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ADAPTABILITY AND GRAIN YIELD STABILITY OF RICE HYBRIDS IN PAKISTAN

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ABSTRACT

To address GxE interaction (GEI), multi-environment testing is necessary for the development of new high-performance and stable cultivars. Using the Additive Main Effects and Multiplicative Interaction Model (AMMI) models, grain yield in rice hybrids was evaluated for adaptability and stability. Seven trials were carried out in Pakistan's principal rice-producing regions during the kharif season of 2020–2021. With hybrid-by-location interaction, ANOVA showed substantial differences in genotype (G), environment (E), and their interaction (GxE), which accounted for 20%, 67%, and 18% of the overall variation, respectively. The first and second principal components of the AMMI biplot models explained 36% and 21% of the GEI, respectively. The hybrid LPSA-04 (H21) as better average performance indicated good adaptability and stability. The hybrid HDR-16 (H49) also stood out with average yield 7258 kg/ha in seven tested locations. Diamond-121 (C) (H70) had a moderate yield (6604 kg/ha) and was the most stable of the two checks (Diamond-121 and GNY-53). To the contrary, the AMMI and GGE biplot models found that FB-1803(H40) and IQS-938 (H9) had high but unstable performances, with special adaptation to the locality Dokri, Sindh (L1). The best-performing genotypes were 137-H (H16) and V-GRO-177 (H4), which were found in two mega environments viz., Dokri 9796 kg/ha and 9617kg/ha: 8600 and 8870kg/ha in Farooq Abad location respectively. In terms of determining the places that are most representative and discriminatory, Gularchi (L5) was found to be the most representative, but genotype discrimination was better at Dokri, site L1. In general, the GEI study benefited from more thorough and insightful insights from the GGE biplot analysis.

