UNDERSTANDING G × E INTERACTION OF ELITE BASMATI RICE (*ORYZA SATIVA* L.) GENOTYPES UNDER NORTH INDIAN CONDITIONS USING STABILITY MODELS

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Abstract. Information regarding the stability of genotypes is critical in expanding the adaptability of released genotypes. But, this information regarding the basmati (scented) rice genotypes cultivated under north Indian conditions are not well known. Therefore, here we have evaluated the twenty-two basmati rice genotypes for stability, based on important traits, and different production system. Genotypes were evaluated for two consecutive Kharif seasons under open field conditions in a randomized complete block design (RCBD). The genotypes were evaluated under four production systems namely, transplanted rice (TPR), system of rice intensification (SRI), direct seeded rice (DSR) in both settings, i.e. wet DSR (W) and dry DSR (D). The stability of genotypes was determined via Eberhart and Russell model, additive main effects and multiplicative interaction (AMMI), and genotype × environment interaction (GGE) biplot model. The stability and adaptability studied using Eberhart and Russell model, AMMI and GGE biplot identified Basmati-370 as the most stable genotype for biological weight; Pusa RH-10 for filled spikelet; CSR-30 for spikelet Number; and Traori Basmati for test grain weight. TPR was the most desirable test environment followed by SRI and DSR (W). Further, we have identified HKR 08-417 as the most suitable genotype for all of the production systems. Overall, this study provides information regarding stable basmati rice genotypes under the north Indian conditions.
Keywords: *rice, G × E, GGE, AMMI, stability model, Eberhart and Russell, SRI, DSR*

Introduction

Rice (*Oryza sativa* L.) production is vital for the growing population (Zhang, 2007; Wu and Cheng, 2014). Although, rice is grown worldwide over an area of around 163.24 mha with a production of around 740.95 mt. besides its productivity is around 4.54 t/ha (Anonymous, 2016). In India rice is cultivated over 43.99 mha which results in the production of 109.69 mt., with a productivity of 2.49 t/ha (Anonymous, 2017). The productivity of rice in India is around half of the world average. This low productivity of rice in the Indian subcontinent is a result of several factors like less water availability, the frequent occurrence of droughts, weed competition, insect pest, and diseases (Silalertruksa et al., 2017; Sreekanth et al., 2017). The rice production areas in India are highly diverse with different production systems due to the area specific soil and climatic features (Singh et al., 1997). Moreover, the improper commercialization of high yielding varieties for non-conventional systems of rice production like system of rice intensification (SRI), direct

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seeded rice (DSR) etc. leads to below average yields under non-conventional systems (Wanjari et al., 2006).

Based on the aroma, rice is divided into two categories namely, basmati (scented) and non-basmati (non-scented) type. Basmati rice is comprised of long slender grain, pleasant aroma and fluffy rice texture (Ashfaq, 2015; Hinge et al., 2016). The scented aroma of basmati varieties is only perceived when basmati rice varieties are grown on the northwestern foothills of Himalayas (Bhattacharjee et al., 2002; Jena and Grote, 2012). Still, most of the basmati genotypes are limited to the environment of their developed institutes, due to less in-depth study regarding the performance of elite verities under diverse environments from their developed institutes (Kamoshita et al., 2008). The researchers are primarily focused on configuring the input demand for the transplanted rice-based production system (Lin, 1994). The new production systems/non-conventional strategies like, SRI, DSR (are intended for the optimum yield per amount of input supplied (Jain et al., 2018).

Genotype × Environment interactions (GEI) plays a pivotal role in the positioning of genotypes from their native to non-native environment, which further hampers the plant breeding advancement (Pham and Kang, 1988). A genotype is termed as stable if it performs statically across different environments. Whereas, the theory of biological stability consider the concept of less variance for yield and yield related characters across unrelated environments (Becker and Leon's, 1988). Rice breeders and agronomists give little attention to biological stability concept (Xu, 2016).

A number of stability analyses models are used to determine the contribution of G × E interaction (GEI), also, to identify genotypes which perform superior under several environments (Génard et al., 2017; Malosetti et al., 2013). Stability model is defined in terms of mean value, regression coefficient, deviation from the regression, and principal component analysis (PCA) (Bernardo, 2002). Stability models like Finlay and Wilkinson (1963), and Eberhart and Russell (1966) are based on two parameter regression coefficient (bi), and deviation from regression (S^2di). Whereas, the additive main effects and multiplicative interaction (AMMI) model is a combination of the main effect due to analysis of variance and their interactions (GEI) (Gauch, 1992).

Yan et al. (2000) created a biplot strategy known as GGE biplot which graphically indicates the genotype (G) primary effects and genotype × environment interaction (GGE). The G and GE are the two fundamental source of variation for genotype evolution under diverse environment. The GGE biplot analysis represents the G+GE of different environment records acquired by plotting the two (or more) PCA score of G × E interaction. The GGE biplot analysis allows the analysis of many characteristics of genotypes and environments (Samonte et al., 2005). Selection and identification of stable and high yielding genotypes over the different environments have been a continuous task to rice breeders (Balestre et al., 2010). Therefore, in our study, we have compared the Eberhart and Russell methodology, AMMI biplot, and GGE biplot analysis of the twenty-two popular basmati rice genotypes under north Indian conditions. Further, these approaches are applied under four different production systems transplanted rice (TPR), SRI, DSR (W) and DSR (D).

Materials and methods

Plant material and experiment layout

Experimental fields were settled at Regional Research Station, Kaul, India (29.98° N latitude and 79.66° E longitude) (*Fig. 1*). Field trials were conducted over two Kharif (July

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to October) seasons in 2014-2015 and 2015-2016 respectively. During both of the years, the nursery was sown in June, for both TPR and SRI. After that, the seedlings were field transplanted in July for TPR and SRI. Whereas, the direct sowing of DSR (D) and DSR (W) was performed in June. Plants were harvested in the month of October for data analysis. The weather during the entire crop period is presented in *Figure 2*. The soil was analysed as a composite sample from the top 0-15 cm (Bandyopadhyay et al., 2012). The soil was sandy loam with the with different percentage of sand (81.4%), slit (7.3%), and clay (11.3%). All plant production related practices were followed based on the package of practices for rice cultivation.

The experimental materials comprised of popular basmati rice genotypes (*Table 1*). These genotypes were laid out in a randomized complete block design (RCBD) with three replications, using four production systems namely, TPR, SRI, DSR (W) and DSR (D) (*Table 2*). Each experimental plot consisted of five rows of 2 m long with 0.20 m row spacing (*Fig. 3*).

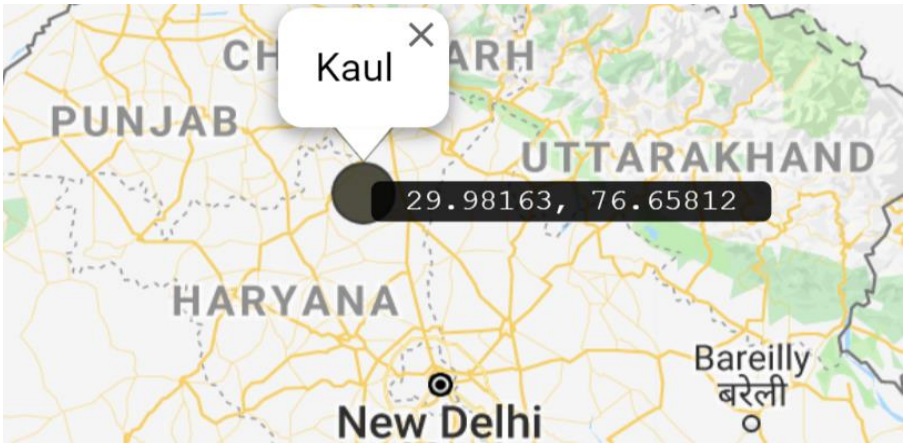
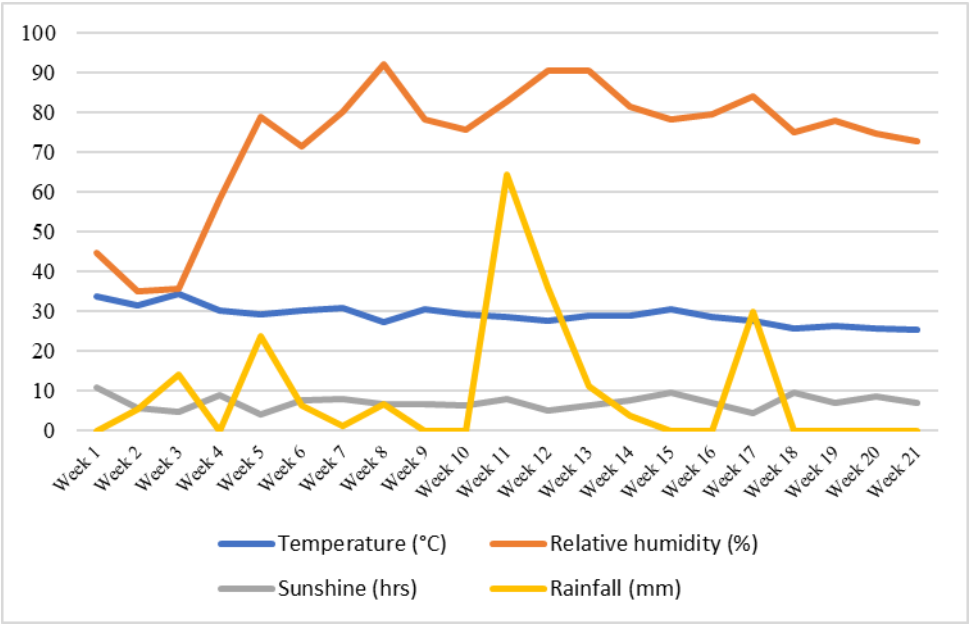


