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Genotype and environment interaction analysis for quality traits in Basmati rice

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A total of 36 rice genotypes including traditional varieties, evolved varieties and some advanced materials were tested for physical and biochemical quality parameters. Experiments were conducted at two locations with four resource-saving environments and two consecutive years in a randomised block designs. Multi-environmental data was analysed using additive main effect and multiplicative interaction (AMMI) and genotype and genotype × environment (GGE) interaction model for quality parameters. Genotype × environment interactions (GEI) were noticed significant for all the studied parameters excluding alkali spreading value, grain breadth before and after cooking and grain length after cooing. Hulling, milling & head rice recovery were observed maximum in transplanted and system of rice intensification production system. Among production systems, SRI recorded a high mean value for all the traits followed by transplanted rice, chemical free cultivation and direct seeded rice. Improved Pusa Basmati 1, Pusa Basmati 1121, Pusa 1884-3-9-175 and SJR-70-3-2 were observed as stable genotypes across the environment coupled with the high mean for amylose content.

Keywords: AMMI, Adaptability, Environment, GGE, Rice

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Rice is the second largest and principal food crop for more than 50% of the world's population, of which nearly 90% is produced and consumed in Asia[1]. The genetic improvement in quality parameters is the second major breeding goal in basmati rice breeding programs after grain yield. It involves the grain look, milling, nutritional importance and cooking quality. Appearance quality of milled rice is measured as grain length, breadth, length-breadth ratio (L/B ratio), grain shape and chalkiness of endosperm. Based on the L/B ratio, rice grains were divided into five different categories: (i) long slender, (ii) short slender, (iii) medium slender, (iv) long bold and (v) short bold[2]. Chalkiness in the rice grains is due to air spaces and small starch granules[3]. Chalky areas weaken the kernels and cause it to break down during the milling process[4]. The milling quality includes brown rice, white rice and head rice recovery. Brown rice is obtained after the removal of husk from the paddy while white rice is obtained after the removal of bran from the brown rice. Head rice recovery involves whole grains and broken kernels of 75% of whole grains. Cooking quality has direct correlation with alkali spreading value (ASV), gel consistency (GC) and amylose content (AC)[5]. ASV determines the cooking time, GC measures the softness of rice after cooking, and AC is responsible for the texture of rice after cooking[6]. AC is present in a negligible proportion in waxy rice, which remains glossy, sticky, firm and does not expand in volume upon cooking. While high amylose rice varieties show high volume expansion and become dry and hard upon cooling. Intermediate amylose rice genotypes cook moist and do not become hard after cooling. In general, rice genotypes with intermediate AC are preferred in rice growing area of world except for Japan where low amylose genotypes is grown[7]. These unique quality characteristics of Basmati are preserved in their original form in traditional varieties (i.e., Basmati 370 and Taraori Basmati) of Basmati rice[8]. In recent past, many new high yielding genotypes have been developed with identical traits to those of traditional Basmati, however, consumers still preferred traditional varieties than newly developed genotypes[9].

In Asian countries, rice is mainly cultivated by the transplanted method which requires continuous

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flooding. However, water deficiency in rice producing areas necessitates the development of alternative production methods which require less amount of water than conventional transplanted method[10]. In recent years, a shift was observed from traditional to non-traditional methods such as direct seeding and rice intensification in Southeast Asia[11]. These techniques require lesser amounts of water and labor as compared to transplanted method. The expression of a trait is the key result of genotype, growing conditions and GEI[12]. Knowledge of GEI is necessary for the selection and identification of better genotype in a particular environment or over a wide range of environments[13]. Nowadays, AMMI and GGE model are the most commonly used statistical models. These models quantify the GEI through PCA and graphical representation[14,15] and help the breeders in identifying better genotypes in the varying environment and also identify better locations or environments where selected genotypes can perform well for quality traits[16]. Therefore, the current research was planned to identify the stable and adaptable genotypes over the different production environments for quality traits.