Additional keywords: Rice, AMMI, GGE biplot, Oryza sativa, hybrids

INTRODUCTION

Rice is cultivated in a wide range of agro-climatic regions across the globe. It is staple diet for more than 3.5 billion people in almost all the latitudes and occupies the second position in production and area of major cereal crops (Pathak et al., 2018). The world's population is expected to increase by 2050 up to nine billion (Béné et al., 2015). To meet the demand of this increasing population, there is a dire need to enhance rice production than the present-day by 60–110% (Pugh et al., 2016). Climate change have impact on national food security and recent estimates shows that high-temperature by 2 °C by 2050 may affect the 20 million ha rice-growing area in Asian countries which consequently reduce the productivity in south Asia (14%), East Asia (10%) and sub-Saharan Africa (15%) (Wassmann, Jagadish, Sumfleth, et al., 2009). Climate change and its influence on genotype × environment interactions (GEI) affect the rice hybridization program to improve its yield potential. Therefore, to mitigate the changing climate, there is a prerequisite to follow the latest technologies which can deliver estimated results. Heterosis (hybrid vigor) in self-pollinated crops as rice, provides an imperative avenue for higher yields where heterozygous F1 hybrids show superior agronomic and physiological performance as compare to their parents (Virmani, Pandey, Singh, & Xu, 2004). The yield of pure line rice varieties in favorable environments have reached to a plateau. The genetic analysis including dominance, over-dominance and epistasis interactions explained the increased yield (10-15%) and biomass in hybrids (Fujimoto et al., 2018) over high yielding pure line varieties. Moreover, hybrid rice (HR) has also shown better cope with adverse conditions like heat, drought and salinity (Wassmann, Jagadish, Heuer, et al., 2009). The better performance of hybrids depends on the genotype, GEI and best growing environments which explores its yield potential (Senguttuvel et al., 2021). Genotype-by-Environment (GxE) studies in rice are conducted to understand the interaction between different rice genotypes and their performance in various environmental conditions (Zhang et al., 2019). These studies help identify the most suitable rice varieties for specific regions or agro-ecological zones in Pakistan. The studies involve evaluating multiple rice genotypes or varieties across different locations or environments to determine their performance and adaptability. The hybrids selection based on its performance in a single environment, is not considered effective, as yield is a complex quantitative inherited trait (Kumar et al., 2017) and influenced by the environment (Gul et al., 2022). Therefore, the evaluation of rice hybrids for yield stability across multiple environments is imperative before released as national hybrids and passed it to the farmers as an end user. Thus, this study was undertaken to evaluate local and exotic imported rice hybrids for high grain yield and their stability across variable environments with different temperature regimes. Multiplicative models, such as the Additive Main Effects and Multiplicative Interaction (AMMI) model and the Genotype Plus Genotype-by-Environment Interaction (GGE) model, are statistical tools used to analyze the response of genotypes to specific environments or to different environments (Abdelrahman et al., 2022). These models help understand the interaction between genotypes and environments and provide insights into the performance and stability of genotypes across multiple environments. The AMMI model combines principal component analysis (PCA) and analysis of variance (ANOVA) to identify significant interactions and represent them in a two-dimensional biplot (Wodebo et al., 2023). The biplot helps visualize the interaction pattern and identifies genotypes that are specifically adapted to certain environments (Ghazvini et al., 2022). The GGE model combines PCA and regression techniques to analyze genotype-by-environment interactions. It provides a graphical representation called a GGE biplot, which helps identify genotypes with stable performance across multiple environments and environments that are most discriminating for genotype performance (Enyew et al., 2021). Both AMMI and GGE models allow researchers to assess the stability, adaptability, and performance of genotypes across different environments. These models are useful for plant breeders, researchers, and policymakers to make data-driven and informed decisions regarding genotype selection, breeding strategies, and variety recommendation for specific environments or agro-ecological zones to enhance crop productivity and adaptation (Sitaresmi et al., 2019). Biometrical models are proposed to analyze the adaptability, GEI and stability. However, multivariate models which involves both main effect and multiplicative components of two way ANOVA, enables a breeder to get more precise estimate on potential genotype and favored environment (Senguttuvel et al., 2021). These methods reduce the biasness caused by outliers and no assumptions are required about the distribution of the observed data. Meanwhile, it is easy to use and interpret and the additions or deletions of one or few genotypes don't cause much variation in results and proposed multivariate models (AMMI) to explore and interpret the GEI (Hashim et al., 2021; Singh et al., 2023).

METHODOLOGY

Seventy rice hybrids including two checks GNY-53 (C) and Diamond-121 (C) (Table 1) grown in seven multi-locational rice producing areas of Pakistan viz; Dokri, D.I.Khan, Kala Shah Kaku, Multan, Gularchi, Farooqabad and Shikarpur during the year 2020 in national uniform hybrid rice yield trial. The sowing was carried out during the Kharif season in the localities presented in Table 2. The agronomic crop production management and crop protection measures are followed in all the locations as per adopted by the farmers in each territory. The experiments were conducted using a randomized complete block design (RCBD), with each treatment replicated three times. The experimental plot size was 12 m², consisting of 8 rows that were 5 m long and spaced 0.30 m apart. The effective harvest area within each plot was 9 m². The character evaluated in this study was grain yield at 12% moisture content.

Table 1. Characteristics of the seven locations used for hybrid rice evaluation in year 2020-21

Locations	**Coordinates**		**Altitude (metres)**	**Mean temperature (°C)**	**Average Rainfall (mm)**
	Latitude	**Longitude**			
Dokri	27° 22'	68° 05'	39.0	33.0	16.22
D.I.Khan	31°50'	70°53'	178.0	31.3	260
Kala Shah Kaku	31°44'	74°15'	236.1	32.2	23.04
Multan	30°9'	71°31'	123.3	31.8	185
Gularchi	24°39'	68°32'	11.5	33.0	20
Farooqabad	25°23'	68°21'	29.44	28.0	30.0
Shikarpur	27°57'	68°38'	71.32	30.0	15.6

STATISTICAL ANALYSIS

A statistical analysis was conducted to examine the effects of location, genotype, and their interactions on grain yield. The study utilized data from ten different genotypes observed across six locations. An analysis of variance (ANOVA) was performed to assess the impact of these factors. To break down the degrees of freedom, the source of genotype variation was categorized into hybrids, locations and their interaction, enabling orthogonal contrasts. The analysis was carried out using the Agricolae Library of the R software (http://www.R-project.org).