Figure 1. *Location and coordinates of the experimental site in India*



a

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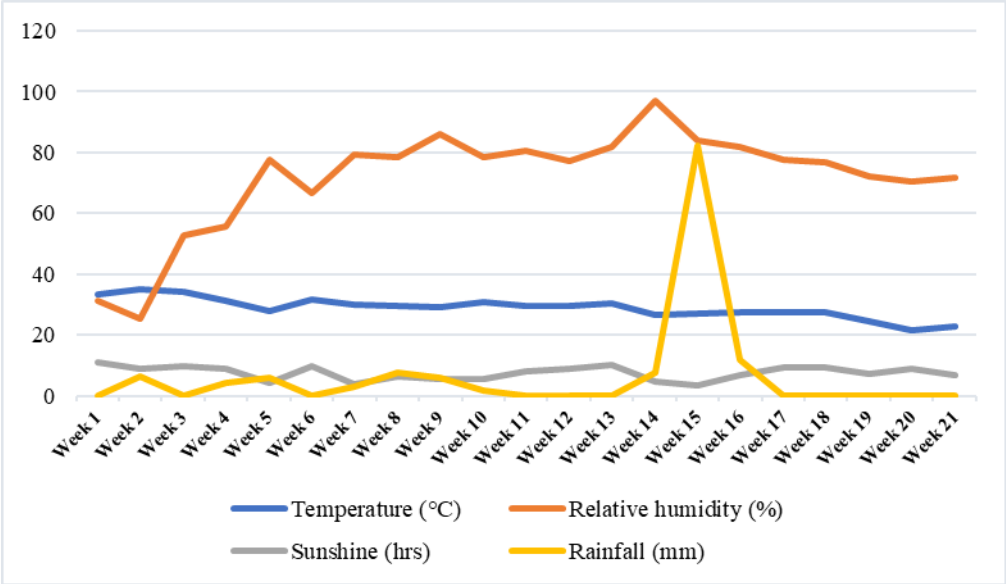

b

Figure 2. *Temperature (°C), relative humidity (%), sunshine (h), and rainfall (mm) during first year and second year of the entire crop season*

Table 1. *List of basmati rice genotypes used in the study*

Code	Genotypes
G1`	Pusa Basmati 1121
G2	Pusa Basmati 1509
G3	Pusa Sugandh 2
G4	Pusa Sugandh 3
G5	Pusa Sugandh 5
G6	Pusa Basmati 6
G7	Pusa Basmati 1
G8	Improved Pusa Basmati 1
G9	HKR 98-476
G10	HKR 03-408
G11	HKR 06-434
G12	HKR 06-443
G13	HKR 06-487
G14	HKR 08-417
G15	HKR 08-425
G16	Haryana Mahek-1
G17	Haryana Basmati-1
G18	Traori Basmati
G19	Super Basmati
G20	CSR-30
G21	Basmati-370
G22	Pusa RH-10

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Table 2. *Description of environments*

Environment	2014	2015
DSR (D)	*E1*	*E2*
DSR (W)	*E3*	*E4*
SRI	*E5*	*
TPR	*E6*	*E7*

Transplanted rice (TPR), system of rice intensification (SRI), direct seeded rice (DSR) in both conditions, i.e. wet (W) and dry (D)
*Filled damage during flood, so data was not included in the analysis

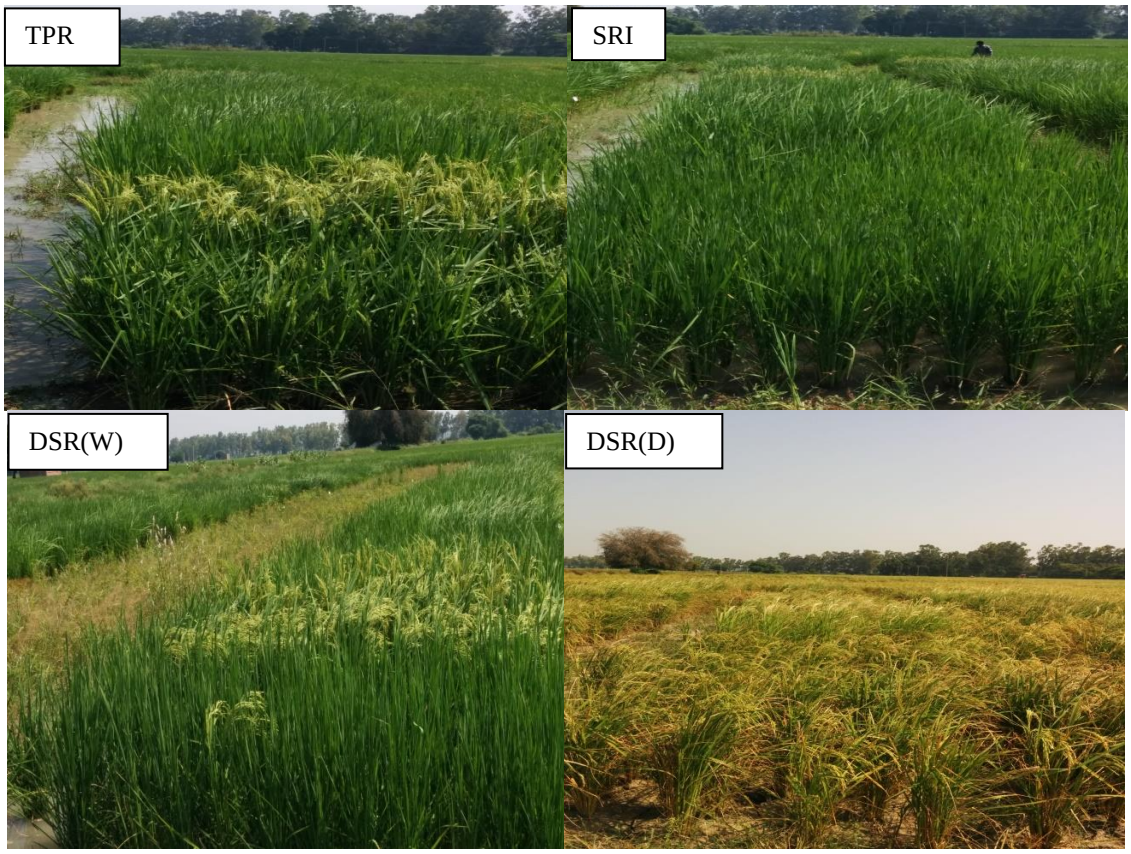

Figure 3. *The four production systems used for the characterization of basmati rice genotypes. Transplanted rice (TPR), system of rice intensification (SRI), direct seeded rice wet (DSR (W)), and direct seeded rice dry (DSR (D))*

Characterization and data analysis

In total seven characters were studied as the mean of five randomly chosen plants per plot. Biological weight is measured as the weight of plant biomass. The biological weight (g) per plant was recorded after harvesting and drying of mature plants. Whereas, the harvest index was determined as the ratio of grain yield/biological yield × 100. Test grain weight (g) was determined from the random sample of 1000 filled grains for each replication. Whereas, the number of spikelet per panicle were determined from a random sample of twenty panicles after harvesting. The percent of filled spikelet was

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estimated as the percentage of grain filled spikelet to the total number of spikelet. While the days to 50% flowering were recorded based on the date of sowing to 50% flowering on a plot basis. Similarly, days to 75% maturity were recorded from the date of sowing until the day when a minimum 75% grains per panicle showed maturity.

The data analysis was performed using the software package PBTools version 1.4 (http://bbi.irri.org/products) and R Statistics (R Core Team, 2017). Unweighted Pair Group Method with Arithmetic Mean (UPGMA) method of hierarchical clustering was applied to the twenty-two genotypes in order to visualize how genotypes are related to each other based on all of the studied descriptors. The AMMI model (Gauch, 1988) is a combination of Additive (ANOVA) and multiplicative interaction (Principal component analysis). The Genotype × Environment interaction was evaluated by considering the first two PCA. The statistical model can be represented as:

$$Y_{ij} = \mu + g_i + e_j + \Sigma\, \lambda_n \alpha_{in} \gamma_{jn} + \theta_{ij} \quad \text{(Eq.1)}$$

where:
Y_{ij}: mean yield of i^{th} genotype in the j^{th} environment;
μ: general mean;
g_i: i^{th} genotypic effect;
e_j: j^{th} location effect.
λ_n: eigenvalue of the Principal Component Axis n;
α_{in}: and γ_{jn} are the i^{th} genotype, j^{th} environment Principle component analysis (PCA) scores for the PCA axis n;
θ_{ij}: residual n is the number of PCA axes retained in the model.