Materials and Methods

The research was carried out at two stations, namely, Rice Research Station, Kaul and Regional Research Station Uchani, during two kharif seasons 2016 and 2017. The plant material involved 36 Basmati rice genotypes including traditional varieties, evolved varieties and some advanced lines. These genotypes were planted in randomized block design under four production methods *viz*., traditional transplanted rice (PTR), chemical free cultivation (CC), direct-seeded rice (DSR) and the system of rice intensification (SRI) (Table 1). The package and practices for these methods were followed as discussed in Kesh *et al.*[17]. Observations were recorded for hulling percent (H), milling percent (M), head rice recovery percent (HRR), grain length (in mm) before cooking (GLBC) and after cooking (GLAC), grain breadth (mm) before cooking (GBBC) and after cooking (GBAC), L/B ratio before cooking (LBBC) and after cooking (LBAC)[18], amylose content[19] percent (AC) and alkali spreading value (ASV). The ASV of kernels was calculated as described in Table 2. To measure the GEI, data were analysed

Table 1 — List of Basmati rice genotypes and production methods

Code	Genotypes	Code	Genotypes	Code	Production methods	Location	Year
G1	Basmati 370	G19	Pusa 1637--2-8-20-5	E1	CC	Kaul	2016
G2	CSR-30	G20	Pusa 1656-10-705	E2	〃	〃	2017
G3	CSR TPB-1	G21	Pusa 1734-8-3-85	E3	〃	Uchani	2016
G4	Haryana Basmati 1	G22	Pusa 1826-12-27-1-4	E4	〃	〃	2017
G5	Haryana Mahak 1	G23	Pusa 1884-3-9-175	E5	DSR	Kaul	2016
G6	HKR -11-509	G24	Pusa 1884-9-12-14	E6	〃	〃	2017
G7	HKR 03-408	G25	PAU 6295-2	E7	〃	Uchani	2016
G8	HKR 08-417	G26	Pusa Basmati 1	E8	〃	〃	2017
G9	HKR 06-434	G27	Pusa Basmati 1121	E9	SRI	Kaul	2016
G10	HKR 06-443	G28	Pusa Basmati 1509	E10	〃	〃	2017
G11	HKR 06-487	G29	Pusa Sugandh 2	E11	〃	Uchani	2016
G12	HKR 08-425	G30	Pusa Sugandh 3	E12	〃	〃	2017
G13	HKR 11-447	G31	Pusa Sugandh 5	E13	PTR	Kaul	2016
G14	HKR 98-476	G32	Pusa Sugandh 6	E14	〃	〃	2017
G15	HUBR-16	G33	SJR-70-3-2	E15	〃	Uchani	2016
G16	Improved Pusa Basmati 1	G34	Super Basmati	E16	〃	〃	2017
G17	PAU-6297-1	G35	Taraori Basmati				
G18	Pusa 1475-03-42-45-119-1	G36	UPR-386-9-1-1				

Table 2 — Different classes of ASV and GT

Score	Kernel Appearance	ASV	GT
1	Kernel not affected; Kernel chalky	Low	High>74°C
2	Kernel swollen; Kernel Chalky, collar powdery	Low	High>74°C
3	Kernel swollen, collar incomplete and narrow; kernel chalky, collar cottony or cloudy	Low, Intermediate	High, Intermediate
4	Kernel swollen, collar complete and wide; centre cottony, collar cleaning	Intermediate	Intermediate (70-74°C)
5	Kernel split or segmented, collar complete and wide; centre cottony, collar clearing	Intermediate	Intermediate (70-74°C)
6	Kernel dispersed, merging with collar; Centre cottony. Collar cleared	High	Low (55-69°C)
7	All kernel dispersed and intermingled; Centre and collar cleared	High	Low (55-69°C)

Table 3 — Overall mean of 36 rice genotypes for various quality traits under different production methods

