



Adaptability and AMMI biplot analysis for yield and agronomical traits in scented rice genotypes under diverse production environments

H Kesh^{*,a,†}, R Kharb^b, K Ram^b, R Munjal^c, P Kaushik^d & D Kumar^e

^aDepartment of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar 125 001, Haryana, India

^bRice Research Station, Kaul-136021, CCS Haryana Agricultural University, Hisar 125 001, Haryana, India

^cDepartment of Botany and Plant Physiology, CCS Haryana Agricultural University, Hisar 125 001, Haryana, India

^dInstituto de Conservación y Mejora de la Agrodiversidad Valenciana, Universitat Politècnica de València, Camino de Vera 14, 46022 Valencia, Spain

^eNational Institute for Plant Biotechnology, IARI, New Delhi 110 012, India

E-mail: [†]harikeshkaul55@gmail.com

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The crucial aspect of the identification of the genotypes adaptable to different production environments (systems) for the thirty-six popular scented rice varieties was countered via adaptability and AMMI biplot analysis. The varieties were evaluated for several agronomical traits (twelve) under four production environments namely, direct-seeded rice (DSR), the system of rice intensification (SRI), chemical-free cultivation (CFC) and transplanted rice (TPR). Among different production environments, SRI was found on the top followed by TPR, CFC and DSR. Genotype \times environment interactions were significant for all of the traits. Based on the AMMI biplot technique, Pusa Sugandh 3, HKR -11-509 and Pusa Sugandh 5 were found suitable for grain yield per plant and general adaptation to all the environments.

Keywords: AMMI, Adaptability, GGE, Rice, Stability

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In India, rice is cultivated over about 44.1 million ha area with the production of 165.3 million tons paddy with the productivity of 3.78 t/ha¹⁻³. Conventionally, rice is generally raised by transplanting 25-30 days old seedlings in puddled and flooded the soil conditions. The benefits of the conventional systems are increased availability of iron, zinc and phosphorus⁴. However, continuous saturation of soil produces suppressive effects on yield by altering the rice root systems due to deformation of their cortex and creation of aerenchyma, with consequent degeneration of roots⁵.

Puddling also results in the formation of hardpan at shallow depths, which reduces permeability in sub-surface layers. Furthermore, a huge amount of water and labor cost is required for puddling and transplanting of rice increasing the cost of rice production⁶. Resources of water at above and below ground are shrinking day by day. About 80% of the available water resources worldwide are used by the

agricultural sector⁷. The high water requirement and labor result in the reduced profit margins in rice. Water scarcity in rice production requires the development and adoption of alternative-irrigated rice systems that demand less water than traditional-flooded rice⁸. Researchers in recent years are trying to develop several water-saving technologies such as alternate wetting and drying, direct-dry seeding, the system of rice intensification (SRI), aerobic rice culture, and non-flooded mulching cultivation⁹⁻¹⁰. Recently, a shift from conventional to non-conventional cultivation techniques namely direct-seeded rice and system of rice intensification has been noticed in several countries of Southeast Asia¹¹.

Following three methods of direct seeding rice are commonly practiced, (1) in Dry DSR, dry rice seeds are broadcasted on unpuddled soil (2) in Wet-DSR, sprouted seeds rice are broadcasted in lines on wet-puddled soil (3) in Water seeding, sprouted seeds of rice are broadcasted in standing water¹². Direct seeding technology doesn't require basic operations, namely, puddling, transplanting and maintaining

*Corresponding author

standing water. Direct-seeded rice is beneficial to the farmers and the environment over traditional practices of puddling and transplanting. Although DSR is labor and cost-saving method, seed yield is generally lower than TPR. But, the area under DSR is increasing as it is more productive and profitable to compensate for the production costs¹³.

Similarly, the system of rice intensification originated serendipitously in Madagascar and first used by Father Henri de Laulanié in 1983. It is a new method gaining popularity in many countries to increase rice production. SRI practices are proclaimed to raise the yields of irrigated rice by 25–50% or even more¹⁴. It is a new methodology of rice cultivation that can raise rice output by reducing water requirements and external inputs¹⁵.