The AMMI model, which stands for Additive Main effects and Multiplicative Interaction, is a biometrical model used to assess adaptability and stability. It describes the mean response of a genotype in a specific environment. The model equation is $\mathcal{Y}ij = \mu + gi + aj + \sum^{N}{}_{n=1} (IPCA_{n}{}^{gi}) (IPCA_{n}{}^{aj}) + dij + \varepsilon ij$, where μ represents the general mean, gi is the genotypic effect, aj is the environment effect, and εij is the experimental error. The Genotype-Environment Interaction (GEI) is denoted as $(IPCA^{gi}{}_{n})$ and represents the score of the Principal Component (PC) of genotype i for the nth axis. Similarly, $(IPCA_{n}{}^{aj})$ is the PC of the environment j for the n^th axis. The variable n represents the number of axes used in a particular analysis, which has a minimum value of [(g-1)(a-1)]. Lastly, dij represents the residual effect of GEI that is not explained by the Principal Component Analysis (PCA).

The Site Regression (SREG) model was utilized to construct the GGE biplot. The biplot was created based on the following model: $\mathcal{Y}ij - \mu - bj = (\lambda 1 \xi i1 n j1) + (\lambda 2 \xi i2 n j2) + \varepsilon ij$. Here, $\mathcal{Y}ij$ represents the average yield of genotype i (i = 1… 10) in environment j (j = 1… 7). μ denotes the general mean, and bj represents the ambient effect of j. The terms $(\lambda 1 \xi i1 n j1)$ and $(\lambda 2 \xi i2 n j2)$ correspond to the first and second principal components (PC1 and PC2) respectively. $\lambda 1$ and $\lambda 2$ represent the eigenvalues associated with PC1 and PC2, while $\xi i1$ and $\xi i2$ represent the autovectors of genotypes i for the first and second principal components. Similarly, $nj1$ and $nj2$ represent the autovectors of environments j for the first and second principal components respectively. Finally, εij represents the experimental error associated with genotype i in environment j. The analysis using the AMMI and GGE biplot was performed using the R software.