Code	Genotypes	H %	M %	HRR %	GLBC	GBBC	LBBC	GLAC	GBAC	LBAC	ASV	AC
G1	Basmati 370	78.60	68.49	53.00	6.24	1.72	3.64	12.82	2.58	4.98	4.44	22.11
G2	CSR-30	77.95	66.80	56.82	6.69	1.67	4.01	12.83	2.50	5.13	4.62	22.64
G3	CSR TPB-1	77.68	66.35	53.67	6.56	1.69	3.88	11.44	2.54	4.51	4.92	22.24
G4	Haryana Basmati 1	80.05	69.89	56.68	6.36	1.72	3.69	11.52	2.58	4.46	5.47	23.17
G5	Haryana Mahak 1	78.09	68.47	54.94	7.50	1.63	4.59	14.74	2.45	6.01	5.65	23.16
G6	HKR -11-509	79.38	68.57	54.40	6.63	1.64	4.04	12.86	2.46	5.22	4.80	21.60
G7	HKR 03-408	79.31	67.17	55.80	7.38	1.70	4.34	14.26	2.55	5.59	5.60	22.69
G8	HKR 06-417	77.73	66.74	52.26	6.99	1.77	3.94	14.65	2.65	5.52	5.32	23.35
G9	HKR 06-434	77.98	67.04	55.81	7.38	1.69	4.36	14.31	2.54	5.63	5.98	22.24
G10	HKR 06-443	77.06	67.00	55.60	7.78	1.72	4.52	15.64	2.58	6.08	5.46	23.58
G11	HKR 06-487	79.22	67.87	53.98	7.46	1.73	4.33	14.30	2.59	5.53	5.49	23.23
G12	HKR 08-425	77.62	67.00	54.71	6.41	1.49	4.32	12.93	2.22	5.82	4.42	23.84
G13	HKR 11-447	79.62	68.87	55.64	7.21	1.75	4.12	13.72	2.63	5.23	6.48	22.90
G14	HKR 98-476	79.40	69.90	56.85	6.70	1.70	3.95	13.64	2.54	5.37	5.52	23.98
G15	HUBR-16	77.39	66.93	53.96	7.50	1.71	4.38	12.84	2.58	4.99	6.51	21.02
G16	Improved Pusa Basmati 1	77.99	67.41	55.48	7.45	1.66	4.50	14.26	2.50	5.72	6.46	24.38
G17	PAU-6297-1	77.78	66.33	55.25	7.10	1.78	3.99	14.64	2.66	5.50	6.68	22.61
G18	Pusa 1475-03-42-45-119-1	77.33	66.11	52.06	7.59	1.67	4.54	13.47	2.51	5.38	6.30	21.98
G19	Pusa 1637--2-8-20-5	77.10	65.71	53.09	7.23	1.62	4.47	13.72	2.42	5.66	6.62	23.54
G20	Pusa 1656-10-705	77.20	66.32	53.71	7.71	1.71	4.51	14.18	2.58	5.52	6.28	22.75
G21	Pusa 1734-8-3-85	77.81	66.17	54.49	7.76	1.73	4.49	15.85	2.59	6.12	6.76	22.80
G22	Pusa 1826-12-271-4	77.90	66.65	49.20	7.86	1.68	4.67	14.75	2.22	5.84	6.32	22.96
G23	Pusa 1884-3-9-175	77.33	66.25	50.99	7.65	1.75	4.39	15.55	2.63	5.94	6.66	23.12
G24	Pusa 1884-9-12-14	77.57	67.37	52.78	7.76	1.70	4.58	15.41	2.54	6.06	6.17	22.21
G25	Pusa 6295-2	77.41	65.71	52.29	7.51	1.68	4.48	15.07	2.58	5.98	6.41	22.39
G26	Pusa Basmati 1	79.71	68.34	58.14	7.19	1.65	4.35	14.29	2.50	5.75	6.56	24.01
G27	Pusa Basmati 1121	78.34	68.74	56.56	8.10	1.74	4.66	17.46	2.66	6.69	6.47	23.75
G28	Pusa Basmati 1509	78.00	67.75	54.85	7.95	1.74	4.58	17.40	2.51	6.69	6.45	23.61
G29	PusaSugandh 2	76.54	65.40	53.64	7.56	1.64	4.60	16.32	2.42	6.63	5.42	23.74
G30	PusaSugandh 3	78.74	67.73	55.03	7.53	1.78	4.22	14.30	2.68	5.33	5.36	24.28
G31	PusaSugandh 5	77.97	67.01	54.43	7.59	1.73	4.38	13.49	2.61	5.18	6.52	23.17
G32	PusaSugandh 6	77.46	65.10	51.34	7.41	1.65	4.48	16.18	2.49	6.51	6.39	23.33
G33	SJR-70-3-2	78.04	66.48	53.02	7.39	1.72	4.30	12.27	2.58	4.76	4.47	24.65
G34	Super Basmati	78.81	68.41	57.30	7.39	1.67	4.41	12.78	2.52	5.07	4.92	22.94
G35	Taraori Basmati	77.56	66.33	49.90	6.71	1.60	4.21	12.70	2.39	5.31	4.64	23.06
G36	UPR-386-9-1-1	78.78	68.41	55.42	6.54	1.70	3.85	12.52	2.55	4.90	6.71	23.50

using AMMI and GGE-biplot techniques with software PB Tools version 1.4.

