Emirates Journal of Food and Agriculture. 2022. 34(3): 229-238
doi: 10.9755/ejfa.2022.v34.i3.2827
http://www.ejfa.me/

RESEARCH ARTICLE

Identification of adaptable rice genotypes under diverse production environments using a multivariate statistical model

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ABSTRACT

Basmati rice is sold at a higher price in both local and international markets due to its superior grain qualities. Identification of high performing and adaptable genotypes under multi-environmental conditions is very crucial to sustain rice production. In the present research, sixteen Basmati rice genotypes were evaluated under three diverse production environments i.e. transplanted (TPR), direct seeded (DSR), and system of rice intensification (SRI) during two consecutive *kharif* seasons. The experiment was laid down in randomized block design with three replications. The primary objective of this research was to identify stable genotypes adaptable to different production environments with a high mean using the GGE biplot model. Genotypes explained a higher proportion (44.25 to 60.71 %) of the total sum of squares while environment attributed only (7.71 to 23.26%). Genotype by environment interaction contributed 31.58% to 36.77% of the total variation for studied traits. Under DSR, Haryana Basmati-1 for hulling%, milling%, and head rice recovery% while Improved Pusa Basmati 1 for amylose content were identified as specifically adapted genotypes. Likewise, under SRI, HKR 98-476 for hulling% and milling%, Pusa Basmati-1 for head rice recovery%, and Improved Pusa Basmati -1 for amylose content were found suitable genotypes. These genotypes can be recommended for commercial cultivation for specific production environments.

Keywords: Adaptability; Basmati; direct seeded; GGE biplot; system of rice intensification

INTRODUCTION

Basmati rice possesses a prominent place in South Asian countries due to its long grain characteristics, excellent quality and high demand in the international market (Awan et al., 2017). It is generally cultivated by transplanting method in puddled and continuously flooded soil. Flooded rice production system produce 1 kg of rice by consuming near about 2500 litre water (Bouman, 2009). However, water deficiency in many areas of the world has adversely impacted sustainable rice production (Jabran et al., 2017). Given the importance of global concern, food security and water scarcity necessitate the development of substitutive water-saving production systems of rice cultivation.

In the past two decades, many water-saving methods like alternate wetting and drying, direct seeding, the system of rice intensification and non-flooded mulching cultivation have been developed (Datta et al., 2017). System of rice intensification (SRI) uses single seedling per hill, reduced planting density, unflooded fields, mechanical weeder, soil organic matter. SRI method increases the rice grain yield by 25-50% (Senthilkumar et al., 2008; Thakur et al., 2010) and reduces the water demands (Satyanarayana et al., 2007; Chapagain and Yamaji, 2010). This method increases the diversity of soil microbes which improves plant growth and productivity (Uphoff, 2003). Several previous studies reported improved grain qualities under SRI over the conventional method. Improved grain yield, water use efficiency, germination %, hulling, milling and head rice recovery % under SRI was observed by Uphoff et al. (2011), Mandal et al. (2014) and Kumar (2014).

Direct seeded rice (DSR) is another method of rice cultivation that consumes less water and labor input as compared to the flooded-transplanted method (Liu et al., 2015). In DSR, seeds are sown directly in dry soil, in

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Received: 17 August 2021; **Accepted:** 25 February 2022

standing water or pre-germinated seeds in wet and puddled soil (Ullah et al., 2017). Many studies observed high grain yield, increased number of spikelet, tiller number, test grain weight and plant height under dry direct deeding compared with flooded transplanted rice (Du et al., 2014; Iqbal et al., 2017). Significant differences in the genotypic performance of rice have been observed under different production environments i.e. DSR, SRI and TPR by Thakur et al. (2011), Jabran et al. (2017), Ullah et al. (2017). High grain yield, root dry matter and high benefit-cost ratio under DSR were reported in comparison to the transplanted method of cultivation (Gangwar et al. 2008). Likewise, a 7-8% saving of labor, 30-50% saving of water and higher grain yield in the comparative study of DSR and TPR have been observed by Manjunatha et al. (2009; Yadav et al. (2011) and Kumar et al. (2015). Thus the selection of better performing and adapted genotypes to these water-saving techniques helps in their wider adaptation in rice-growing areas. However, to date, no specific cultivars have been developed for these water-saving techniques using breeding efforts.

Grain qualities parameters such as hulling, milling, head rice recovery and amylose content play a very important role in deciding the rate and demand of rice in the market. Rice with high milling % and intermediate level of amylose content is generally preferred by consumers (Jabran et al., 2017). Besides genetics, these traits are also influenced by environmental conditions such as soil type, temperature, aerobic and flooded conditions, rainfall and harvesting methods, etc. (Zhao and Fitzgerald, 2013). Some studies reported equal or better performance of rice genotypes under DSR than TPR however, many other reports observed significantly poor performance under DSR. To what extent, the well-adapted genotypes in TPR interact with these alternative methods is the main focus of research. Hence, the present study was undertaken (i) to analyze the effect of GEI on quality parameters of Basmati rice and (ii) to identify genotypes better adapted to different production environments like DSR and SRI.