Both plant growth and yield are greatly affected by environmental fluctuations due to significant genotype and environment interaction. It is seen that a specific genotype not perform similarly under diverse environmental conditions or contrasting genotypes behave differently to a particular environment. The presence of genotype and environment interaction reduces the association between genotype and phenotype and makes it difficult to know the actual worth of a genotype. Therefore it is necessary to determine the magnitude of genotype and environment interaction and stability of genotypes before its commercial release. The most efficient way to assess the genetic potential and adaptability of genotype is to raise it in different environments for

several years¹⁶. The evaluation of genotypes at convenient testing locations is necessary to the progress of a plant breeding program. Because an ideal test location not only provides the estimates of genetic differences among the genotypes but also discriminate environments for which the identified genotypes are best adapted¹⁷. Therefore, looking into the importance of these components in evaluating the stability and adaptability of the genotypes, this study was undertaken for the evaluation of basmati rice genotypes for yield and its components in different production environments along with the estimation of genotype \times environment interaction.

Materials and Methods

Field experiments were conducted at two locations, Rice Research Station, Kaul, Kaithal and Regional Research Station Uchani, Karnal during two wet seasons' Kharif 2016 and Kharif 2017, respectively. The experimental material comprised of thirty-six basmati rice genotypes as listed in Table 1. The genotypes were grown in a Randomized Block Design (RBD) in three replications in four production environments viz., conventional transplanted rice (TPR), the system of rice intensification (SRI), direct-seeded rice (DSR) and chemical-free cultivation (CFC) as given in Table 2 and Table 3. Plot size consisted of 5 row of 1 m length with a spacing of 20 cm from row to row. All other plant production-related instructions were followed as described elsewhere¹⁸. Observations were recorded on a plot basis for days to 50% flowering (DF)

Table 1 — List of Basmati rice genotypes used in the present study.

Code	Genotypes	Source	Pedigree
G1	Basmati 370		Selection from local material
G2	CSR-30	CSSRI, Karnal	BR 4-10
G3	CSR TPB-1		Trichy 1
G4	Haryana Basmati 1	RRS, Kaul	Sona/Basmati 370
G5	Haryana Mahak 1	RRS, Kaul	IR 50/ Taraori Basmati
G6	HKR -11-509	RRS, Kaul	Pusa Sugandha-3/HBC 19
G7	HKR 03-408	RRS, Kaul	HKR 240/Taraori Basmati
G8	HKR 08-417	RRS, Kaul	Super Basmati/ Taraori Basmati
G9	HKR 06-434	RRS, Kaul	PB 1
G10	HKR 06-443	RRS, Kaul	Super Basmati/HBC 19
G11	HKR 06-487	RRS, Kaul	HBC 19
G12	HKR 08-425	RRS, Kaul	Super Basmati/ Taraori Basmati
G13	HKR 11-447	RRS, Kaul	Sikandri/HBC 19
G14	HKR 98-476	RRS, Kaul	HKR 239/HBC 5
G15	HUBR-16	BHU, Varanasi	Taroari Basmati dwarf mutant-2/PusaSugandh-2
G16	Improved Pusa Basmati 1	IARI, New Delhi	PB 1/PB 1/IRBB 55
G17	PAU-6297-1	PAU, Ludhiana	IET1794811

(Contd.)

Table 1 — List of Basmati rice genotypes used in the present study. (*Contd.*)