Whereas GGE biplots are a combination of both G (Genotype) linear effect and G × E interaction and it is based on sites regression linear, bilinear model (Kang, 1993; Cornelius et al., 1996; Crossa and Cornelius, 1997; Crossa et al., 2002).

Results

Genotypic performance of different traits

A diverse range of variation in the means was detected for yield and yield-related traits for all of the 22 basmati rice genotype in a different production system. During the two seasons; wide-ranging genotypic fluctuation or variation was detected and ranged for biological weight (32.49 to 44.26); harvest Index (%) (27.54 to 41.17); test grain weight (19.62 to 29.95); number of Spikelet (57.49 to 109.71); filled spikelet (%) (73.06 to 87.62); 50% flowering (86.00 to 108.40); 75% maturity (107.60 to 137.60) among different genotype under study as shown in *Table 3*. Considering the two season average mean, genotypes G22 recorded the highest number of spikelet per plant, whereas, genotype G16 recorded the highest biological weight per plant. Genotype G2 was short duration with lowest unfilled grain and highest test grain weight in all the production system (*Table 3*). Further, using the Unweighted Pair Group Method with Arithmetic Mean (UPGMA) technique the clustering results of the twenty-two basmati rice genotypes are presented in *Figure 4*. More related genotypes were clustered together. Genotype G2 clustered apart from rest of the genotypes. Whereas, seven genotypes clustered together, while, the remaining fourteen genotypes were together (*Fig. 4*).

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Table 3. *Mean performance of genotypes for the studied characters over a period of two years*

Genotype	Biological weight (g)	Harvest index (%)	50 flowering (%)	75 maturity (%)	Filled spikelet (%)	Test grain weight (g)	No. of spikelet
G1	43.76	32.32	101.60	128.30	75.41	27.46	62.05
G2	32.49	39.54	86.00	107.60	85.22	29.95	66.91
G3	36.63	36.66	89.50	113.60	81.39	27.45	91.05
G4	36.85	33.97	99.00	120.70	77.71	22.94	88.10
G5	35.86	35.43	99.80	119.60	79.21	25.44	92.38
G6	38.31	34.85	110.30	135.90	73.06	21.85	80.48
G7	35.52	34.84	107.50	136.80	77.42	21.85	89.10
G8	33.94	36.51	107.60	136.60	76.15	21.19	87.41
G9	39.55	30.16	107.40	135.40	77.21	21.50	57.50
G10	41.29	28.20	109.10	136.20	81.59	21.16	64.79
G11	44.11	27.55	111.40	137.00	82.17	22.63	66.00
G12	39.51	30.33	102.00	130.00	78.84	26.29	53.95
G13	39.14	30.02	108.40	134.10	84.26	19.62	84.95
G14	37.21	41.17	98.80	127.60	86.40	21.90	72.59
G15	40.14	37.31	99.40	129.10	84.67	21.52	81.10
G16	44.27	27.49	114.00	137.60	82.14	23.58	76.33
G17	36.63	34.13	101.50	127.90	79.42	22.61	83.77
G18	40.14	33.59	103.50	128.60	87.63	23.63	56.19
G19	38.88	32.71	96.70	127.80	82.54	21.44	77.58
G20	36.97	26.99	105.60	132.80	84.75	22.82	51.95
G21	43.83	29.20	101.00	130.10	83.23	22.10	81.24
G22	38.11	40.61	92.30	116.90	73.32	24.75	109.71
Mean	38.78	33.34	102.38	128.65	80.62	23.35	76.14
Standard error	3.19	2.18	1.70	2.30	2.20	0.95	4.99

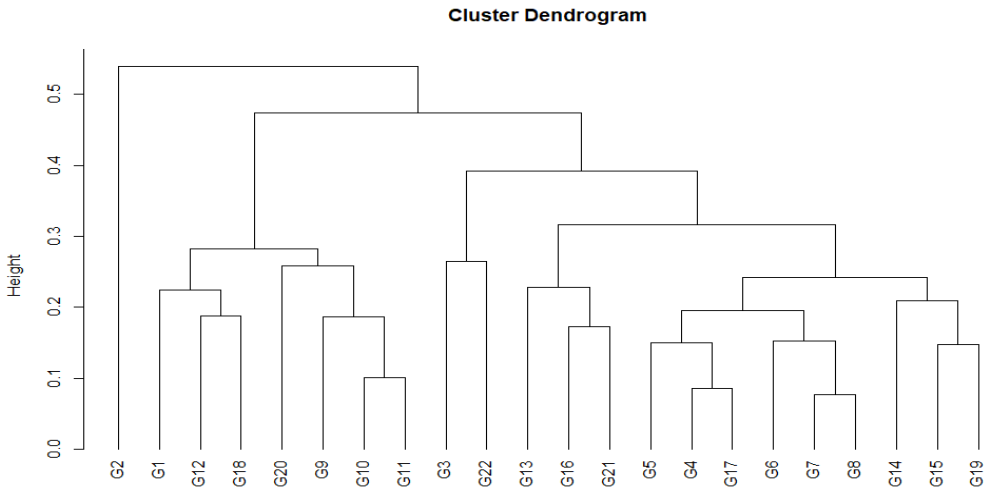

Figure 4. *Clustering dendrogram of twenty-two basmati rice genotypes based on the Unweighted Pair Group Method with Arithmetic Mean (UPGMA) clustering method with on log-normalized descriptors values. The cophenetic correlation coefficient of clustering is 0.8*

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Pooled analysis and stability analysis

Interpretations on the yield-related traits for two-year data were then subjected to pooled analyses by using Eberhart and Russel (1966), Additive Main Effect and multiplicative interaction (Gauch and Zobel, 1989) and GGE Biplot (Yan and Kang, 2003). In the analysis, the environment defined by every arrangement of location or Kharif season with the production system. First Analysis of variance was conducted for each location (environment) then combined analysis of two-year data was subjected to stability analysis using PB tools and R software. The pooled analysis results showed that the genotypic and environmental variances were significant ($p < 0.05$) for all the traits. Similarly, the mean sum of squares due to G × E interaction was significant for all of the seven traits studied. Furthermore, the partitioning of the combined environment, and genotype × environment variance into linear and non-linear components showed that environment linear and combined deviation was significant given in *Table 4*.

Table 4. *Pooled analysis of variance over different environments for different traits in rice (Eberhart and Russell, 1966 model)*

Source of variations	DF	Biological weight (g)	Harvest index (%)	50 Flowering (%)	75 Maturity (%)	Filled spikelet (%)	Test grain weight (g)	No. of spikelets
Rep within Env.	14	3.5	1.81	0.81	0.5	8.23	0.53	13.32
Varieties	21	73.87*	127.58**	354.36**	480.49**	120.46**	45.29**	1536.44**
Env.+ (Var.* Env.)	132	249.73***	76.312**	32.56**	52.85**	63.66**	8.37*	435.22**
Environments	6	4600.33***	937.039**	325.86**	442.44**	679.10**	67.58**	5072.60**
Var.* Env.	126	42.56**	35.32*	18.59*	34.30*	34.35*	5.55*	214.39*
Environments (Lin.)	1	27601.99***	5622.23**	1955.21**	2654.67**	4074.60**	405.52**	30435.60**
Var.* Env.(Lin.)	21	63.49*	62.66**	20.33	44.27	54.03*	4.83015871	502.62**
Pooled Deviation	110	36.63***	28.50**	17.41**	30.84**	29.03**	5.44**	149.62**
Pooled Error	294	5.73	2.31	1.32	1.07	6.67	0.69	14.74
Total	153	225.59	83.34	76.72	111.55	71.45	13.44	586.37

*, **Significant at 5% and 1% respectively

The stability model proposed by Eberhart and Russell (1966) was adopted to analyse the data over different environments and in this model is the most popular technique of studying Genotype × Environment interaction and genotypic stability. It used two parameters (bi and $S^{-2}di$) to define stability. $S^{-2}di$; is primarily used to rank the relative stability of cultivars. The indication is that bi may be utilized to depict the standard response to the goodness of environmental conditions though S-2di measures the predictability. According to this model, a stable variety is one that has a high mean (Xi), unit regression coefficient (bi=l) and the deviation from regression as small as possible ($S^{-2}di = 0$). The stability analysis revealed the genotypes in case of with significant regression coefficient (bi) and non-significant deviation from the regression ($S^{-2}di$) Genotype G21 (50% flowering) and G17 (filled spikelet (%)) exhibited non-significant $S^{-2}di$, regression coefficient significantly greater than one and mean higher than the population mean was found suitable for a better environment (E6 and E5). Genotype G2 in biological weight, G18 and G21 in a filled spikelet (%), G2 and G12 in Number of spikelet with regression coefficient significantly less than one and non-significant deviation from regression and mean higher than the population mean was identified suitable for unfavourable environments E1, E2, E3, E4. Genotype G9 and G19 were