MATERIALS AND METHODS

Plant material and testing environments

Sixteen genotypes were assessed during *kharif* season 2016 and 2017 under three production environments namely system of rice intensification, transplanted and direct seeded condition. The experiment was organized at Rice Research Station, Kaul and Regional Research Station, Uchani using randomized block design in three replications. The soil was clay loam. The list of genotypes used in the study is given in Table 1. The detailed description of agronomic practices like seed rate per hectare, number of seedlings per hill used for transplanting, seedling age, spacing, number of irrigation applied, weeding and date of sowing or transplanting are given in Table 2. Observations were recorded for four important quality traits hulling %, milling %, head rice recovery % and amylose content %. Hulling %, milling % and head rice recovery % were measured by using the method of Khush et al. (1979). Amylose content in % was measured as per the protocol suggested by (Juliano, 1971).

Statistical analysis

Data of sixteen genotypes were pooled for two years to assess the mean performance of genotypes under different production environments over the locations. Codes were used for genotypes as G1 to G16 (Table 1) and for environments as E1 to E6 (Table 3) to represent them on biplots. GGE biplot theory has been used for the statistical analysis (Yan and Kang, 2003) and data were subjected to singular value decomposition (SVD) for environment-centered matrix. Biplot analysis was done without scaling to generate a test-centered biplot (Yan and Tinker, 2006) using GGEBiplot and GGEbiplotGUI software. Singular value partitioning, using the mean versus stability option was used for genotype evaluation and the relation among testers option was used for environment evaluation (Yan,

Table 1: Code and name of sixteen rice genotypes used in the study

Code	Genotypes	Code	Genotypes
G1	Basmati 370	G9	Pusa 1637-2-8-20-5
G2	CSR 30	G10	Pusa 1656-10-705
G3	Haryana Basmati 1	G11	Pusa 1734-8-3-85
G4	HKR 11-509	G12	Pusa Basmati1
G5	HKR 08-425	G13	Pusa Basmati1121
G6	HKR 11-447	G14	Pusa Basmati1509
G7	HKR 98-476	G15	Pusa Sugandh 2
G8	Improved Pusa Basmati 1	G16	Pusa Basmati 6

Table 2: Agronomic practices followed in different production environments

Production environments	DSR	SRI	TPR
Seed rate/hectare	5 kg	20 kg	20 kg
Sowing/ transplanting	20 June 2016/2017	3 July 2016/2017	17 July 2016/2017
Seedling age	Seed sowing	14 days	27 days
Spacing	15 × 20 cm^2	25 × 25 cm^2	15 × 20 cm^2
Seedlings/hill	2-3	1	2-3
Irrigations	13-14	18-20	30-33
Weeding	Manual	Herbicide	Herbicide

Table 3: Codes used for different production environments in the study.

Code	Production system	Code	Production system	Code	Production system
E1	DSR- K	E3	SRI- K	E5	TPR- K
E2	DSR- U	E4	SRI- U	E6	TPR- U

E- Environment, K- Kaul, U- Uchani

2001) Which-won-where pattern option was used for the identification of different mega-environments.

RESULTS AND DISCUSSION

Analysis of variance (ANOVA) and mean performance

The pooled ANOVA indicated that genotype (G), environment (E) and genotype × environment interaction (GEI) were significant ($p < 0.05$) for all the studied traits viz., hulling %, milling %, head rice recovery % and amylose content. The percent contribution of each source of variation was given in Table 4. This is an indication of the broad genetic base of studied genetic material and the diversity of different production environments. Genotypes accounted, 51.17 %, 58.12 %, 60.71 % and 44.25%, GEI explained 36.77%, 31.77%, 31.58% and 32.49% and environments accounts 12.05%, 10.11%, 7.71% and 23.26% of total variation for hulling %, milling %, head rice recovery % and amylose content, respectively. The sum of square percent contribution for each trait suggested that the highest percentage was accounted for genotypes followed by interaction effect and production environments. Multi environment screening and identification of stable and adaptable genotypes is an integral step of the variety release process (Bishaw and Van Gastel, 2009). It was noticed that about 80% of the total variation in multi environmental trials is contributed by the environment (Gauch and Zobel, 1997). However, a little lesser variation of 43.32% was reported in rice by Hashim et al. (2021) and 63.07% in okra by Sanwal et al. (2021). Based on the GGE biplot several studies have been conducted even to study disease reaction and combining ability besides using for the identification of stable genotypes in India, Nigeria, Bangladesh and Brazil (Tabien et al., 2008; Balestre et al., 2010; Nassir, 2013; Fotokian et al., 2014; Akter et al., 2015).