Code	Genotypes	Source	Pedigree
G18	Pusa 1475-03-42-45-119-1	IARI, New Delhi	Pusa Basmati 1/IRBB60//Pusa1302
G19	Pusa 1637--2-8-20-5	IARI, New Delhi	Pusa Basmati 1 / IRBL 9-W //Pusa Basmati 1*3
G20	Pusa 1656-10-705	IARI, New Delhi	Pusa 1592 / Pusa 1612
G21	Pusa 1734-8-3-85	IARI, New Delhi	PB1121/FL478// Pusa Basmati 121*3
G22	Pusa 1826-12-27-1-4	IARI, New Delhi	Pusa Basmati 1509/Pusa Basmati 6
G23	Pusa 1884-3-9-175	IARI, New Delhi	Pusa 1727
G24	Pusa 1884-9-12-14	IARI, New Delhi	Pusa 1727
G25	PAU 6295-2	PAU, Ludhiana	IET 17948
G26	Pusa Basmati 1	IARI, New Delhi	Pusa 150/Karnal Local
G27	Pusa Basmati 1121	IARI, New Delhi	P 614-1-2/P 614-2-4-3
G28	Pusa Basmati 1509	IARI, New Delhi	Pusa 1301/ Pusa1121
G29	Pusa Sugandh 2	IARI, New Delhi	Pusa 1238-1/Pusa 1238-81-6
G30	Pusa Sugandh 3	IARI, New Delhi	Pusa 1238-1/Pusa 1238-81-6
G31	Pusa Sugandh 5	IARI, New Delhi	Pusa 3 A
G32	Pusa Sugandh 6	IARI, New Delhi	Pusa 1121-92-8-2-7-1
G33	SJR-70-3-2		Vasumati
G34	Super Basmati		IR 662
G35	Taraori Basmati		Selection from local Basmati Collection
G36	UPR-386-9-1-1		UPR 2724-15-1-1

Table 2 — Description of production environments

Description	CFC	DSR	SRI	TPR
Seed rate (Kg)	20	5	20	20
Seedling age (Days)	30	Direct Sowing	14	30
Spacing (cm ²)	15×20	15×20	25×25	15×20
Sedlings/hill	2-3	2-3	1	2-3

CFC chemical free cultivation, *DSR* direct seeded rice, *SRI* system of rice intensification and *TPR* transplanted rice

and days to 75% maturity (DM) while on five randomly selected plants in each plot for Plant height (PH) in cm, Number of tiller per plant (NTPP), Panicle length (PL) in cm, Panicle weight (PW) in gm, number of spikelets per panicle (NSPP), percent filled spikelets per panicle (PFS) in %, test grain weight (TGW) in gm, grain yield per plant (GYPP) in gm, biological yield per plant (BYPP) in gm and Harvest index (HI) in %.

Stability analysis

The stability model suggested by Eberhart and Russell¹⁹ was used for the determination of stability. The numbers of PCA axes retained in AMMI analysis were determined with the F-statistic^{20,21}. All these analyses were carried out using PB Tools version 1.4t^{22,23}.

Results and Discussion

Mean

Based on the overall mean across the sixteen environments a broad range of variation was realized among the thirty-six genotypes used in this study

(Table 4). The mean ranged from 84.88 to 109.50 for days to flowering. Similarly, for the plant height (86.69 to 144.06 cm), number of tillers per plant (9.62 to 16.48), grain yield per plant (11.34 to 18.54 gm) and harvest index (29.78 to 39.23 %) a large amount of variation was determined (Table 4). Among the thirty-six genotypes studied the Pusa basmati 1 chronicled the maximum values for grain yield, panicle length and harvest index (Table 4). Whereas HKR 06-434 showed the highest biological yield per plant, Pusa Sugandh 5 documented the most number of spikelets per panicle and thousand-grain weight (Table 4).

Stability analysis based on Eberhart and Russell's model

Pooled analysis of variance

The results of the pooled analysis of variance for stability as based on the model of Eberhart and Russell; showed that there was a presence of highly significant genotypes, environment and genotype × environment interaction. Mean sum of squares due to environments + (genotypes × environments) were highly significant for all the character studied depicted the distinct nature of environments and genotype × environment interaction on phenotype expression (Table 5). Mean sum of squares due to environments + (genotypes × environments) found significantly high for all the character studied

Table 3 — Code used for production environments during 2016 and 2017

Direct Seeded Rice (DSR)		System of Rice Intensification (SRI)		Chemical Free Cultivation (CFC)		Transplanted Rice (TPR)	
E1	E2	E3	E4	E5	E6	E7	E8
CFCK16	CFCK17	CFCU16	CFCU17	DSRK16	DSRK17	DSRU16	DSRU17
E9	E10	E11	E12	E13	E14	E15	E16
SRIK16	SRIK17	SRIU16	SRIU17	TPRK16	TPRK17	TPRU16	TPRU17

K16 Kaul 2016, *K17* Kaul 2017, *U16* Uchani 2016 and *U17* Uchani 2017

Table 4 — Overall mean (\pm SD) of the thirty-six Basmati rice genotypes for the agronomical traits under different environments.