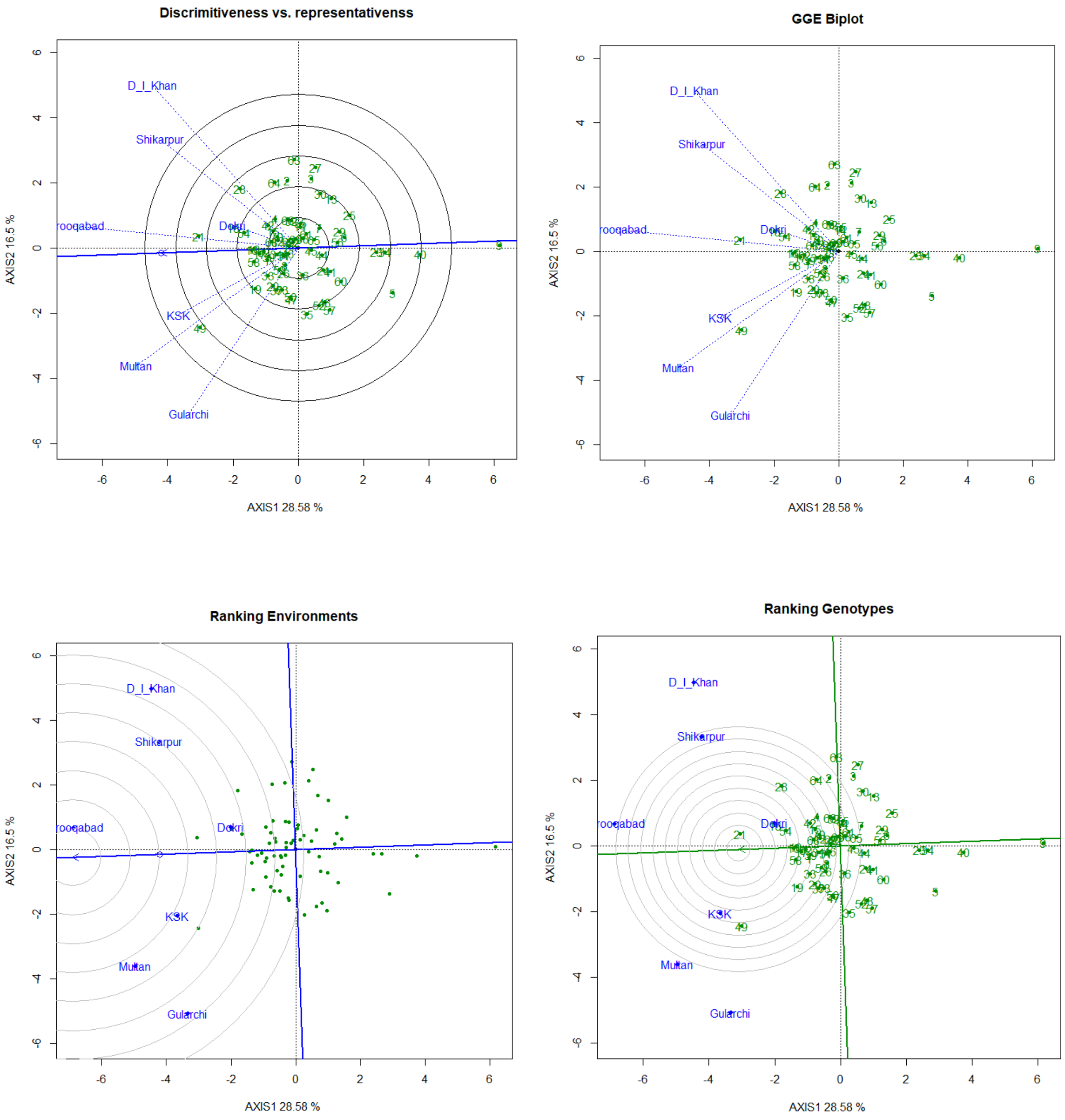
The REML/BLUP model was utilized for conducting stability and adaptability analysis. The harmonic mean of genotypic values was calculated using the equation HMGV = $e \sum (1/GVij)$, where (e) represents the number of environments in which genotype (i) was evaluated and $(GVij)$ corresponds to the genotypic value of genotype (i) in environment (j). To assess adaptability, the relative performance of genotypic values (RPGV) across environments was obtained using the equation RPGV = $(1/e) \sum (GVij/\mu j)$, where μj represents the mean of environment (j). The RPGV values were expressed as a proportion of the general mean (GM) for each location, and the average value of these ratios from all locations was calculated. Lastly, a simultaneous analysis of yield, stability, and adaptability was conducted using the harmonic mean of relative performance of genotypic values (HMRPVG) with the equation HMRPVG = $e \sum (1/RPGVj)$.