In the present study, a total of sixteen genotypes were evaluated and their mean performance across the environment is present in Table 5. Genotypic mean ranged from 76.69 to 80.46 % for hulling %, 65.41 to 70.23% for milling %, 51.54 to 57.96% for head rice recovery and 21.14 to 24.68% for amylose content. The highest hulling %, milling % and head rice recovery % were reported in HKR 98-476 (G7), Haryana Basmati 1 (G3), HKR 11-447 (G6) and Pusa Basmati 1 (G12). The highest amylose content was observed in Improved Pusa Basmati 1 (G8) followed by HKR 98-476 (G7) and Pusa Sugandh 2 (G15). These genotypes do not only show high mean performance but are also identified as stable in one or another production environment. Therefore, these genotypes can be considered as potential selection and recommended for their cultivation in direct seeded condition or system of rice intensification (Hashim et al. 2021; Kesh et al., 2021; Aristya et al., 2021).

Table 4: ANOVA and percentage of total variation contributed by genotype (G), environment (E) and genotype×environment interaction (GEI) for studied characters

Traits	G	E	GEI
Hulling %			
MS	7.43*	5.25*	1.07*
% Contribution	51.17	12.05	36.77
Milling %			
MS	15.72*	8.20*	1.72*
% Contribution	58.12	10.11	31.77
Head rice recovery %			
MS	18.60*	7.08*	1.93*
% Contribution	60.71	7.71	31.58
Amylose content %			
MS	4.60	7.25	0.68
% Contribution	44.25	23.26	32.49

Significance @ P<0.05

Genotype evaluation

The mean value and stability of Basmati rice genotypes were sharply represented using the GGE biplot based on the average environment coordination (AEC) method (Yan, 2002). The first two principal components (PC) explained 83.79% variation for hulling, 83.81% for milling, 83.05% for head rice recovery % and 82.16% for amylose content (Fig. 1 a-d). A single arrowed horizontal line moving through the origin of biplot pointing towards the high mean values is the AEC abscissa and vertical line on AEC abscissa crossing the center of biplot origin is referred to as AEC ordinate which points the genotype by interaction effect stability on either direction (Aristya et al., 2021; Frutos et al., 2014). The small vector length of genotypes indicates high stability (Kaya et al., 2006). HKR 11-447 (G6) and

Table 5: Genotypic means are calculated for 3 production environment data for 2 years and 2 locations

Code	Hulling %	Milling %	Head rice recovery %	Amylose content %
G1	78.93	68.83	53.28	22.11
G2	77.63	66.15	56.21	22.90
G3	80.10	69.96	56.77	23.20
G4	78.98	67.99	53.87	21.14
G5	77.89	67.22	54.88	23.87
G6	80.46	69.80	56.54	23.04
G7	79.75	70.23	57.34	24.34
G8	77.99	67.12	55.21	24.68
G9	76.85	65.50	52.86	23.74
G10	77.39	66.30	53.67	22.78
G11	77.90	66.36	54.78	22.62
G12	79.35	68.17	57.96	23.89
G13	78.33	68.68	56.52	23.88
G14	77.92	67.62	54.70	23.89
G15	76.69	65.53	53.76	23.91
G16	77.99	65.41	51.54	23.56
Range	76.69 – 80.46	65.41 – 70.23	51.54 – 57.96	21.14 – 24.68
Mean	78.38	67.55	54.99	23.35
CV (%)	1.42	2.41	3.25	3.83
Variance	1.23	2.64	3.18	0.80