Results

Mean performance

The mean value across the production methods showed a narrow range of variation was among the genotypes for various quality traits. The mean value ranged from 76.54-80.05% for hulling, 65.10-69.90% for milling, 49.20-58.14% for head rice recovery, 6.24-8.10 mm for GLBC, 1.49-1.78 mm for GBBC, 3.64-4.67 for L/B ratio before cooking, 11.44-17.46 mm for GLAC, 2.22-2.68 mm for GBAC, 4.467-6.69 for L/B ratio after cooking, for alkali spreading value and 21.02-24.65% for AC (Table 3). Genotype SJR-70-3-2 had the highest AC over the multi-environments followed by Improved Pusa Basmati 1 (Table 3). With regard to environments, AC was lower under DSR and CFC and higher under SRI as compared to TPR. The hulling percent, milling percent, head rice recovery percent, grain length and breadth and L/B ratio were found to be higher under SRI than TPR due to better grain filling in SRI production system (Table 3).

AMMI biplot analysis

AMMI biplot graph between main effect and PCA I was used for the interpretation of AMMI results. Based

on AMMI 1 biplot, genotypes G4 and G14 for hulling percent; G4, G5 and G14 for milling percent; G4, G14 and G17 for head rice recovery percent; G7, G24 and G28 for grain length before cooking; G7, G9 and G29 for L/B ratio before cooking, G9, G26 and G29 for L/B ratio after cooking; and G23, G27 and G36 for AC were found suitable for general adaptation to all the environments (Fig. 1). For hulling percent, genotypes G3, G9, G31 and G33 were found ideal for TPR; G6, G26 and G27 for CC; G8, G10 and G35 for SRI and none of the genotypes were found suitable for DSR. For milling percent, genotypes G16, G20, G22, G26, G28 and G31 were found suitable for TPR; G3 and G6 for CC; G1, G12, G24 for SRI; and G13 for DSR. For head rice recovery, genotypes G12, G16, G28, G31 were found suitable for TPR; G2, G6, G25 for CC; G15, G21, G23, G30, G36 for SRI; and none of the genotypes was found suitable for DSR. For GLBC, genotypes G11, G15 and G34 were found ideal for TPR; G5, G19 and G30 for CC and G16 and G29 for DSR. For L/B ratio before cooking, genotypes G5, G15, G23, G24 and G34 were found suitable for TPR; G7 and G33 for CC; G26 and G34 for SRI and G12 for DSR were ideal. For L/B ratio after cooking, genotypes G19 and G23 were found suitable for TPR; G8, G9, G17 and G33 for CC; G10 and G25 for SRI and G12 for DSR. For AC, genotypes G10, G12 and G29 were found suitable for TPR; G22 for SRI; and G3, G14, G17, G19, G23, G24, G27 and G28 for DSR were ideal (Fig. 1).