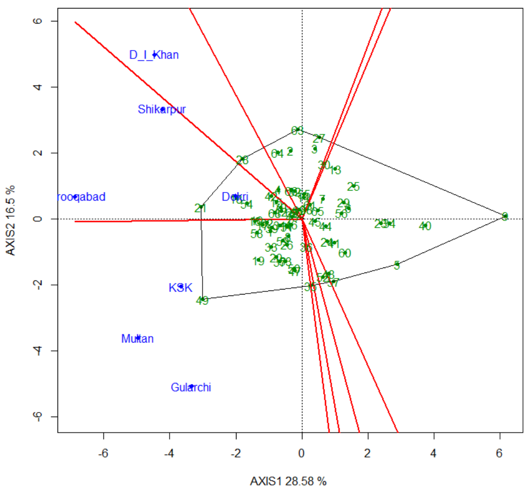
RESULTS AND DISCUSSION

The basic premise of multiplicative models is that the response of a genotype in a particular environment can be decomposed into two components (Krishnamurthy et al., 2021): the main effects of the genotype and the environment, and the interaction effect between the genotype and the environment. The main effects represent the overall performance of the genotypes and the environments independently. These effects capture the average behavior of genotypes across all environments and the average performance of environments across all genotypes. The interaction effect captures the deviation from the overall average performance and describes how a genotype's response varies across different environments. It signifies the differential response of genotypes to specific environments and provides insights into genotype-by-environment interactions. In our analysis of genotype-environment interaction (GEI) using the Additive Main Effects and Multiplicative Interaction (AMMI) model, we observed a complex interaction pattern in terms of mean yield across different locations. This complexity arose from variations in how genotypes were classified across the various locations. AMMI analysis allowed us to distill this complexity into two principal components (PC1 and PC2), which collectively explained 77% of the total GEI. Specifically, PC1 accounted for 58%, and PC2 explained 19% of the interaction variability. These results are consistent with findings in previous studies involving hybrids and rice varieties, where the first two PCs explained varying proportions of the GEI. To visually represent the performance of different genotypes in specific environments, we employed biplots (see Figure 1). Genotypes with both high yield and stability across most locations are considered the best performers. In this study, five materials (H6, V4, V1, H3, and H2) displayed yields above the general mean. Notably, three of these were hybrids, and two were local varieties. Genotypes with low PC1 scores, approaching zero, are considered to have minimal influence on the interaction. Among these, hybrids H3, H6, and H2, along with variety V3, demonstrated stability. Hybrid H6 emerged as the most desirable genotype due to its high yield and stability, followed closely by the HIAAL H3 hybrid. These findings shed light on the performance and stability of various genotypes under diverse environmental conditions and can inform future breeding and selection efforts. The first and second principal components of the AMMI biplot models explained 36% and 21% of the GEI, respectively. The hybrid LPSA-04 (H21) as better average performance indicated good adaptability and stability. The hybrid HDR-16 (H49) also stood out with average yield 7258 kg/ha in seven tested locations. Diamond-121 (C) (H70) had a moderate yield (6604 kg/ha) and was the most stable of the two checks (Diamond-121 and GNY-53). To the contrary, the AMMI and GGE biplot models found that FB-1803(H40) and IQS-938 (H9) had high but unstable performances, with special adaptation to the locality Dokri, Sindh (L1). The best-performing genotypes were 137-H (H16) and V-GRO-177 (H4), which were found in two mega environments viz., Dokri 9796 kg/ha and 9617kg/ha: 8600 and 8870kg/ha in Farooq Abad location respectively. In terms of determining the places that are most representative and discriminatory, Gularchi (L5) was found to be the most representative, but genotype discrimination was better at Dokri, site L1. In general, the GEI study benefited from more thorough and insightful insights from the GGE biplot analysis. rop improvement is followed by genetic diversity, with various characteristics screened. In this study, different hybrids were studied in 2019 under in-house trials for yield and yield-related traits and their adaptation to changing climatic conditions. With respect to yield, all the Honglian hybrid rice varieties showed more than 30% more yield potential over check variety. As Honglian hybrid rice varieties have desirable yield and yield related traits, i.e., high yield, high quality, heat tolerant, drought tolerant, high tillering ability, high fertility and good grain quality parameters, etc., PCA and correlation analysis displayed significant genetic differences among the genotypes along with all the desired traits indicating the existence of variability (Ashfaq et al., 2023). The association of different rice traits and patterns of influence on the grain yield of rice was investigated. Such types of evaluation are very important to determine the direct effects of various traits on yield to determine the selection criteria for high grain yield. We found that some of traits have greater value, including seed length, seed width, seed thickness, curling%, bursting %, cooked grain length, head rice recovery%, etc., which have accounted for high grain yield. The positive associations of yield with other desirable traits were found to be significant, providing the information for selecting desirable rice hybrids/genotypes which are more favorable to acclimatize to changing environments. Positive significant genetic differences and correlation studies among the genotypes, along with desired traits, provide information to the researcher for the better selection of genotypes (Ishfaq et al., 2021). The hybrid varieties were also analyzed using PCA to compare characteristics of HP varieties over check varieties. Principal components with more than one eigenvalue showed more variability among the traits studied for each genotype. Those principal components with more than one eigenvalue showed a collective variation of 67.42% in the year 2020. The PC1 had 22.62%, PC2 showed 19.45%, PC3 exhibited 13.56%, and PC4 had 11.79% variability between the rice varieties and their various traits in 2020. The variance and eigenvalue associated with principal components decreased gradually and stopped at 0.18%. In the year 2021, the first six components showed maximum variability of 82.13% (Ahmed et al., 2024). Stability analysis for multi-location data has been evaluated in both univariate and multivariate statistics (Zaid et al., 2022). Among the multivariate methods, the additive main effects and AMMI analysis are widely used for G × E interactions. The AMMI model combines ANOVA and G × E interactions to identify the genotypes and environmental variables (Naeem et al., 2022). The relative contributions of the total sum of squares of location, genotype, and GL interactions in the AMMI model of two-year data for grain yield per plant showed a similar pattern in the previous rice stability analysis (Kashif et al., 2023). Significant interactions between locations and tested genotypes in plant height and tillers per plant, as a high portion of the first two interaction principal components (IPCA1 and IPCA2), have been reported (Habib et al., 2024). In our study, the univariate stability analysis screened out highly stable (GSR 112 and GSR 252) GSR lines for most of the studied traits. The GGE biplot analysis showed that IIRI-6 was the most stable genotype for plant height. GSR-305 and Kissan basmati were the most stable genotypes for tillers per plant. GSR 305 was closed to the biplot origin, depicting less response than the vertex genotypes. Moreover, it also reveals low environmental interaction in terms of grain and straw yield per plant. On the contrary, the other genotypes were farther from the biplot origin and demonstrated higher vulnerability towards environmental factors that affect their stability. Based on the adaptation pattern, Narowal and Dokri were found to be the most dynamic locations for genotypes plant height, Muzaffargarh and the NARC for tillers per plant, and Swat and Muzaffargarh for grain and straw yield per plant in 2020 and 2021, respectively. However, the tested genotypes showed different yields concerning their locations for the yield traits. Similar observations of the biplot model for multi-location studies using rice genotypes were also concluded earlier (Sabar et al., 2024). However, high-performing GSR lines for yield traits with less stability across locations can be stabilized following the backcross approach with the most stable GSR line (Riaz et al., 2023).