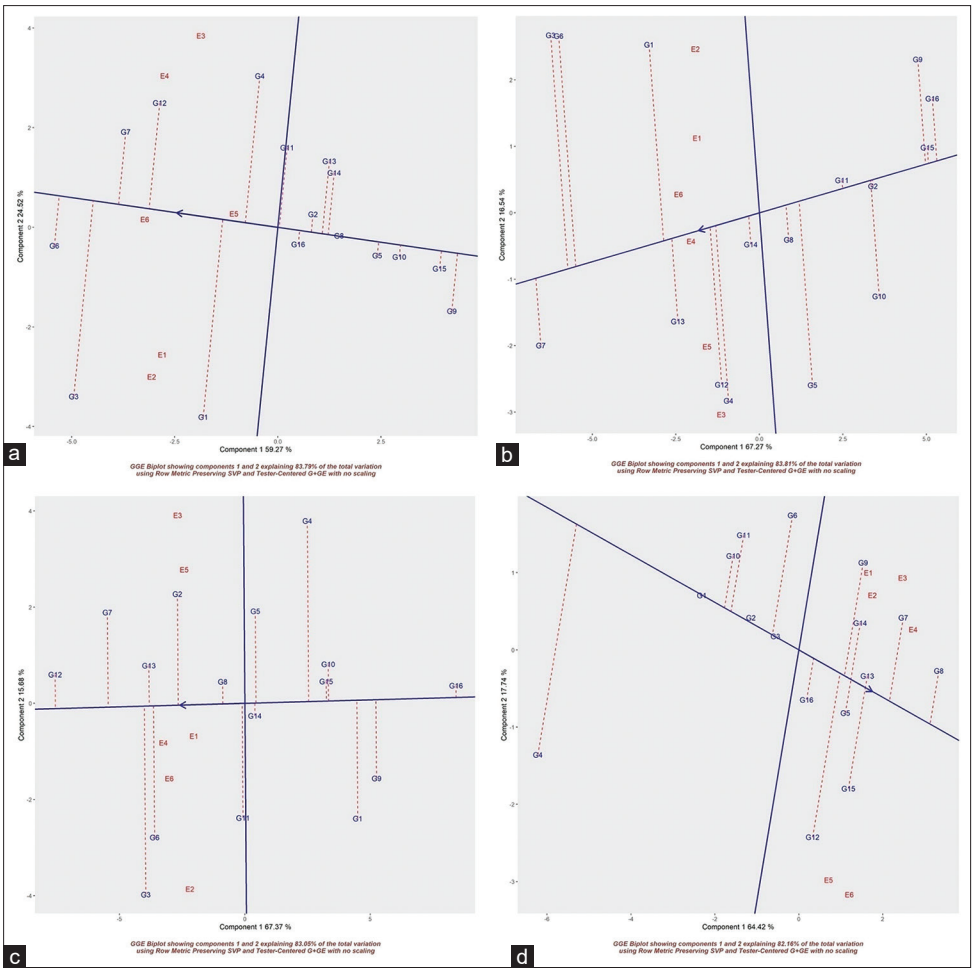

Fig 1. GGE biplot analysis: mean vs stability for (a) hulling %, (b) milling %, (c) head rice recovery % and (d) amylose content %.

HKR 98-476 (G7) were the best performings while Pusa Sugandh 2 (G15) and Pusa 1637-2-8-20-5 (G9) were poor performing genotypes for hulling %. It may be found that Haryana Basmati 1 (G3), Basmati 370 (G1) and HKR 11-509 (G4) were the least stable genotypes owing to the greater vector length from the AEC abscissa. Pusa Basmati 6 (G16), CSR-30 (G2) and Improved Pusa Basmati 1 (G8) were observed as stable genotypes but have low hulling % in comparison to other genotypes. For milling %, HKR 98-476 (G7), Pusa Basmati 1121 (G13) and Pusa Basmati 1509 (G14) were the best performing genotypes with relatively more stability. On other hand, Pusa Sugandh 2 (G15) and Pusa Basmati 6 (G16) were poor performings. Basmati 370 (G1), Haryana Basmati 1 (G3), HKR 11-509 (G4), HKR 11-447 (G6) and Pusa Basmati 1 (G12) were the least stable genotypes for milling %. Pusa Basmati 1 (G12), Pusa Basmati 1121 (G13) and Improved Pusa Basmati 1 (G8) had maximum while Pusa Basmati 6 (G16) had minimum head rice recovery percentage with high stability across the environments. Similarly, for amylose content Improved Pusa Basmati 1 (G8), Pusa Basmati 1121 (G13) and HKR 08-425 (G5) were more stable genotypes with better performance. Genotypes HKR 11-509 (G4) and Pusa Basmati 1 (G12) were less stable for amylose content. This technique has been used commonly in several crops to identify the stable and high yielding genotypes in multi-environmental trails like wheat (Kaya et al., 2006), barley (Dehghani et al., 2006), Sorghum (Rakshit et al., 2012) and Sugarcane (Otieno and Owuor, 2019). Fig. 2 (a-d) represents the ranking of sixteen genotypes concerning the ideal genotype. Ideal genotype has a high mean value with high stability across the multi-environment, which could be identified by the larger vector length and present near the center of the concentric circles (Rakshit et al., 2012). Genotypes present in the vicinity of ideal genotypes are preferable to remaining genotypes due to their stability and better performance (Otieno and Owuor, 2019; Hashim et al., 2021). In the present study, HKR 11-447 (G6) and HKR 98-476 (G7) for hulling %, HKR 98-476 (G7) and Pusa Basmati 1121 (G13) for milling %, Pusa Basmati 1 (G12) and Pusa Basmati 1121 (G13) for head rice recovery % and Improved Pusa Basmati 1 (G8) and Pusa Basmati 1121 (G13) for amylose content were present in the vicinity of ideal genotype and are most valuable among the studied genotypes.

