the biplot and the position of genotypes indicates the performance of genotypes across the environments. Genotypes closer to the origin perform consistently stable across environments and farther of origin indicate the more variation of performance across the different environments. In GGE biplot, genotypes were distributed across on the biplot and the position of genotypes indicate the performance of genotypes across the environments. Distance from the origin represents the magnitude of genotype performance and Genotypes closer together are more similar in performance across environment [19]. In this study, genotypes GojalGoria, J 6 IR 520 (Wc693), PSBRC 88, Maloba (Dissi Rouge), BengalyMorimo, IR 77390-1-6-4-19-1-B, PSBRC 18, LudiGochya, Aus 295, Kalalan and IR13f167 are closer to the origin and considered as stable genotypes which has less affected by across environments. The genotype DamnoeubKhseSaut, Ta Pai Maung, B 12, Bw 295-5, G 25, Moshi, RD 15, H 6, Hua Li Zao, and Noh Hai has away from origin might be adapted to specific environment. Biplot based on position of genotypes and vectors in quadrants. Quadrants are formed by the intersection of PC1 and PC2. Genotypes in the same quadrant respond similarly to the main sources of variation. in our result QI has 44 Genotypes with positive scores on both PC1 and PC2. That means all 44 genotypes across QI has performed well across environments [32,19]. In QII, 34 Genotypes with positive PC1 and negative PC2 may be perform well in certain environments. In QIII 64 Genotypes with negative scores on both PC1 and PC2 that means they poorly performance and QIV, 44 Genotypes with negative PC1 and positive PC2 may be perform better in specific environment and Genotype RD 15 and DamnoeubKhseSaut were highly adopted in E1 and E2 respectively. The most stable with high yielding genotypes which is present in QI were selected, IR13f167, IR93354, F50, Mekenzie Small, Ngalongyi, Sadajira 19-317, War 72-2-1-1, ARC 13156, Kula Karuppan and IRRI 123 across the environment.

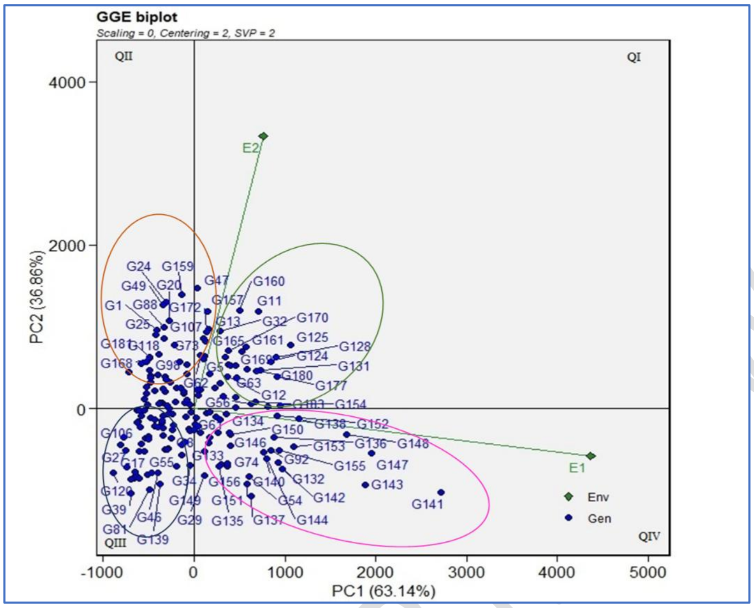

Fig1. GGE biplot of genotype across the E1 and E2 (green color circle- stable genotypes across environment, Brown color- adaptable in E2 and pink color circle – adaptable in E1 and blue color- unstable genotypes).

The selected genotypes havefulfilled all stability analysis criteria, including low W2i, low S2i, low KSi, low ASV, and low YSi, while consistently have high mean yield across seasons. (Table 4). Selected genotypes i.e., IR13f167(631.06), ARC13156(601.88), IR93354(579.50), F50(562.31), Ngalongyi (556.31), Giza 178(527.94), Arc 10159(525.63), Sadajira 19-317(515.63), Arith (508.75), IR 57920-Ac 25-2-B (480.31), Pesagro 102 (472.5), Mekenzie small (465.93), Nasaenge (464.06), Kula Karuppan (462.81), Vary gony (460.62), MR 69 (407.18), Kanu Dam (442.5), IRRI 123 (434.06), sativa IRGC17083-1 (420.93), Kalia (418.12) and Swarna (367.65)

Formatted: Highlight

Table 4. Most stable genotypes across the environment with highest mean yield performance.