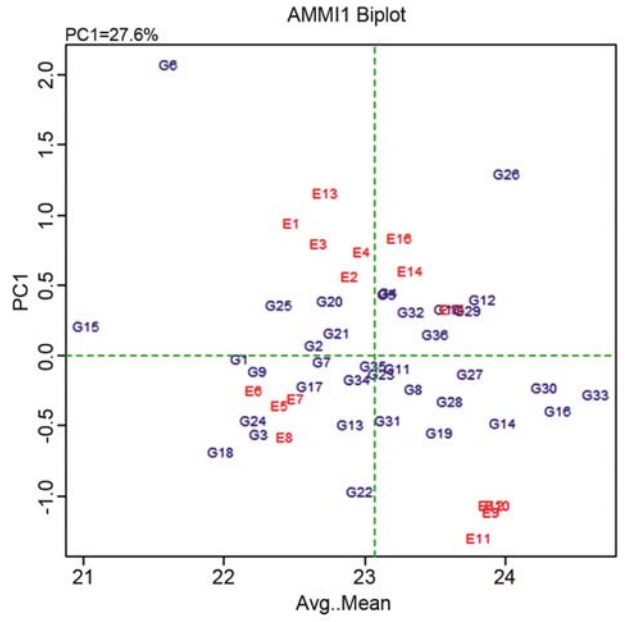

Fig. 1 — AMMI I biplot for amylose content over the production methods

GGE Biplot

Relationship among the tested production methods

The Biplot showed in Figure 2 explained 63.9% of total variability for AC and can be used for measuring the relationship among the tested production methods (Fig. 2). Based on the angles of environment, vectors were clustered into five groups, group 1 (E9, E10, E11 and E12); group 2 (E5, E6, E7and E8); group 3 (E15); group 4 (E2, E3, E4, E13, E14, E16) and group 5 (E1). The minimal angle between E2, E16 & E4 entails that there is a highly positive correlation between them, implying that these production methods produce similar information for the genotypes (Fig. 2). Obtaining similar information with lesser number of environments diminishes the cost of screening and enhances the breeding efficiency. Representativeness and discriminating ability are the decisive properties of an ideal environment. A small blue circle in Figure 3 shows an ideal environment. Ideal environment has longest vector length of all tested production methods and located on AEC abscissa[20]. Figure 3 depicted that E7 is an ideal production method as E7 has large PC1 and low PC2 score. E2 is the most representative and discriminating and was an ideal production method for the selection of generally adapted genotypes (Fig. 3). E11 and E13 were most discriminating production methods but are non-representative (Fig. 3). So these production methods are advisable for selecting the specifically adapted genotypes.

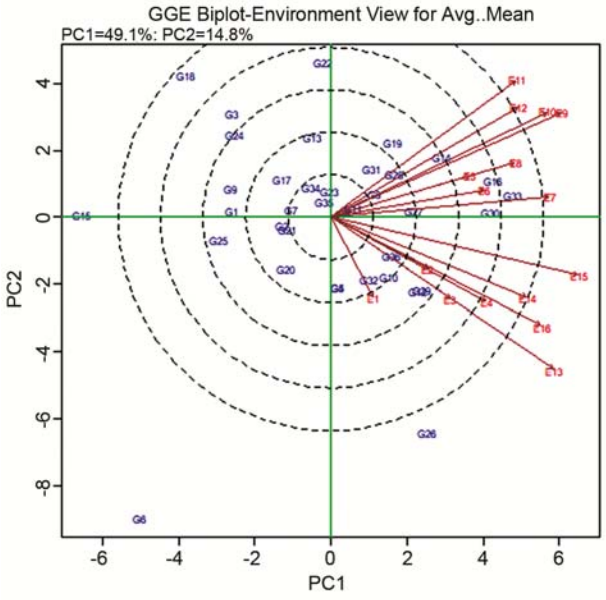

Fig. 2 — Relationship among tested production methods

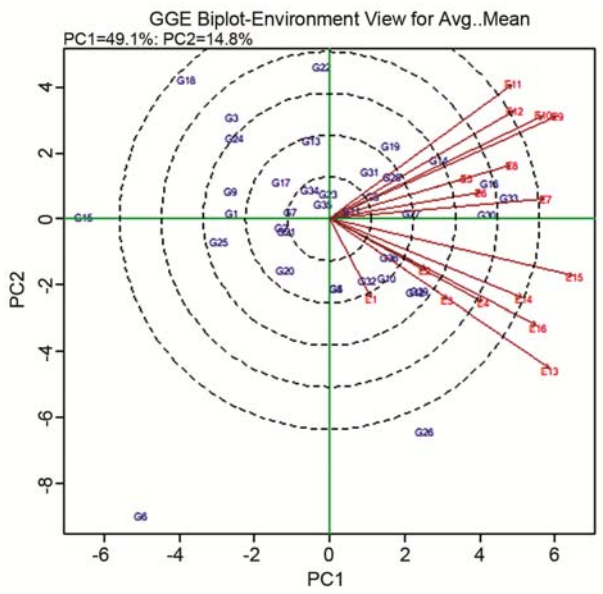

Fig. 3 — Discriminating ability and representativeness of different production methods