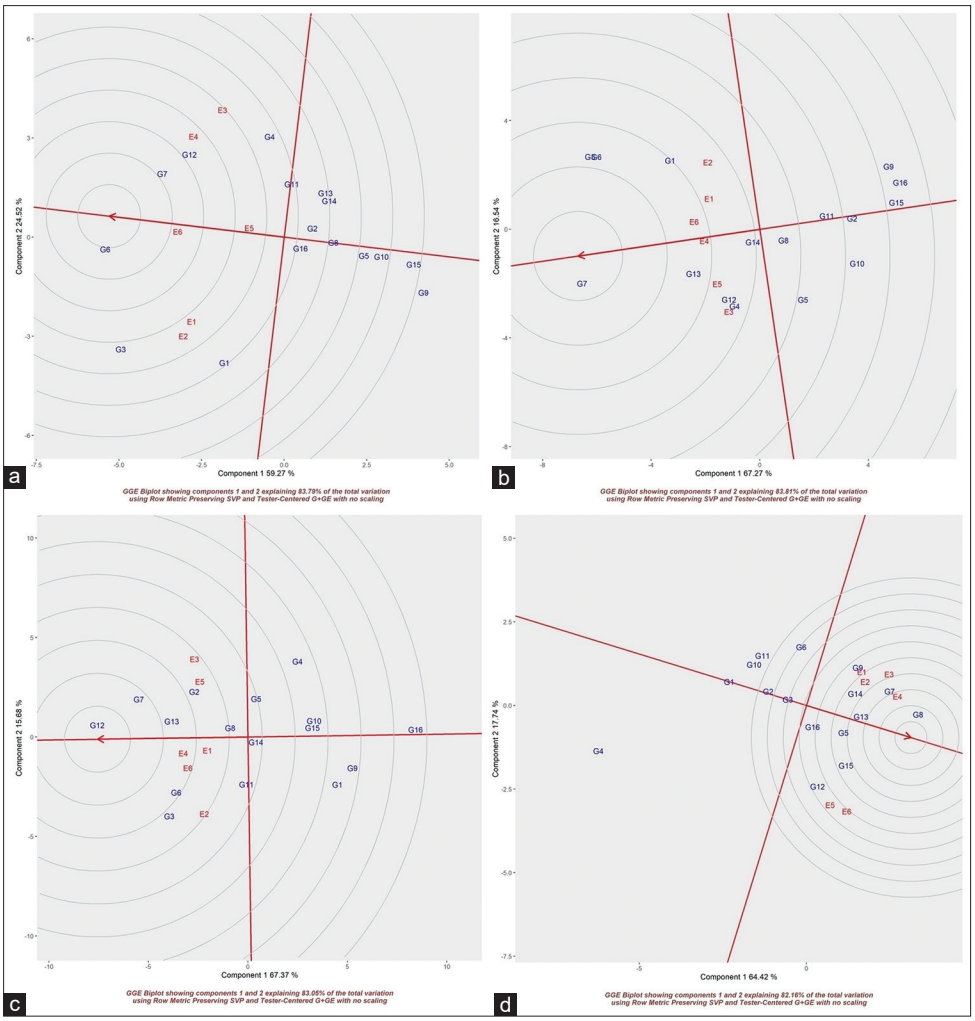

Fig 2. GGE biplot analysis: ranking of genotypes relative to an ideal genotype for (a) hulling %, (b) milling %, (c) head rice recovery % and (d) amylose content %.

Environment evaluation

The angle between the environmental vectors defines the association among them. The presence of an acute angle shows a positive or closer association between the tested environments. It indicates the non-existence of crossover GE, suggesting that similar kinds of information can be drawn from the minimum number of environments and ranks of genotype do not vary from environment to environment. While a 90° angle among them indicates no association. An obtuse angle between environmental vectors shows a negative association among the tested environments and is an indication of strong crossover GE interaction. The genotype good in one environment may be worse in another environment (Rakshit et al., 2012; Inabangan-Asilo et al., 2019; Frutos et al., 2014). Relationship among the different environments for hulling % (Fig. 3a), milling % (Fig. 3b), head rice recovery % (Fig. 3c) and amylose content (Fig. 3d) showed that most of the angles between the environmental vectors are acute indicating the positive or close association among them with an exception between E2 (DSR-U) and E3 (SRI-K) for hulling % and milling %. This suggests that E2 and E3 environments showed significant differences in genotypic performance for these two traits. Plant breeder always wants to select genotypes that gave the best performance across environments with minimum GEI; however, this happens seldom (Krishnamurthy et al., 2017). Discriminating ability, an important feature of GGE biplot, is represented by vector length i.e. larger the vector length of an environment means greater discriminating ability (Yan, 2001; Yan, 2002). The six environments can be divided into three groups for hulling % i.e. group 1: E1 (DSR-K), E2 (DSR-U); group 2: E3 (SRI-K), E4 (SRI-U); group 3: E5 (TPR-K) and E6 (TPR-U), three groups for milling % i.e. group 1: E1 (DSR-K), E2 (DSR-U); group 2: E3 (SRI-K), E5 (TPR-K); group 3: E4 (SRI-U), E6 (TPR-U), three groups for head rice recovery % i.e. group 1: E2 (DSR-U); group 2: E3 (SRI-K), E5 (TPR-K) and group 3: E1 (DSR-K), E4 (SRI-U), E6 (TPR-U), and two groups for