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found stable for filled Spikelet (%) trait for all the environments that have high mean (Xi), unit regression coefficient (bi=l) and the deviation from regression as small as possible ($S^{-2}di = 0$) given in *Table 5.*

Table 5. *Stability parameters for yield contributing traits of rice genotypes tested over different environments*

Genotypes	Parameter	Biological weight (g)	Harvest index (%)	50 flowering (%)	75 maturity (%)	Filled spikelet (%)	Test grain weight (g)	No. of spikelets
G1	Mean	43.762	32.323	101.571	128.286	75.414	27.462	62.048
	bi	1.22	1.273	0.830	1.022	1.123	0.666	0.229
	S^2di	29.395	25.010	5.55	6.638	9.777	0.579	21.705
G2	Mean	32.490	39.535	86.000	107.619	85.224	29.952	66.905
	bi	0.555	0.898	0.837	-0.019	-0.136	0.316	0.709
	S^2di	-0.537	49.719	2.062	39.809	9.969	4.788	13.008
G3	Mean	36.633	36.658	89.476	113.571	81.386	27.452	91.048
	bi	0.905	1.019	0.863	0.271	-0.256	0.657	1.399
	S^2di	12.465	29.494	6.785	51.342	22.906	-0.115	106.416
G4	Mean	36.848	33.966	99.000	120.714	77.714	22.943	88.095
	bi	0.800	0.814	1.827	0.010	1.351	0.001	1.462
	S^2di	26.09**	20.80**	34.35**	83.90**	163.25**	6.35**	202.05**
G5	Mean	35.857	35.430	99.762	119.571	79.205	25.438	92.381
	bi	0.563	0.077	1.448	0.542	0.496	0.927	1.176
	S^2di	33.21**	41.67**	67.98**	64.73**	4.772	4.63**	103.31**
G6	Mean	38.314	34.851	110.33	135.857	73.062	21.848	80.476
	bi	1.177	1.095	1.545	0.962	0.773	1.079	1.95*
	S^2di	1.449	65.10**	6.74**	7.94**	63.60**	7.64**	88.68**
G7	Mean	35.521	34.839	107.524	136.762	77.424	21.848	89.095
	bi	0.891	1.004	1.373	1.293	1.498	1.517	1.76*
	S^2di	13.74**	3.12*	11.95**	5.77**	22.20**	5.30**	96.96**
G8	Mean	33.943	36.507	107.571	136.619	76.148	21.186	87.410
	bi	0.95*	0.769	1.675	1.411	1.545	0.898	2.08*
	S^2di	5.064	25.12**	23.41**	5.19**	42.22**	12.85**	152.05**
G9	Mean	39.552	30.159	107.381	135.381	77.214	21.495	57.495
	bi	1.119	1.98*	1.368	1.85*	1.04*	0.940	0.649
	S^2di	33.88**	31.48**	4.035**	7.72**	5.894	6.11**	87.83**
G10	Mean	41.286	28.195	109.095	136.238	81.586	21.162	64.790
	bi	1.276	0.956	0.949	1.61*	0.765	1.22*	0.42*
	S^2di	53.30**	23.55**	3.42**	2.48**	6.991	0.352	23.62*
G11	Mean	44.114	27.547	111.380	137.048	82.167	22.633	66.000
	bi	1.393	0.844	0.710	1.456	0.887	1.565	0.639
	S^2di	84.97**	26.12**	0.019	8.31**	14.27**	10.01**	67.03**
G12	Mean	39.514	30.332	102.048	129.952	78.843	26.286	53.952
	bi	0.910	1.237	0.971	0.800	1.838	0.722	0.43**
	S^2di	35.55**	1.504	9.04**	26.35**	44.09**	0.86*	2.899
G13	Mean	39.143	30.022	108.381	134.143	84.257	19.624	84.952
	bi	0.863	1.126	0.424	1.618	1.312	1.26*	1.465
	S^2di	25.75**	6.71**	15.26**	31.78**	4.260	0.045	730.35**
G14	Mean	37.210	41.173	98.810	127.571	86.395	21.895	72.590
	bi	1.067	0.585	0.745	1.727	0.910	1.767	0.556
	S^2di	19.43**	11.83**	35.85**	29.08**	13.32*	1.34*	143.06**
G15	Mean	40.143	37.314	99.381	129.095	84.667	21.524	81.095
	bi	1.18*	1.283	0.547	1.054	0.40*	1.324	0.835
	S^2di	2.343	3.39*	29.93**	2.51*	6.654	0.824	194.79**
G16	Mean	44.267	27.488	114.048	137.571	82.138	23.576	76.333
	bi	1.356	1.482	0.818*	1.728	1.403	0.651	0.346
	S^2di	47.98**	29.54**	1.440	38.51**	12.31*	6.02**	90.42**
G17	Mean	36.631	34.130	101.476	127.905	79.419	22.614	83.767
	bi	0.929	1.252	1.639	-0.150	1.38*	2.220	1.839
	S^2di	21.85**	12.24**	12.94**	81.51**	4.067	8.47**	287.84**

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G18	Mean	40.143	33.592	103.476	128.571	87.629	23.629	56.190
	bi	1.032	0.111	0.760	1.049	0.81*	0.846	0.503
	S^2di	25.98**	89.14**	5.79**	18.90**	-1.576	3.14**	76.25**
G19	Mean	38.876	32.708	96.667	127.762	82.537	21.438	77.581
	bi	0.959	1.58*	-0.178	1.450	1.01*	0.842	1.304
	S^2di	8.91*	8.95**	65.42**	26.44**	5.813	8.94**	162.68**
G20	Mean	36.971	26.992	105.571	132.810	84.752	22.819	51.952
	bi	1.163	1.74*	0.555	1.079	1.186	1.340	0.035*
	S^2di	68.91**	16.08**	5.47**	27.05**	12.07*	6.64**	170.01**
G21	Mean	43.829	29.196	101.048	130.143	83.233	22.095	81.238
	bi	0.839	0.708	1.18*	0.787	0.83*	0.965	0.874
	S^2di	96.98**	14.17**	0.789	4.49**	-1.604	7.06**	32.28*
G22	Mean	38.114	40.610	92.333	116.905	73.324	24.752	109.714
	bi	0.828	0.149	1.104	0.439	1.796	0.270	1.304
	S^2di	35.11**	41.67**	6.27**	84.99**	25.17**	2.65**	115.49**

*, **Significant at 5% and 1% respectively

Genotypes or general genotypic adaptation

GGE and AMMI biplots described stability across genotypes or general genotypic adaptation. Comparative position of diverse genotypes on the biplots is based on its projection onto the O-axis in AMMI Biplot and GGE biplot. Biplots can identify GEI effects on each trait which contribute towards yield. AMMI1 biplot interpreted results by main effect and IPCA1 of both genotype and environment revealed that genotypic differences were important in term of direction and magnitude along both axis (X axis and Y axis). AMMI biplot represent that shift along the X-axis reflected changes in main effects, however, shift along the Y-axis reflected differences in interaction effects and adaptation of a genotype to specific environment showed by high PCA score, IPCA scores nearly to zero gave information about stable genotype in different environments. The AMMI biplot analysis is provided in *Table 6*.

Table 6. *AMMI analysis for different traits in rice across different production system*

Source of variations	**Biological weight (g)**	**[+]SS (%)**	**Harvest index (%)**	**SS (%)**	**50 Flowering (%)**	**SS (%)**	**75 maturity (%)**	**SS (%)**	**Filled spikelet (%)**	**SS (%)**	**Test grain weight (g)**	**SS (%)**	**No. of spikelets**	**SS (%)**
Trials	225.60		83.35		76.73		111.55		71.46		13.44		586.37	
Genotypes	73.87*	4.49	127.58*	21.01	354.36*	63.39	480.50*	59.12	120.46*	23.14	45.30*	46.24	1536.45*	35.96
Environments	4600.33*	79.97	937.02*	44.09	325.87*	16.65	442.45*	15.55	679.10*	37.27	67.59*	19.71	5072.60*	33.92
G × E interaction	42.56*	15.54	35.33*	34.90	18.59*	19.96	34.30*	25.32	34.36*	39.59	5.56*	34.04	214.40*	30.11
PCA I	81.72*	39.62	69.32*	40.49	69.68*	77.33	92.63*	55.72	60.61*	36.40	8.61*	31.96	423.70*	40.78
PCA II	45.87*	20.53	40.67*	21.93	14.60*	14.96	66.63*	37.00	41.36*	22.93	7.00*	24.00	352.16*	31.29
PCA III	40.34*	16.55	36.31*	17.95	3.66*	3.44	7.61*	3.88	39.00*	19.82	5.64*	17.72	148.17*	12.07
PCA IV	27.33*	10.19	19.02*	8.55	2.59*	2.21	4.01*	1.86	24.37*	11.26	4.85*	13.84	88.33*	6.54
PCA V	25.72*	8.63	16.19*	6.55	1.57*	1.21	2.44*	1.02	13.37*	5.56	3.45*	8.87	90.64*	6.04
Residual	15.00	4.48	12.60	4.53	1.24	0.85	1.44	0.53	10.90	4.03	1.58	3.60	55.52	3.29
Pooled residual	23.14*		22.01*		18.59*		34.30*		34.36*		5.56*		214.40*	
Error	5.64		2.30		1.30		1.05		6.74		0.69		14.68	
Total	78.64		29.20		26.33		37.72		28.22		4.92		204.42	

*, **Significant at 5% and 1%, respectively. [+]Mean sum of squares (SS)

AMMI analysis (*Figs. 5, 6, 7, 8* and *9*) showed that genotype G22 for filled spikelet (%); G20 for number of spikelets; G18 for test grain weight; G8 for Harvest index.