Code	Genotypes	DF	DM	PH	NTPP	PL	PW	NSPP	PFS	TGW	BYPP	GYPP	HI
G1	Basmati 370	99.19 \pm 4.65	142.81 \pm 5.22	137.56 \pm 4.34	11.01 \pm 1.85	27.93 \pm 1.16	2.04 \pm 0.18	97.31 \pm 10.40	83.13 \pm 1.70	23.13 \pm 0.76	41.90 \pm 4.86	12.53 \pm 1.91	29.78 \pm 1.85
G2	CSR-30	99.81 \pm 3.33	141.81 \pm 3.33	127.19 \pm 3.29	14.43 \pm 1.62	28.76 \pm 1.22	1.76 \pm 0.06	82.19 \pm 6.24	85.78 \pm 3.29	25.25 \pm 1.07	42.92 \pm 3.30	15.73 \pm 1.61	36.63 \pm 1.80
G3	CSR TPB-1	107.19 \pm 3.58	138.19 \pm 3.58	96.19 \pm 3.82	9.62 \pm 2.00	26.82 \pm 1.21	2.23 \pm 0.33	71.94 \pm 5.67	76.57 \pm 1.73	23.76 \pm 1.34	35.48 \pm 4.44	11.34 \pm 2.25	31.62 \pm 2.75
G4	Haryana Basmati 1	99.94 \pm 4.01	130.56 \pm 4.99	115.19 \pm 3.53	12.02 \pm 3.67	28.37 \pm 1.81	2.48 \pm 0.37	110.56 \pm 14.17	83.99 \pm 1.73	23.43 \pm 0.46	40.87 \pm 5.57	13.80 \pm 3.73	33.10 \pm 5.33
G5	Haryana Mahak 1	96.88 \pm 4.05	137.88 \pm 4.05	135.56 \pm 2.92	12.29 \pm 1.41	28.51 \pm 1.22	2.42 \pm 0.12	105.38 \pm 10.46	81.25 \pm 1.63	26.21 \pm 1.17	43.86 \pm 3.47	13.60 \pm 1.26	30.97 \pm 1.58
G6	HKR - 11-509	109.44 \pm 3.24	139.63 \pm 3.30	130.06 \pm 3.57	14.48 \pm 2.66	29.16 \pm 0.97	2.08 \pm 0.19	102.25 \pm 9.65	81.60 \pm 2.69	25.48 \pm 0.59	45.59 \pm 4.58	15.99 \pm 2.33	34.93 \pm 2.33
G7	HKR 03-408	102.19 \pm 3.69	142.19 \pm 3.69	138.75 \pm 3.28	10.75 \pm 2.24	27.95 \pm 1.21	1.87 \pm 0.16	76.38 \pm 8.33	83.52 \pm 2.47	24.38 \pm 0.68	39.29 \pm 6.20	12.22 \pm 2.10	31.02 \pm 1.79
G8	HKR 06-417	96.56 \pm 2.97	126.50 \pm 3.03	116.81 \pm 4.17	11.64 \pm 3.11	28.32 \pm 1.54	1.99 \pm 0.13	81.06 \pm 9.86	84.66 \pm 2.97	24.77 \pm 0.60	37.62 \pm 5.32	13.17 \pm 3.16	34.53 \pm 4.21
G9	HKR 06-434	102.63 \pm 3.90	142.63 \pm 3.90	134.56 \pm 3.48	14.51 \pm 2.00	29.16 \pm 1.20	2.14 \pm 0.14	112.56 \pm 8.41	84.23 \pm 3.74	25.82 \pm 0.68	50.58 \pm 4.44	16.05 \pm 2.10	31.70 \pm 3.26
G10	HKR 06-443	95.00 \pm 2.58	125.06 \pm 2.84	132.88 \pm 4.06	11.94 \pm 2.30	28.36 \pm 1.14	1.79 \pm 0.11	87.75 \pm 10.47	81.03 \pm 3.27	28.95 \pm 0.45	40.51 \pm 4.50	13.49 \pm 2.29	33.16 \pm 3.56