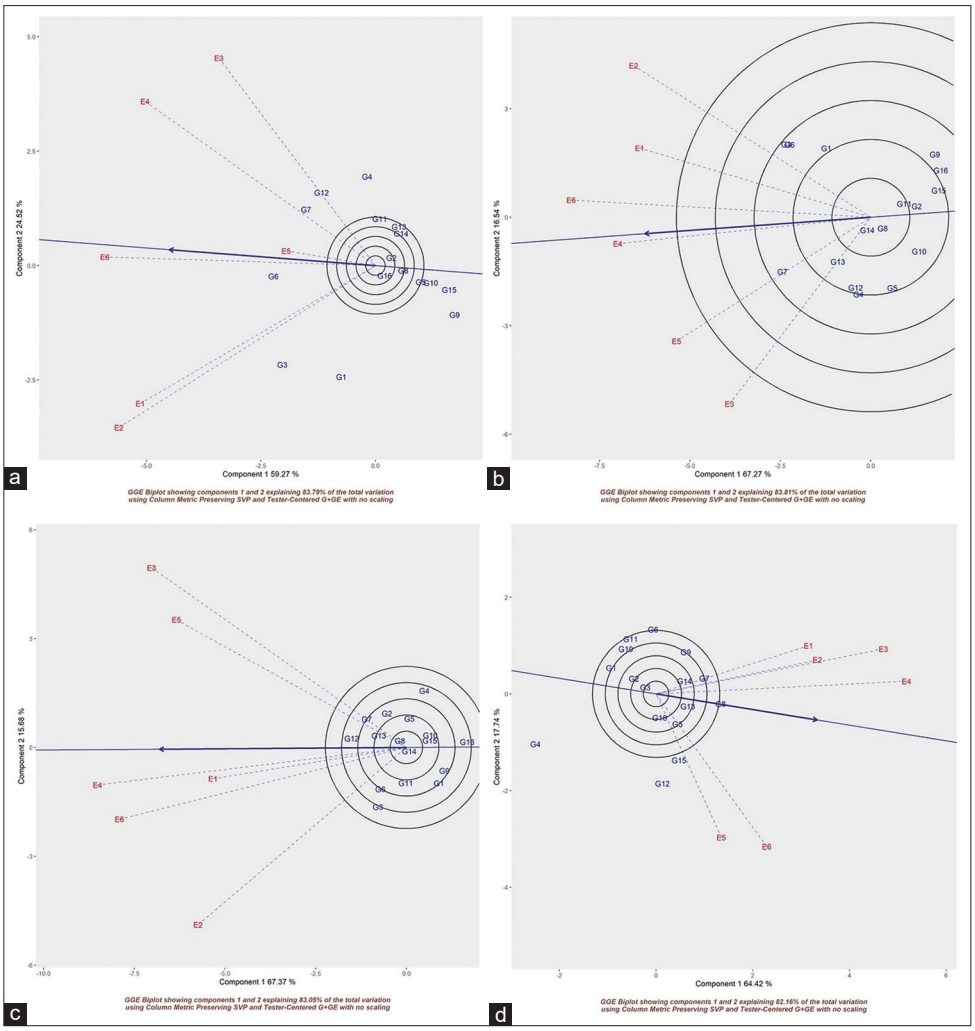

Fig 3. GGE biplot analysis: relations among, discriminating ability and representativeness of test environments for (a) hulling %, (b) milling %, (c) head rice recovery % and (d) amylose content %.

amylose content i.e. group 1: E1 (DSR-K), E2 (DSR-U), E3 (SRI-K), E4 (SRI-U) and group 2: E5 (TPR-K), E6 (TPR-U). The arrow present on the average environment axis (AEA) denotes the average environment. A test environment with a smaller angle with AEA is more representative than others (Rakshit et al., 2012). For hulling %, E5 (TPR-K) and E6 (TPR-U); for milling %, E4 (SRI-U) and E6 (TPR-U); for head rice recovery % and amylose content, E4 (SRI-U) were found as most representative environments. A representative and discriminating environment is good for choosing generally adapted, while non-representative and discriminating environments are good for choosing specifically adapted genotypes (Yan and Tinker, 2006). In the present study, E5 (TPR-K) and E6 (TPR-U) for hulling %, E4 (SRI-U) and E6 (TPR-U) for milling %, E4 (SRI-U) for head rice recovery % and E4 (SRI-U) for amylose content were both discriminating as well as representative and ideal for selecting genotypes for general adaptation (Inabangan-Asilo et al., 2019). Similarly, E2 (DSR-U) and E3 (SRI-K) for hulling, milling and head rice recovery % and E1 (DSR-K) and E5 (TPR-K) for amylase content were most discriminating environments but non-representative and best for selecting specifically adaptable genotypes (Senguttuvel et al., 2021). These environments differentiate among the genotypes and are better for culling out inferior genotypes.