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Environment E5, E6 were more responsive for the traits Biological weight, number of Spikelets, Test Grain Weight, filled Spikelet (%) and environment E7 was responsive for traits filled Spikelet (%), Test grain weight, Harvest index. From the AMMI biplot was concluded that environment interaction was extremely diverse and entirely the four Production systems were extremely interactive for most of the yield-related traits. Environment E5, E6 seemed to be a favourable environment for all the yield-related traits; E7, E2 for filled spikelet (%), Test Grain Weight, Harvest Index. Environment E1 and E3 unfavourable for Harvest Index, Test grain weight, number of spikelet and filled spikelet (%).

Specific genotypic adaptation

Specific genotypic evaluation centred on two GGE biplots "which-won-where pattern" biplot and adaptation biplot displayed specific genotypic adaptation to limited environment condition or the adaptability of genotypes for each environment. The biplot *Figure 10* represents a polygon where some of the genotypes were placed on the crests, while the rest were surrounded by the polygon. As the genotypes placed on the peak had the longest detachment from the biplot origin and they were expected to be the most responsive. The genotypes on the crests could be called the ideal/vertex genotype. In the present study, the genotypes G15 in E1 and E5 are the vertex genotype, which had the highest test grain weight. The genotype G20 is only apex genotype for environment E4 and Genotype G14 for E2 and E6 environment. None of the environments fell in the sectors with genotypes G1, G7 and G3 that these genotypes were not appropriate for growing in these environments.

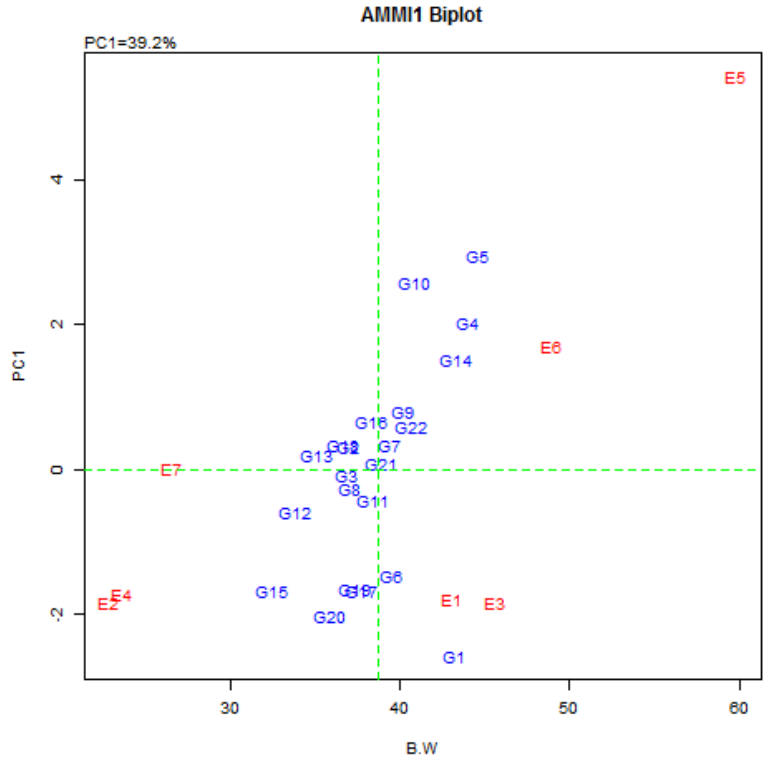

Figure 5. *AMMI1 biplot for biological weight (g)*

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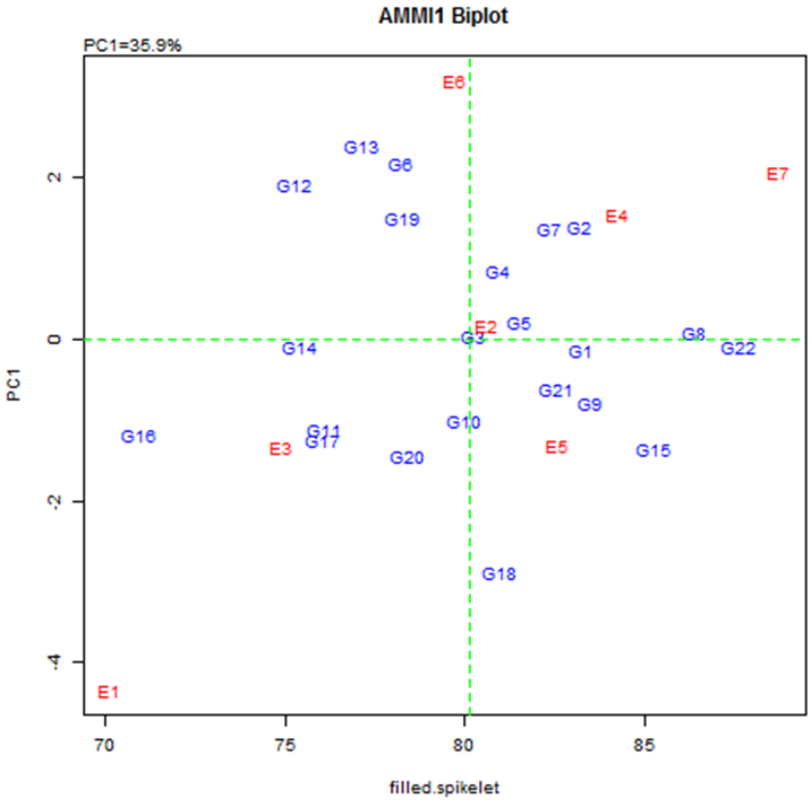