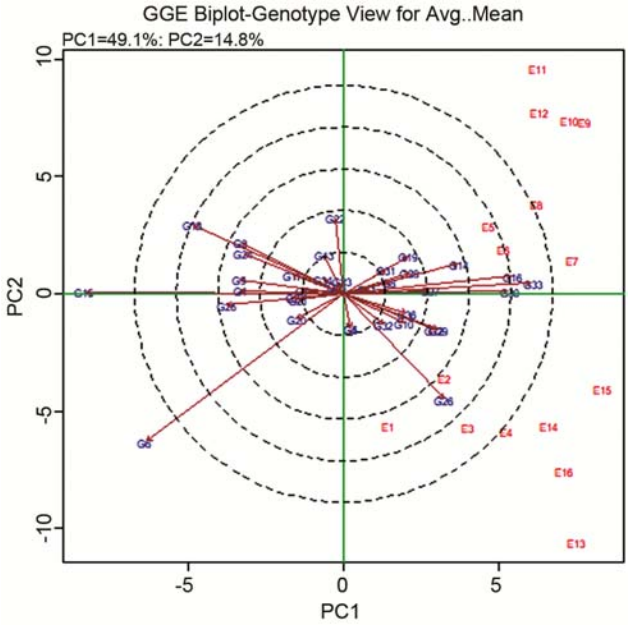

Fig. 4 — Genotypic ranking across the production methods

Genotype evaluation

Genotypes ranked based on the mean performance and stability of genotypes are presented in Figure 4. PC 1 in biplot depicts the mean performance and PC 2 defines the G × E interaction. Genotypes G6, G22 and G26 can be observed as a more fluctuating and less durable while G23, G27, G30, G36, G33 and G16 are high yielder and more stable (Fig. 4). In GGE biplot, the high yielding and stable genotypes were identified

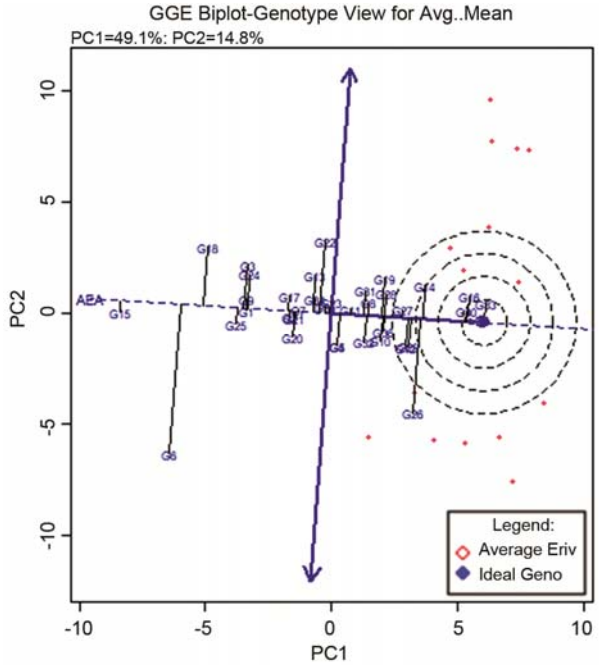

Fig. 5 — Genotypic ranking relative to the ideal genotype

by AEA axis (average environmental axis, AEA) method[21]. The dark blue dot in the figure is an indicator of the ideal genotype. The ideal genotype has large PC 1 scores and low PC 2 scores. The genotypes located near to the perfect genotype are more desirable. Hence, G16, G30 and G33 are present near the ideal genotype and therefore were more desirable than remaining (Fig. 5). Although genotypes G1, G15 and G21 were durable, they are seen as undesirable due to their distant location from ideal genotype (Fig. 5). In addition, genotypes with shorter vector length showed more stability than with longer vector length. Thus, genotypes G23, G27, G30 and G233 were identified as more stable genotypes (Fig. 5).

Polygon view

The polygon view of Basmati rice genotype which is drawn by linking the distantly located genotypes with straight lines is shown in Figure 6. Genotypes G33, G22, G18, G15, G6 and G26 were distantly placed and were either good or poorly performing genotypes in a specific method or across the production methods. The equality lines partitioned the biplot into five sectors and all the production methods fall under only 2 sectors. The apex genotypes in these two sectors were having maximum AC. The G11, G8, G31, G28, G27, G19, G14, G16, G30 fell into sector 1 with G33 as the apex genotypes, implying good