Polygon view

Which-Won-Where is the most important feature of GGE biplot (Yan and Tinker, 2006) which helps in the differentiation of mega-environments and identification of specifically adaptable genotypes (Hashim et al., 2021). Polygon is constructed by associating the genotypes present farther from the biplot origin. These genotypes are either better or poor performing in some or all environments. The HKR 11-509 (G4), G12, HKR 98-476 (G7), HKR 11-447 (G6), Haryana Basmati 1 (G3), Basmati 370 (G1), Pusa 1637-2-8-20-5

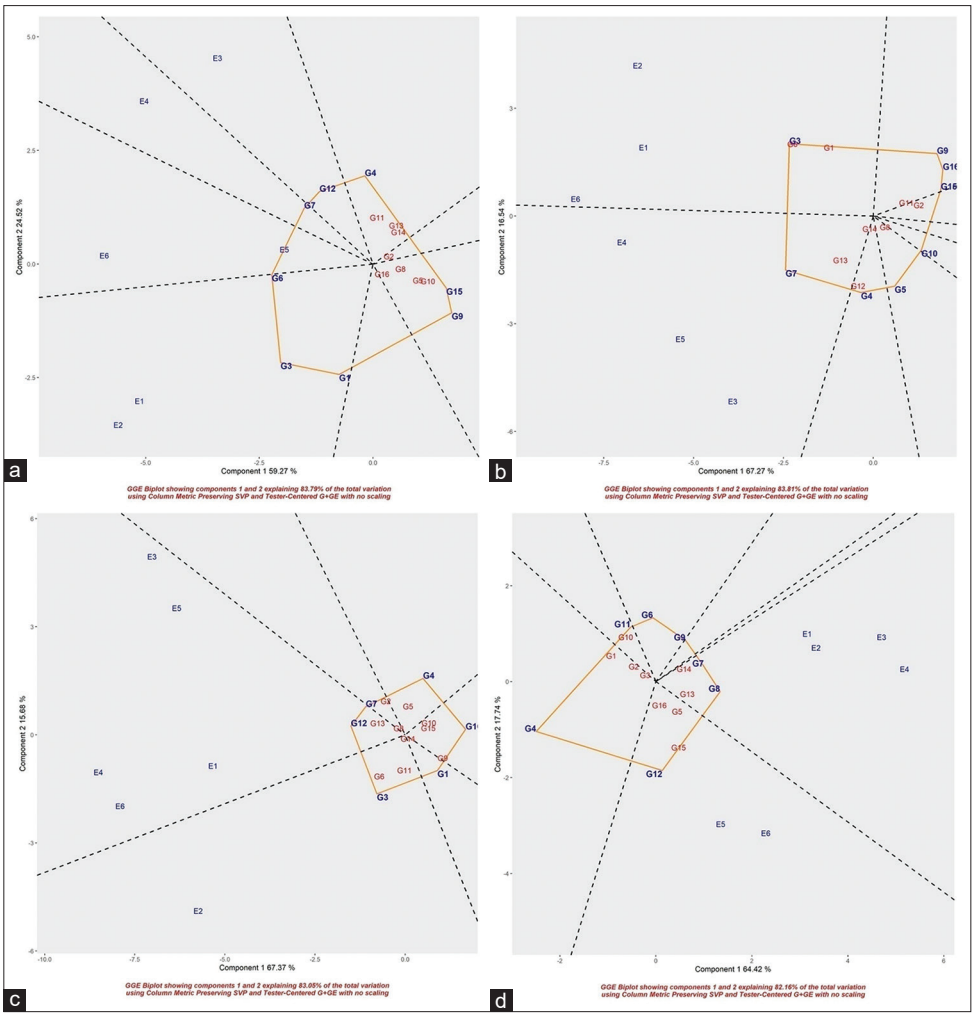

Fig 4. GGE biplot analysis: Identification of winner genotypes and their mega-environments for (a) hulling %, (b) milling %, (c) head rice recovery % and (d) amylose content %.