Figure 6. *AMMI1 biplot for filled spikelet (%)*

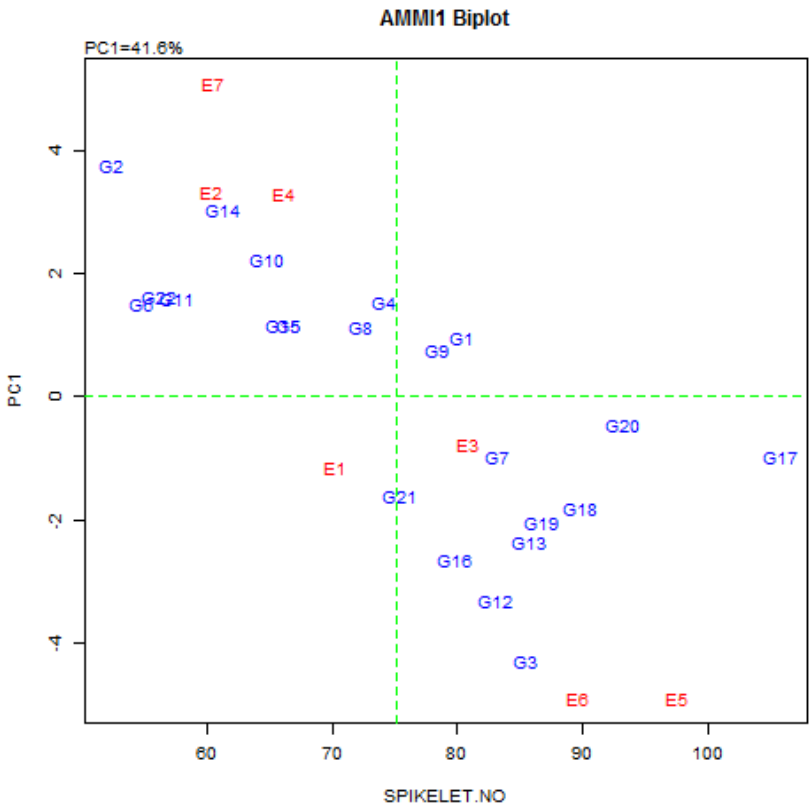

Figure 7. *AMMI1 biplot for number of spikelets*

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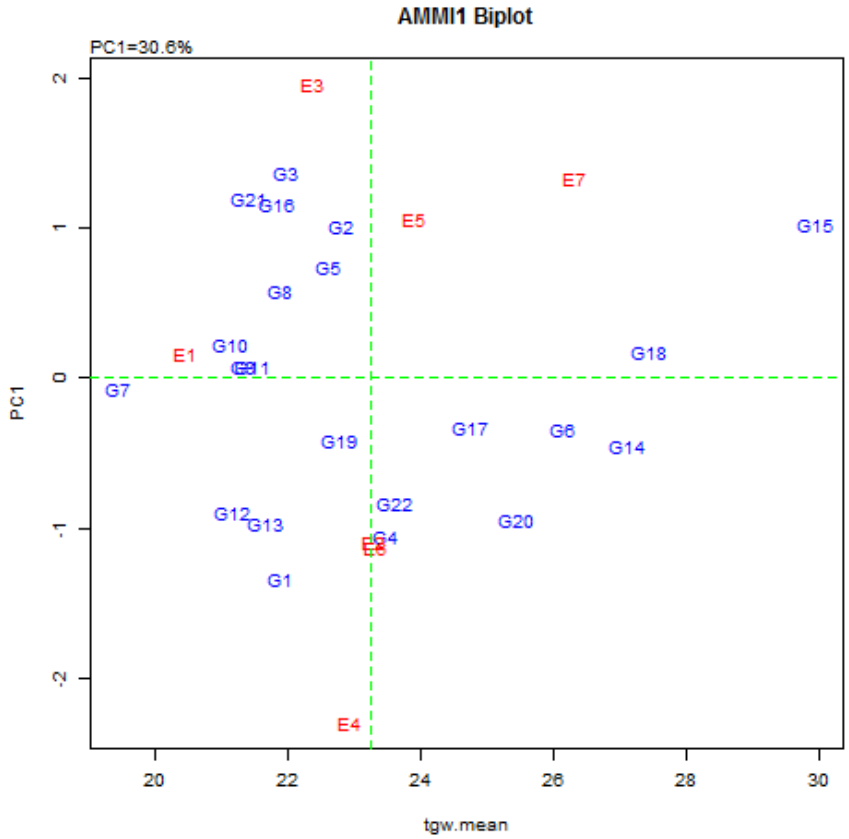

Figure 8. *AMMI1 biplot for test grain weight (g)*

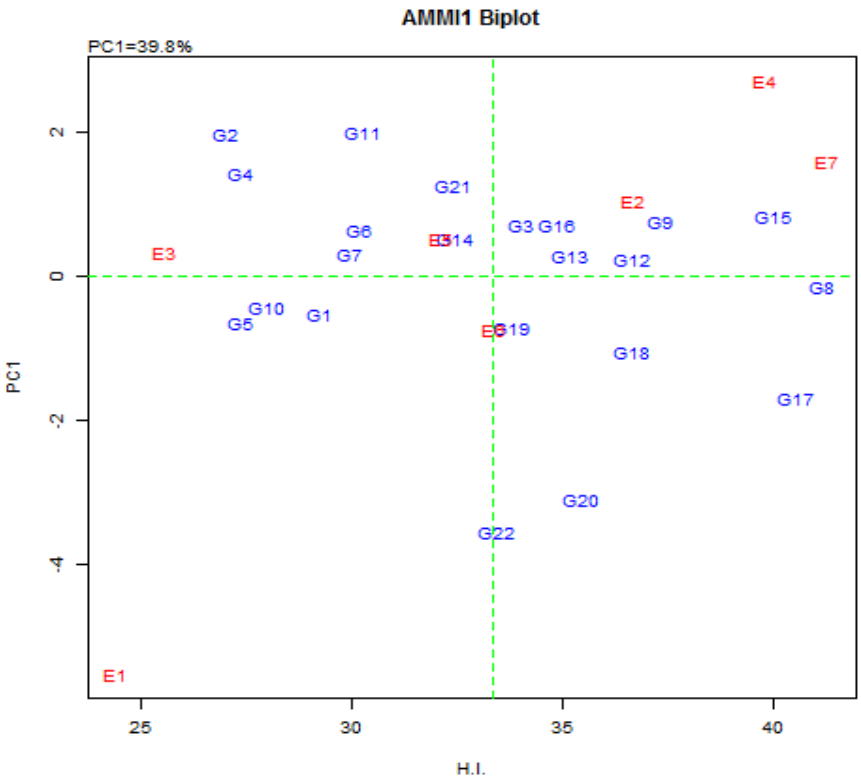

Figure 9. *AMMI1 biplot for harvest index (%)*

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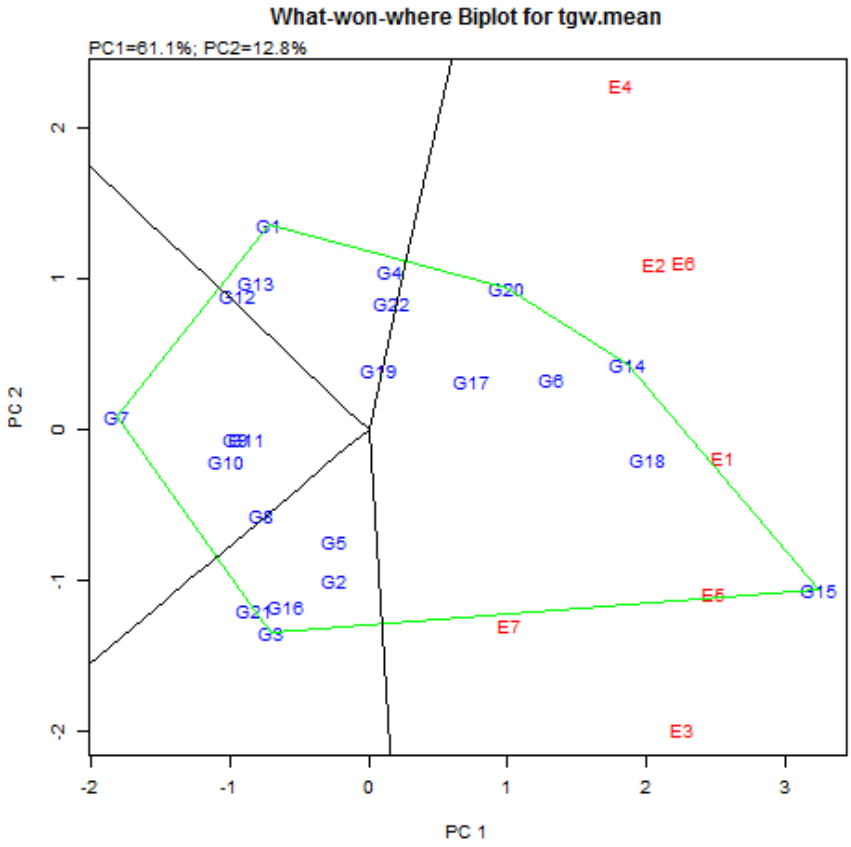

Figure10. *Polygon views of the GGE biplot based on symmetrical scaling for "which-won-where" pattern of rice genotypes in three environments "which-won-where pattern biplot test grain weight (g)"*

In case of biological weight (*Fig. 11*) Vertex genotypes are G4, G5, G10 and G1 at E6, E5, E7 and E1 respectively. In case filled spikelet (*Fig. 12*) Vertex genotypes are G22, G2, G12, G18 and G15 at E2, E4, E7, E1 and E3, E5 respectively.

In *Figure 13* average tester coordinate (ATC X-axis) or the performance line passes through the biplot origin with an arrow indicating the positive end of the axis. The average biological Weight of the genotypes is estimated by the projections of their markers to the ATC X-axis. Genotypes G2 and G5 had the highest biological Weight and genotype G15 had the poorest biological Weight. Mean biological weight of the genotypes were in the following order: G2 > G5 > G14 > G1 > G10 > G9 > G11 > G22 > G2 > G16 (*Fig. 13*). The performance of genotypes G10 and G1 were the most variables (least stable), whereas genotypes G4, G9 and G22 were highly stable with high biological weight.

The discriminating power vs representativeness view of the GGE biplot as shown in *Figure 14* indicated that environments E1 and E5 with the most extended projection from the biplot origin were found large discriminating power of the genotypes (i.e., provided information regarding differences among genotypes). On the other hand, E2 and E3 with its shortest vector from the biplot origin was found less discriminating of the different genotypes. Environments E2, E3, E4 and E6 were found to be more representative of other test environments because they have smaller angles with the AEAs (*Fig. 14*). E6 was therefore identified as an ideal environment that has both discriminating abilities of

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the genotypes and representative of the other test environments. Therefore, environment E6 can be used to effectively select superior rice genotypes that can perform consistently across environments.

Ranking genotypes relative to the ideal genotypes

An ideal genotype is one that has both high mean yield and high stability. The centre of the concentric circles (*Fig. 15*) represents the position of an ideal genotype, which is defined by a projection onto the mean-environment axis that equals the longest vector of the genotypes that had above-average mean biological weight and by a zero projection onto the perpendicular line (zero variability across environments). Therefore, genotypes G21 and G16 which fell into the centre of concentric circles, were ideal genotypes in terms of higher yield ability and stability, compared with the rest of the genotypes. In addition G6, G7, G22, G9, G2 located on the next concentric circle, may be regarded as desirable genotypes.

Ranking environment relative to the ideal environment

The GGE biplot way of measuring representativeness is to define an average environment and use it as a reference or benchmark. The average environment is indicated by small circle (*Fig. 16*). The ideal environment, represented by the small circle with an arrow pointing to it, is the most discriminating of genotypes and yet representativeness of the other tests environments. Therefore, E1, E2 and E3 were the most desirable test environment followed by E7.