G11	HKR 06-487	99.25 \pm 3.42	129.25 \pm 3.42	119.44 \pm 4.94	13.31 \pm 2.09	28.73 \pm 1.00	1.92 \pm 0.11	84.56 \pm 7.73	82.44 \pm 2.77	24.89 \pm 1.12	40.90 \pm 4.50	14.87 \pm 1.91	36.29 \pm 1.49
G12	HKR 08-425	94.13 \pm 5.23	124.38 \pm 4.87	122.19 \pm 5.24	15.07 \pm 2.74	29.55 \pm 1.16	2.17 \pm 0.18	110.00 \pm 8.24	78.83 \pm 2.36	24.78 \pm 0.64	45.01 \pm 5.76	16.80 \pm 3.03	37.11 \pm 2.40
G13	HKR 11-447	109.50 \pm 3.20	140.50 \pm 3.20	122.06 \pm 3.15	15.00 \pm 3.08	29.33 \pm 1.30	2.29 \pm 0.21	102.25 \pm 10.67	83.13 \pm 2.61	25.31 \pm 1.16	45.07 \pm 4.47	16.39 \pm 2.97	36.19 \pm 4.32
G14	HKR 98-476	97.00 \pm 3.22	127.94 \pm 3.23	128.44 \pm 3.83	12.80 \pm 1.31	29.09 \pm 0.91	1.85 \pm 0.09	87.00 \pm 6.46	86.06 \pm 1.45	24.84 \pm 0.58	43.92 \pm 4.18	13.89 \pm 1.18	31.70 \pm 2.22
G15	HUBR- 16	97.06 \pm 4.96	126.94 \pm 4.82	102.69 \pm 3.22	12.93 \pm 3.11	28.81 \pm 1.44	3.05 \pm 0.48	92.81 \pm 7.78	84.50 \pm 1.88	26.28 \pm 1.24	39.25 \pm 5.73	14.43 \pm 3.19	36.37 \pm 3.79
G16	Improved Pusa Basmati 1	94.19 \pm 4.53	126.19 \pm 4.53	101.19 \pm 3.33	14.14 \pm 2.77	29.29 \pm 1.20	2.27 \pm 0.18	99.31 \pm 13.44	80.51 \pm 2.85	25.74 \pm 0.68	42.34 \pm 6.01	15.60 \pm 2.90	36.65 \pm 2.72
G17	PAU- 6297-1	92.94 \pm 3.97	125.13 \pm 3.65	104.44 \pm 4.10	12.69 \pm 1.33	28.13 \pm 1.01	2.02 \pm 0.19	89.88 \pm 6.06	86.91 \pm 3.29	26.13 \pm 0.86	43.91 \pm 1.76	13.81 \pm 0.88	31.46 \pm 1.98
G18	Pusa 1475-03- 42-45-119-1	87.25 \pm 2.86	118.06 \pm 3.04	86.69 \pm 4.85	11.86 \pm 2.00	28.07 \pm 0.81	2.15 \pm 0.13	83.56 \pm 9.64	80.73 \pm 3.68	24.87 \pm 1.40	39.45 \pm 3.79	13.61 \pm 1.96	34.35 \pm 2.45
G19	Pusa 1637--2- 8-20-5	91.19 \pm 3.67	121.19 \pm 3.67	101.56 \pm 2.99	14.92 \pm 2.07	29.63 \pm 0.92	2.39 \pm 0.22	108.69 \pm 10.81	82.82 \pm 2.99	25.64 \pm 0.83	44.27 \pm 4.11	16.83 \pm 1.97	38.01 \pm 2.94
G20	Pusa 1656- 10-705	89.56 \pm 2.31	119.56 \pm 2.31	103.75 \pm 3.97	14.49 \pm 1.46	29.53 \pm 1.09	2.37 \pm 0.26	114.88 \pm 9.99	86.00 \pm 3.44	27.15 \pm 0.7 2	42.25 \pm 3.08	16.35 \pm 1.95	38.63 \pm 3.10
G21	Pusa 1734- 8-3-85	104.50 \pm 3.85	135.63 \pm 4.40	104.63 \pm 5.28	16.48 \pm 2.13	29.96 \pm 0.87	2.40 \pm 0.10	113.31 \pm 10.64	80.06 \pm 3.50	26.62 \pm 1.18	48.77 \pm 3.64	18.16 \pm 2.19	37.12 \pm 2.38