(G9) and Pusa Sugandh 2 (G15) for hulling % (Fig. 4a), Haryana Basmati 1 (G3), HKR 98-476 (G7), HKR 11-509 (G4), HKR 08-425 (G5), Pusa 1656-10-705 (G10), Pusa Sugandh 2 (G15), Pusa Basmati 6 (G16) and Pusa 1637-2-8-20-5 (G9) for milling % (Fig. 4b), HKR 11-509 (G4), HKR 98-476 (G7), Pusa Basmati 1 (G12), Haryana Basmati 1 (G3), Basmati 370 (G1) and Pusa Basmati 6 (G16) for head rice recovery % (Fig. 4c), and Improved Pusa Basmati 1 (G8), HKR 98-476 (G7), Pusa 1637-2-8-20-5 (G9), HKR 11-447 (G6), G11, HKR 11-509 (G4) and Pusa Basmati 1 (G12) for amylase content (Fig. 4d) were present on the vertices of the polygon. It was reported that genotypes present inside the polygon and near to origin are tolerant to environmental fluctuations (Oladosu et al. 2017). If all environment falls in one sector, indicates that a single genotype performs well among the environments. Conversely, genotypes placed on the vertices of sectors with no environment had poor performance in all tested environments (Herawati et al., 2021). Equality lines were drawn from the biplot origin which divides the biplot into different sectors with a vertex genotype (Yan, 2001). The vertex genotype is the best performer in the environments present within the sectors (Yan, 2002). In the present study, the testing environments were separated into four mega environments for hulling % (Fig. 4 a): first with E3 (SRI-K) have Pusa Basmati 1 (G12), second with E4 (SRI-U) have HKR 98-476 (G7), third with E5 (TPR-K) and E6 (TPR-U) have HKR 11-447 (G6) and fourth with E1 (DSR-K) and E2 (DSR-U) have Basmati 370 (G1) and Haryana Basmati 1 (G3) as winner genotypes. For milling % (Fig. 4b), two mega-environments were formed: one with E1 (DSR-K), E2 (DSR-U) and E6 (TPR-U) has Haryana Basmati 1 (G3) and second with E3 (SRI-K), E4 (SRI-U) and E5 (TPR-K) have HKR 98-476 (G7) as winner genotypes. For head rice recovery % (Fig. 4c), one mega-environment had E1 (DSR-K), E3 (SRI-K), E4 (SRI-U), E5 (TPR-K) and E6 (TPR-U) with Pusa Basmati 1 (G12) and second encompassing E2 (DSR-U) with Haryana Basmati 1 (G3) as winner

genotype. Similarly, for amylose content (Fig. 4d), mega environment one with E1 (DSR-K), E2 ((DSR-U), E3 (SRI-K) and E4 (SRI-U) have Improved Pusa Basmati 1 (G8) and second with E5 (TPR-K) and E6 (TPR-U) have Pusa Basmati 1 (G12) as winner genotypes. Based on this analysis, inferences can be made from one or two representatives of each mega-environment which reduces the cost of multi-environment testing. However, this pattern needs to be confirmed by using the same set of genotypes and environments across the years (Yan et al., 2000). A reproducible which-won-where pattern is necessary for drawing a better conclusion from the mega-environments (Zobel et al., 1998; Yan et al., 2007; Krishnamurthy et al., 2017). Partitioning of test environment into different mega-environments was reported earlier in rice, wheat, cotton and sorghum (Navabi et al., 2006; Rakshit et al., 2012; Luo et al., 2015; Yan et al., 2015).

CONCLUSION

The estimation of GEI is very important for the identification of rice genotypes with specific and wide adaptation. Analysis of variance showed significant differences among the genotypes, environments, GE effect and interaction principal components 1 and 2 for all the investigated traits. The significance of GEI and principal components should be taken simultaneously to make the recommendation of stable and adaptable genotypes accurately. It has been brought out from the study, those genotypes showing adaptability for one trait do not mean its adaptability for remaining traits. Thus plant breeders need to identify the principle traits to target during the genetic improvement programs. Across the environments, HKR 98-476 for hulling % and Pusa basmati 1121 for milling %, head rice recovery and amylose content were identified as high performing and stable genotypes. Haryana Basmati-1 and Improved Pusa Basmati 1 under DSR while HKR 98-476, Pusa Basmati-1 and Improved Pusa Basmati -1 under SRI was better performing and highly adaptable genotypes. Further, this research is expected to sort out the problem of varietal identification and recommendation for the alternative and resource-conserving method of rice planting with wider adaptation, stability and high mean performance.

AUTHOR CONTRIBUTIONS

Hari Kesh- Conceptualization of research; Hari Kesh and Satender Yadav- Execution of field experiments and data collection; Mujahid Khan, Hari Kesh and Akshay Kumar Vats- Analysis of data and interpretation; Hari Kesh and Akshay Kumar Vats- Preparation of the manuscript.

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