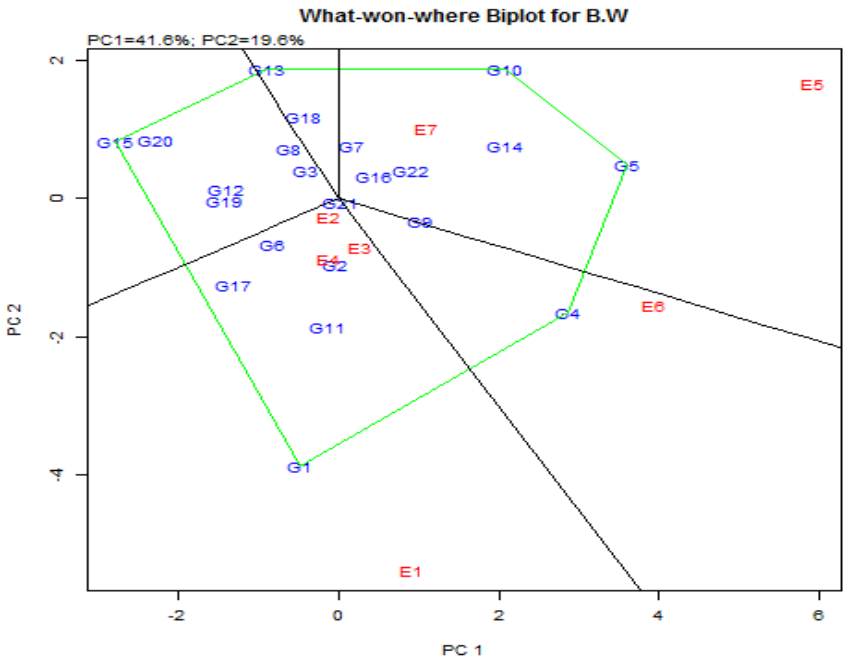

Figure 11. *Polygon views of the GGE biplot based on symmetrical scaling for "which-won-where" pattern of rice genotypes in three environments "which-won-where biplot biological weight (g)"*

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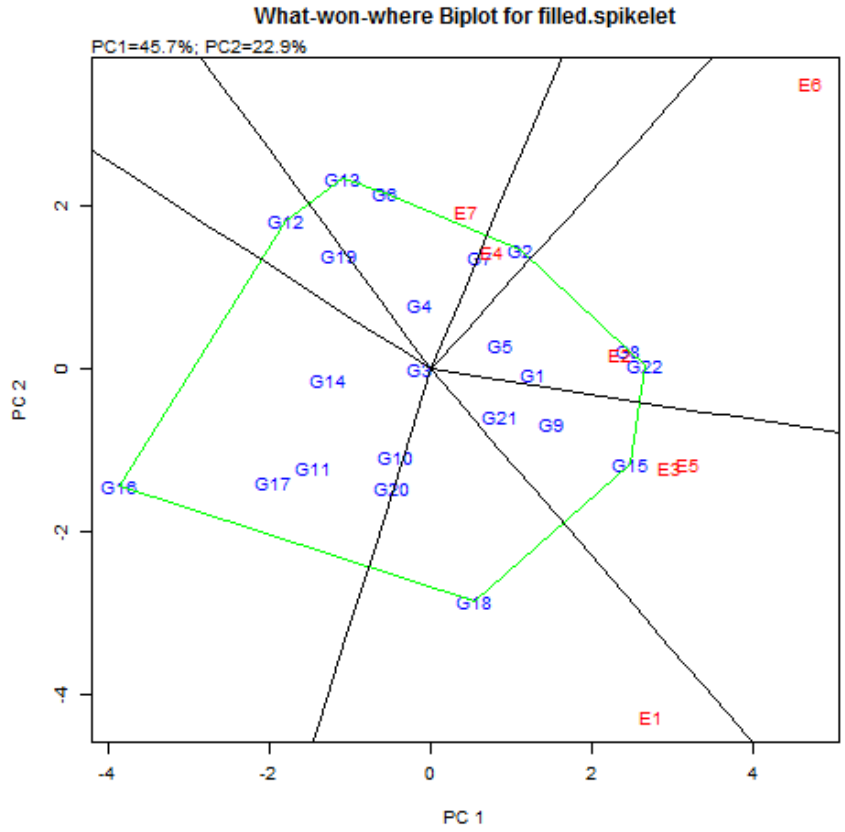

Figure 12. *Polygon views of the GGE biplot based on symmetrical scaling for "which-won-where" pattern of rice genotypes in three environments "which-won-where biplot filled spikelet (%)"*

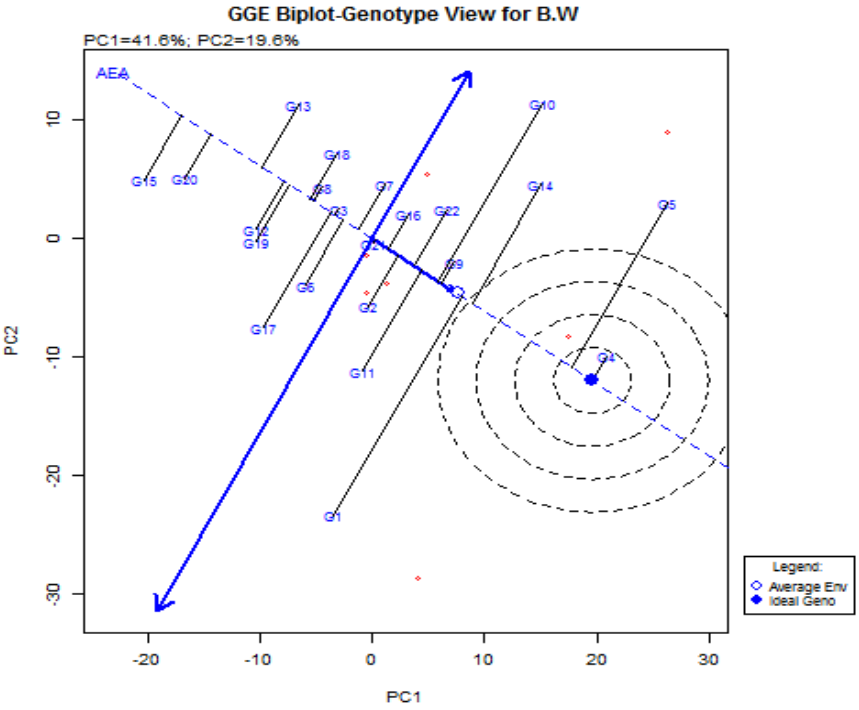

Figure 13. *Polygon view biological weight (g)*

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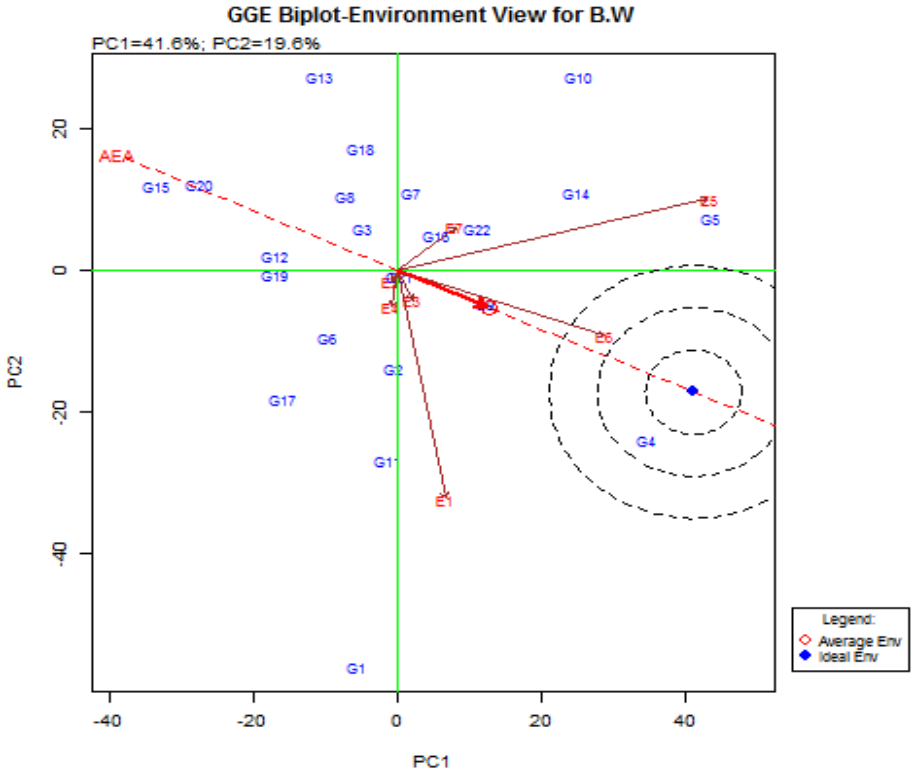