(Contd.)

Table 4 — Overall mean (\pm SD) of the thirty-six Basmati rice genotypes for the agronomical traits under different environments. (Contd.)

Code	Genotypes	DF	DM	PH	NTPP	PL	PW	NSPP	PFS	TGW	BYPP	GYPP	HI
G22	Pusa 1826-12-271-4	100.44 \pm 3.05	130.44 \pm 3.05	98.56 \pm 3.48	13.45 \pm 1.74	29.06 \pm 0.89	2.28 \pm 0.26	95.25 \pm 9.64	83.01 \pm 2.99	25.50 \pm 0.63	43.12 \pm 3.49	15.06 \pm 1.94	34.83 \pm 2.68
G23	Pusa 1884-3-9-175	92.56 \pm 3.93	123.56 \pm 3.93	98.06 \pm 4.71	13.82 \pm 2.98	28.85 \pm 1.45	2.22 \pm 0.26	99.63 \pm 8.95	78.59 \pm 3.63	25.08 \pm 1.10	43.46 \pm 4.93	15.25 \pm 3.07	34.73 \pm 3.54
G24	Pusa 1884-9-12-14	96.19 \pm 3.90	128.19 \pm 3.90	106.63 \pm 4.54	10.88 \pm 2.35	27.71 \pm 1.18	1.76 \pm 0.23	75.88 \pm 6.35	86.61 \pm 2.87	24.46 \pm 1.22	38.96 \pm 4.86	12.18 \pm 2.18	31.01 \pm 2.16
G25	Pusa 6295-2	102.75 \pm 3.59	132.81 \pm 3.47	87.75 \pm 3.42	14.62 \pm 1.73	28.67 \pm 1.59	2.02 \pm 0.20	94.38 \pm 9.08	87.93 \pm 2.67	27.76 \pm 1.86	44.95 \pm 3.25	15.77 \pm 1.50	35.02 \pm 1.49
G26	Pusa Basmati 1	92.50 \pm 3.48	123.50 \pm 3.48	104.75 \pm 3.68	16.20 \pm 2.77	30.26 \pm 1.44	2.70 \pm 0.26	133.13 \pm 11.69	82.59 \pm 1.74	24.89 \pm 0.67	47.13 \pm 7.51	18.54 \pm 3.30	39.23 \pm 2.09
G27	Pusa Basmati 1121	95.50 \pm 2.90	125.44 \pm 3.05	134.94 \pm 4.64	15.87 \pm 4.38	29.59 \pm 1.46	1.95 \pm 0.14	88.63 \pm 10.63	82.02 \pm 3.47	29.22 \pm 0.37	45.18 \pm 7.99	16.73 \pm 4.07	36.62 \pm 2.76
G28	Pusa Basmati 1509	84.88 \pm 4.11	115.38 \pm 4.24	91.50 \pm 3.85	15.37 \pm 2.16	29.51 \pm 1.32	2.53 \pm 0.18	104.19 \pm 7.91	83.64 \pm 4.40	28.27 \pm 0.70	42.78 \pm 4.13	16.81 \pm 2.13	39.18 \pm 2.27
G29	Pusa Sugandh 2	91.69 \pm 3.70	123.69 \pm 3.70	103.88 \pm 3.54	13.07 \pm 1.96	28.79 \pm 1.09	2.96 \pm 0.37	99.69 \pm 9.62	82.16 \pm 3.22	27.84 \pm 1.24	40.10 \pm 3.74	14.35 \pm 2.01	35.64 \pm 2.59
G30	Pusa Sugandh 3	96.44 \pm 3.41	126.44 \pm 3.41	109.75 \pm 3.04	14.48 \pm 2.46	29.43 \pm 1.15	2.28 \pm 0.23	112.94 \pm 10.26	81.23 \pm 4.16	25.10 \pm 0.69	41.98 \pm 5.05	16.05 \pm 2.30	38.15 \pm 2.16
G31	Pusa Sugandh 5	90.38 \pm 4.13	121.31 \pm 4.09	103.13 \pm 3.59	15.48 \pm 2.30	29.47 \pm 1.19	2.91 \pm 0.18	141.13 \pm 12.86	81.27 \pm 2.88	30.23 \pm 1.28	44.26 \pm 4.73	16.87 \pm 2.20	38.08 \pm 2.60
G32	Pusa Sugandh 6	95.25 \pm 2.86	125.25 \pm 2.86	89.06 \pm 3.36	15.42 \pm 3.48	29.39 \pm 1.56	2.33 \pm 0.12	112.31 \pm 14.10	78.05 \pm 2.30	26.04 \pm 0.84	44.93 \pm 7.58	16.72 \pm 3.50	37.04 \pm 2.91
G33	SJR-70-3-2	96.31 \pm 3.05	126.31 \pm 3.05	109.31 \pm 3.98	14.99 \pm 3.19	29.01 \pm 1.57	2.27 \pm 0.19	104.56 \pm 12.17	78.00 \pm 3.58	26.05 \pm 0.94	46.68 \pm 5.24	16.43 \pm 3.01	35.28 \pm 5.35
G34	Super Basmati	104.50 \pm 3.56	134.50 \pm 3.56	120.50 \pm 3.44	12.22 \pm 2.82	28.32 \pm 1.31	1.58 \pm 0.33	90.94 \pm 9.57	81.37 \pm 2.92	24.12 \pm 0.99	42.89 \pm 7.50	13.88 \pm 2.87	32.20 \pm 2.07
G35	Taraori Basmati	100.88 \pm 4.63	143.31 \pm 3.59	144.06 \pm 3.30	11.47 \pm 2.41	28.13 \pm 1.21	1.80 \pm 0.15	81.06 \pm 8.73	89.32 \pm 2.57	24.61 \pm 0.25	41.83 \pm 6.70	12.82 \pm 2.41	30.52 \pm 2.14
G36	UPR-386-9-1-1	89.75 \pm 4.07	120.69 \pm 4.05	107.88 \pm 5.45	13.41 \pm 1.92	28.68 \pm 1.17	2.26 \pm 0.19	93.19 \pm 8.02	81.52 \pm 3.92	24.28 \pm 0.71	40.30 \pm 4.23	14.77 \pm 1.79	36.62 \pm 2.14
	Range	84.88-109.50	115.38-143.31	86.69-144.06	9.62-16.48	26.82-30.26	1.50-3.05	71.94-141.13	76.57-89.32	23.13-30.23	35.48-50.58	11.34-18.54	29.78-39.23