CONCLUSIONS

The present findings conclusively demonstrate that the yield of 9338 kg/ha of HP3 in 2020 and 7863 kg/ha of HP1 in 2021 were higher than the average yield of all the hybrids tested in both years and over check varieties. We found that some of the traits, i.e., seed length, width, thickness, cooked grain length, brown rice, milled rice and yield per hectare of HP3 and HP1, respectively, were greater than the check varieties (D-121, Guard-53). These hybrids and their parent material could be further used for the development of new distinct uniform homozygous plant population son the basis of the desired characteristics. The performance of Honglian type hybrid rice was more stable and considerably better than other hybrids/varieties in high temperature locations, which indicates its better adaptation and acclimatization in various ecological zones of Pakistan. Finally, we summarize that HP1, HP2 and HP3, as the new generations of Honglian type hybrids with advanced characteristics, are beneficial for introduction into Pakistan for future development and industrialization. The NUYT and DUS analysis convincingly showed that they are suitable to grow in Pakistan. Based on the historical economical contributions of the old varieties of Honglian type hybrid rice, it is promising that development and industrialization of these new varieties would contribute well to Pakistan and benefit the people both in China and Pakistan. In the current scenario, this type of study and the genetic material could be very useful for the production of high yielding varieties that would be more fruitful to the farmers community and strengthen the country's economy.