Figure 14. *GGE biplot for biological weight (g)*

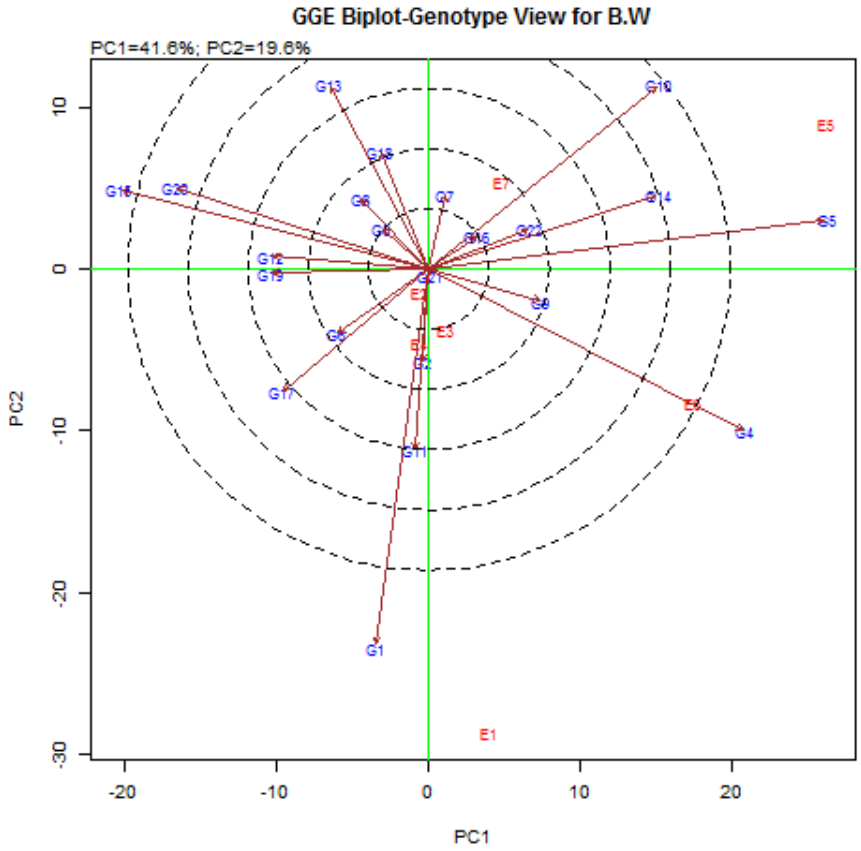

Figure 15. *Ranking genotypes relative to the ideal genotypes*

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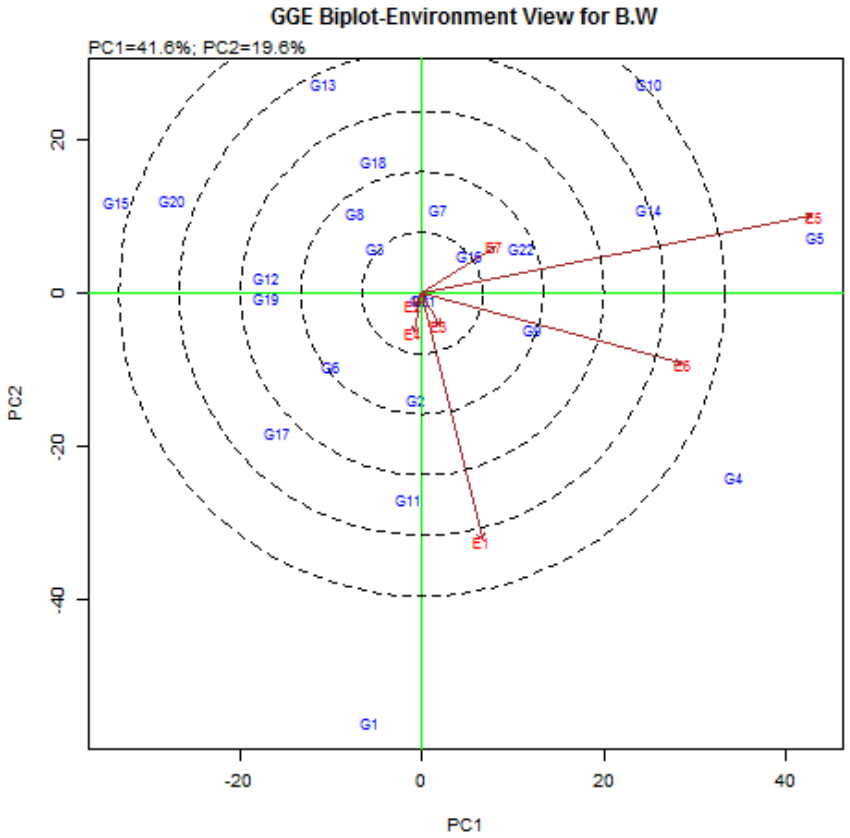

Figure 16. *Ranking environment relative to the ideal environment*

Discussion

Due to the Cultivation of rice under several agroecological zones and in different production systems the evaluation of rice genotypes for stability and adaptability is of prime importance (Bose et al., 2012). The changes in environmental conditions significantly affect rice production (Bose et al., 2014). Therefore, here we have identified stable rice genotype to sustain with innovative production systems like the system of rice intensification, and direct seeded rice using stability models. Previously, researchers have used GGE biplot analysis mainly for assessment of varietal stability cultivar evaluation and mega-environment evaluation (Kang, 1993; Yan and Hunt, 2001; Yan and Kang, 2003; Dehghani et al., 2006; Navabi et al., 2006; Blanche et al., 2007; Ding et al., 2007; Jalata, 2011; Mohammadi et al., 2012; Rakshit et al., 2012; Amiri et al., 2015). The simultaneous selection for stability and high mean results in the selection of better genotypes with non-significant stability variance, and it enhances the quality of selection (Nassir, 2013). Pooled analysis study stipulates that a significant basis of variation in the basmati rice genotypes was due to genotype by environment interaction. In the present study, two-year data under four production system of rice was primarily subjected to stability analysis of the traits.

The GGE and AMMI1 biplots recognised Genotype G21 most stable genotype for biological weight; G22 for Filled spikelet (%); G20 for Number of spikelets; G18 for Test Grain weight; G8 for Harvest index was identified as most stable genotypes. Similarly, it has been proved that for multi-environment trails both GGE and AMMI biplots were important for judging stable and adaptable genotypes (Hagos and Abay,

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2013; Stojaković et al., 2010; Mitrovic et al., 2012; Rad et al., 2013). Genotypes G21 and G16 were ideal genotypes for biological weight. Further, E1, E2 and E3 were the top three most desirable test environments. Whereas, the GGE biplot analysis has identified E3 as the ideal environment having a long vector length (discriminating ability) and a small angle (representativeness) and G18 as a superior genotype across environments. Similar research finding by Khalil et al. (2011).

This study uncovered that the GGE biplot hence clarified better Genotype + Genotype-Environment interaction than the AMMI1 biplot so that better precise explanation of the GGE of the basmati rice genotype in a diverse production system. This might likely be due to the truth that in spite of the fact that, the AMMI1 biplot (Zobel et al., 1988) has been demonstrated to be exceptionally effective in identifying significant sources of variation of Genotype × Environment interaction effects and has moreover been pronounced as either superior or equal GGE biplot analysis (Gauch, 2006), but it isn't capable to successfully show the virtual execution of each genotype in each environment i.e., does not have the foremost critical property of a true biplot. As a result, the performance of a given genotype in a given environment cannot be precisely visualized even in case it completely shows the data.

Also, Yan et al. (2007) concluded that the GGE biplot is predominant in the AMMI1 biplot in mega-environment analysis and genotype assessment, as it clarifies more G+GE and pinpointed that, the AMMI1 biplot is way better seen as a tool for displaying conclusions instead of as a tool for finding which-won-where designs. Contrastingly, the GGE biplot was criticised by Ebdon and Gauch (2002) and Gauch (2006) for not being able to uncover which-won-where designs in case more than two PCs are required to surmise the information.

Conclusion

We showed the significance of Genotype × Environment interaction by evaluating the genotypic potential of twenty-two basmati rice genotypes using stability models. Basmati rice genotypes were compared for their stability under different production systems (both conventional and non-conventional) for yield-related traits. Results from the analysis with Eberhart and Russell model, AMMI and GGE biplots showed Genotype G21 as the most stable genotype for biological weight; G22 for filled spikelet (%); G20 for number of spikelets; G18 for test grain weight; and G8 for harvest index. Whereas, among the different environments E7 was the most desirable test environment followed by E5 and E4. Overall, a summary list of best genotypes under all of the four production system is provided in *Table 7*. Further, the HKR 08-417 (G14) was determined to be stable under all of the production systems.

Table 7. *List of best three genotypes for all of the four production system*

Production system	Genotype
TPR	HKR 98-476 (G9) Haryana Mehak-1 (G16) HKR 08-417 (G14)
SRI	HKR 98-476 (G9) Imp Pusa Basmati 1,(G8) HKR 08-417 (G14)

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DSR (W)	Imp Pusa Basmati1, (G8) Haryana Mehak-1 (G16) HKR 08-417 (G14)
DSR (D)	Super Basmati (G19) HKR 06-487 (G13) HKR 08-417 (G14)

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