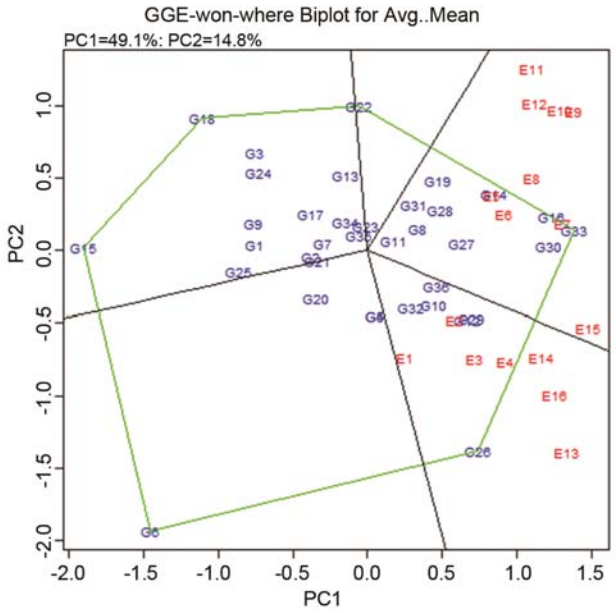

Fig. 6 — Polygon view for amylose content

performing genotypes for E5 to E12 production methods (Fig. 6). Similarly, G32, G10, G29, G36 fell into sector 2 with G26 as the apex genotype, indicating the high mean of these genotypes under E1 to E4 and E13 to E16 production methods.

Discussion

Multi-environmental trials are commonly conducted to collect clues regarding the identification, recommendation and release of new genotypes. However, GEIs complicate the evaluation and selection of genotypes; therefore, proper analysis and interpretation of GEIs is very important[22]. Stability is the fitness of a genotype across the environments and adaptability is the ability of a genotype to survive better under a particular environment. Which may be acquired either through genetic or through physiological homeostasis of genotypes for fluctuating environments[23]. Effect of genotype, varying environmental conditions and their interaction measures the performance of a genotype and its common and specific adaptation to varying environments[24]. The knowledge of interaction effect is very essential for the identification of ideal production methods to select the genotypes for quality traits[25,26]. In the current study, two mostly used approaches, AMMI biplot and GGE biplot, have been implemented. AMMI was found a powerful tool to estimate the GEI and to select adaptable genotypes[27]. Likewise, GGE is another powerful technique to measure the adaptability of genotypes for multi-environment data. This technique divides the genotypic and interaction effects into principal components via singular value decomposition of environments[20]. In our study, the percent contribution of genotype and environment interaction is 43.0 6%, indicating that the interaction effect is a main role player in the phenotypic expression of AC. Further, the ideal genotype is one which shows good performance and stability across the environments[24]. But a stable genotype with moderate to high AC is advised to be more desirable. Therefore, genotype G27 was identified with the high mean and stability value of AC. These findings were in conformity to those of Kesh *et al.*[17], Akter *et al.*[28] and Fasahat *et al.*[29]. According to GGE biplot analysis, an ideal genotype had more PC I and low PC II score. The distance between the vectors of sixteen production methods divided them into 5 different groups: group 1 (E9, E10, E11 and E12), group 2 (E5, E6, E7and E8), group 3 (E15), group 4 (E2, E3, E4, E13, E14, E16) and group 5 (E1). The test environment should be differentiating for the genotypes and representative of the mega environment[25]. E11 and E13 were found most discriminating and advisable for the selection of specifically adapted genotypes. AC was significantly higher in SRI and TPR because of longer period of grain filling[30,31]. Polygon view of GGE biplot is the finest way to identify adaptable and high yielding genotype and the interaction patterns between genotypes and environments and to adequately interpret a biplot[32]. However, the GGE biplot was criticized by Ebdon and Gauch[33,34] for not being able to uncover “which-won-where” designs.

Conclusions

GEIs are the major challenge for agronomists and plant breeders which are frequently involved in the evaluation of genotypes. GEIs affects the association between the genotypic and phenotypic value which reduces the probability for the identification of stable and adaptable genotypes. Therefore, proper analysis of multi-environmental data is necessary for the recommendation and release of a genotype for a particular area or across the environments. Two most commonly used methods, AMMI and GGE biplot, were employed to measure the genotype and interaction effect on each quality trait. In the present study, Improved Pusa Basmati 1, Pusa Basmati 1121, Pusa 1884-3-9-175 and SJR-70-3-2 were found to be stable and better performing genotypes across the environments. These genotypes were least affected by

environmental fluctuation and perform well over a broad range of environmental conditions.

Conflict of Interest

Authors declare no conflict of interest

Authors' Contributions

Conceptualization by KRB and HK; Supervision by KRB and PK; Data analysis by HK, PK and DK; Final draft, corrections and writing: HK, KRB and PK.

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