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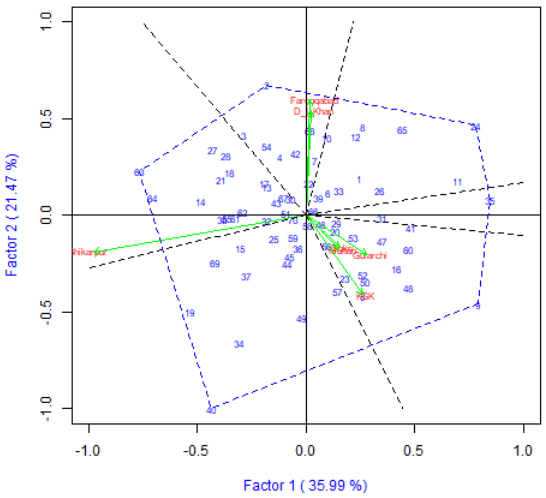
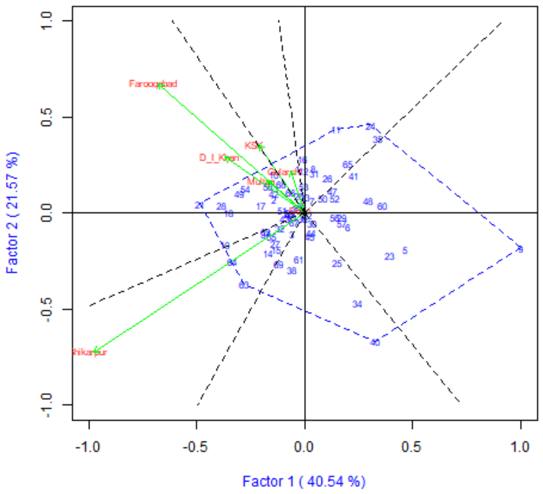
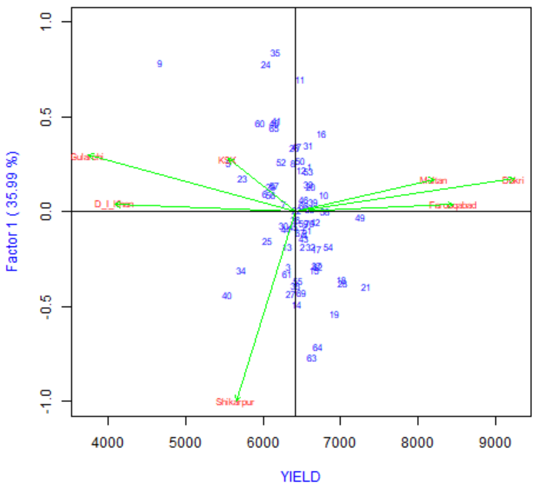

AMMI YIELD from a LSMeans


SREG YIELD from a LSMeans


AMMI PCA1 Score vs YIELD from a LSMeans

CONCLUSION

It was concluded that rice yield and growth increased by their different varieties the hybrid LPSA-04 (H21) as better average performance indicated good adaptability and stability. The hybrid HDR-16 (H49) also stood out with average yield 7258 kg/ha in seven tested locations and Diamond-121 (C) (H70) had a moderate yield (6604 kg/ha). The best-performing genotypes were 137-H (H16) and V-GRO-177 (H4), which were found in two mega environments viz., Dokri 9796 kg/ha and 9617kg/ha: 8600 and 8870kg/ha.

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