Accessions	Mean Yield (g/sq. m)	Mean Rank	W2i	S2i	KSi	ASV	ASV rank	YSi
IR13f167	631.0625	4	5255.054	4895.8	4	49045051	44	48
ARC 13156	601.875	6	38055.21	38052.5	121	1.32E+08	115	121
IR93354	579.5	7	5255.054	4895.8	7	49045051	44	51
F50	562.3125	8	5255.054	4895.8	57	49045051	44	52
Ngalongyi	556.5625	10	25339.24	25198.3	109	1.08E+08	99	109
Giza 178	527.9375	12	5255.054	4895.8	12	49045051	44	56
Arc 10159	525.625	13	6484.462	6138.6	67	54678377	54	67
Sadajira 19-317	515.625	15	3708.225	3332.2	47	41361834	33	48
Arith	508.75	16	5819.175	5466	68	51797171	52	68
IR 57920-Ac 25-2-B	480.3125	24	16359	16120.4	108	86851847	84	108
Pesagro 102	472.5	26	36482.09	36462.3	137	1.3E+08	111	137
Mekenzie Small	465.9375	28	3111.12	2728.6	28	37871340	28	56
Nasaeng	464.0625	30	13265.14	12992.9	107	78208228	77	107
Kula Karuppan	462.8125	31	267.2399	-146.2	43	11109167	12	43
Vary Gony	460.625	33	4596.601	4230.2	33	46034758	40	73
MR 69	407.1875	51	2973.656	2589.6	78	37040024	27	78
Kanu Dam	442.5	39	508.2049	97.4	52	15301891	13	52
IRRI 123	434.0625	43	10821.97	10523.2	113	70654098	70	113
Sativa IRGC 17083-1	420.9375	45	21036.86	20849.1	136	98505759	91	136
Swarna	367.625	60	19824.15	19623.3	148	95624553	88	148

Wricke'secovalence (W2i), Shukla stability variance (S2i), Kang stability statistic (KSi), AMMI stability value (ASV), Yield stability index (YSi)

Comment [MMAA5]: False values

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

Formatted: Highlight

4. CONCLUSION

The performance of the rice genotypes has been significantly affected by the environment, however some of the genotypes IR13f167, ARC13156, IR93354, F50, Ngalongyi, Giza 178, Arc 10159, Sadajira 19-317, Arith, IR 57920-Ac 25-2-B, Pesagro 102, Mekenzie small, Nasaenge, Kula Karuppan,varygony, MR 69, Kanu Dam, IRRI 123, sativa IRGC17083-1, Kalia and Swarna have performed stably over a period of two years. Ten genotypes were found to be more adapted and perform better in specific environments. The Genotypes that fulfilled the major criteria of different stability analyses methods were identified as the most stable. Out of these 25 high-yielding genotypes were selected as genotypes with better breeding value and further use in breeding programs. Stability analyses aided in the discovery of unique genotypes for all environments studied, as well as a stable genotype that can be cultivated in all the environments studied and in areas with similar characteristics to the test environments. This can be used as a preliminary study for future breeding programs and also to understand the plasticity of rice to changing climate conditions.

REFERENCES

1. Babarmanzoor A,Tariq MS,Ghulam A, Muhammad A. Genotype x environment interaction for seed yield in Kabuli Chickpea (*Cicer arietinum* L.) genotypes developed through mutation breeding. Pakistan Journal of Botany. 2009; 41:1883-1890.
2. Bajpai PK, Prabhakaran VT. A new procedure of simultaneous selection for high yielding and stable crop genotypes. Indian Journal of Genetics and Plant Breeding.2000; 60:141-146.
3. Becker, H.C., and J. Leon. 1988. Stability analysis in plant breeding. Plant Breeding 101:1-23.
4. Bernardo R. Breeding for Quantitative Traits in Plants, Stemma Press, Woodbury, Minn, USA, 2010.
5. CRAN. 2014. The comprehensive R archive network. Comprehensive R Archive Network for the R programming language. [cited 2016 December 1). Available from: http:// cran.r-project.org/web/packages/available_packages_by name.html available-packages-A.
6. Dashiell KE, Ariyo OJ, Bello L. Genotype x environment interaction and simultaneous selection for high yield and stability in soybeans (*Glycine max* (L.) Merr.) Annals of Applied Biology. 1994; 124:133-139.
7. Eskridge KM. Selection of stable cultivars using a safety-first rule. Crop Science. 1990; 30:369-374.
8. Farshadfar E. Incorporation of AMMI stability value and grain yield in a single non-parametric index (GSI) in bread wheat. Pakistan Journal of Biological Science. 2008; 11:1791-1796.
9. Farshadfar N,Mahmodi, Yaghotipoor A. “AMMI stability value and simultaneous estimation of yield and yield stability in bread wheat (*Triticum aestivum* L.),” Australian Journal of Crop Science. 2011; vol. 5, no. 13, pp. 1837–1844.
10. Gauch HG, Zobel RW. AMMI analysis of yield trials. In: MS Kang, HG Gauch, editor. Genotype by environment interaction.1996; p. 85–122.
11. Gauch HG. Statistical analysis of regional yield trials: AMMI analysis of factorial designs. Amsterdam (Netherlands): Elsevier;1992 p. 278.
12. Hagos HG, Abay F. “AMMI and GGE biplot analysis of bread wheat genotypes in the northern part of Ethiopia,” Journal of Plant Breeding and Genetics.2013; vol. 1, pp. 12–18.

Formatted: Font: Italic

Formatted: Font: Italic

Formatted: Font: Italic

13. Hall AJ, Richards RA. Prognosis for genetic improvement of yield potential and water-limited yield of major grain crops. Field Crop. Res. 2013; 143, 18–33.
14. Kang MS, Miller JD, Darrah LL. A note on relationship between stability variance and ecovalence. J Hered.1987; 78:107–107.
15. Kang MS, Pham HN. Simultaneous selection for high yielding and stable crop genotypes. Agron J. 1991; 83:161–165.
16. Kang MS. Breeding: genotype-by-environment interaction. In: Encyclopedia of plant and crop science. p.2004; 218–221.
17. Kang MS. Simultaneous selection for yield and stability in crop performance trials: consequences for growers. Agron J. 1993; 85:754–757
18. Karimizadeh R, Mohammadi M, Sabaghni N, Mahmoodi AA, Roustami B, Seyyedi F, Akbari F. GGE biplot analysis of yield stability in multi-environment trials of lentil genotypes under rainfed condition. Not Sci Biol. 2013; 5:256–262.
19. Kaya Y, Akcra M, Taner S. GGE-biplot analysis of multienvironment yield trial in bread wheat. Turkish Journal of Agriculture and Forestry.2006; 30, 325–337. https://journals.tubitak.gov.tr/agriculture/vol30/iss5/3.
20. Kebede G, Worku W,Jifar H,Feyissa F. GGE biplot analysis of genotype by environment interaction and grain yield stability of oat (Avena sativa L.) in Ethiopia. *Agrosystems, Geosciences & Environment*, 2023; *6*(3), p.e20410.
21. KhanMMH, Rafii MY, Ramlee SI, Jusoh M, Mamun AI, AMMI M. GGE biplot analysis for yield performance and stability assessment of selected Bambara groundnut (Vignasubterranea L. Verdc.) genotypes under the multi-environmental trials (METs). Sci. Rep. 2021; 11, 22791.
22. Li R, Li M, Ashraf U, Liu S, Zhang J. Exploring the relationships between yield and yield-related traits for rice varieties released in China from 1978 to 2017. Front. Plant Sci. 2019; 10, 543.
23. Mekbib F. Yield stability in common bean (Phaseolus vulgaris L.) genotypes. Euphytica. 2003; 130:147–153.
24. Mohammadi R,Abdulahi A, Haghparast R, Armion M. Interpreting genotype- environment interactions for durum wheat grain yields using non-parametric methods. Euphytica. 2007; 157:239-251.
25. Mohammadi R, Amri A. Comparison of parametric and non-parametric methods for selecting stable and adapted durum wheat genotypes in variable environments. Euphytica. 2008; 159:419-432.
26. Purchase JL, Hatting H, van Deventer CS. Genotype x environment interaction of winter wheat (Triticum aestivum L.) in South Africa: II. Stability analysis of yield performance. South African Journal of Plant and Soil. 2000; 17:101-107.
27. Rao AR, Prabhakaran VT. Use of AMMI in simultaneous selection of genotypes for yield and stability. Journal of the Indian Society of Agricultural Statistics. 2005; 59:76-82.
28. RStudio. 2014. RStudio: Integrated development environment for R (Computer software v0.98.1074). RStudio. [cited 2016 December 1]. Available from: http://www.rstudio.org/
29. Shukla GK. Some statistical aspects of partitioning genotype environmental components of variability. Heredity. 1972; 29: 237–245.
30. Tumuhimbise R,Melis R,Shanahan P, Kawuki R. “Genotype * environment interaction effects on early fresh storage root yield and related traits in cassava,” The Crop Journal, 2014; vol. 2, no. 5, pp. 329–337.
31. Wricke G. Evaluation Method for Recording Ecological Differences in Field Trials. Plant Breed. 1962; 47:92–96.

31. Yan W, Cornelius PL, Crossa J, Hunt L. Two types of GGE biplots for analyzing multi-environment trial data. Crop. Sci. 2001; 41, 656–663.

33. Yan W, Hunt LA, Sheng Q, Szlavnics Z. Cultivar evaluation and mega-environment investigation based on the GGE biplot. Crop Science. 2000; 40, 597–605. https://doi.org/10.2135/cropsci2000.403597x
34. Yan W, Kang MS, Ma B, Woods S, Cornelius PL. GGE biplot vs. AMMI analysis of genotype-by-environment data. Crop Sci.2007; 47:643–653.
35. Yan W, Kang MS. GGE biplot analysis: A graphical tool for breeders, geneticists, and agronomists. New York (USA): CRC press. 2002; p. 71.
36. Zobel RW, Wright MJ, Gauch HG. Statistical analysis of a yield trial. Agron J. 1988; 80:388–393.