Table 5 — Pooled analysis of variance across the environments for different traits (Eberhart and Russell model, 1966).

Source	df	DF	DM	PH	NTPP	PL	PW	NSPP	PFS	TGW	BYPP	GYPP	HI
Genotype (Gen.)	35	552.47**	1002.72**	4159.95**	47.43**	7.97**	1.88**	3739.35**	138.63**	42.49**	151.48**	49.33**	119.95**
Environment (Env.)	15	345.46**	353.48**	349.70**	170.67**	28.17**	1.14**	2602.66**	48.32**	12.00**	521.69**	170.80**	180.87**
Gen. \times Env.	525	4.37**	4.27**	5.88**	1.43**	0.78**	0.02**	24.74**	7.32**	0.58*	11.26**	1.40**	3.25**
Env. + Gen. \times Env.	540	13.85**	13.97**	15.43**	6.13**	1.54**	0.049**	96.36**	8.46**	0.886**	25.44**	6.11**	8.181**
Env. (Linear)	1	5181.88**	5302.16**	5245.10**	2560.01**	422.53**	17.06**	39047.61**	724.79**	180.27**	7825.28**	2562.00**	2713.01**
Env. \times Gen. (Linear)	35	8.36**	8.45**	6.68	8.55**	1.82**	0.126**	88.04**	14.49**	1.70**	46.63**	9.43**	17.67**
Pooled deviation	504	3.97**	3.86**	5.66*	0.89*	0.69**	0.009**	19.65**	6.62**	0.48	8.49**	0.81*	2.16**
Pooled error	11200.90		1.23	4.48	0.78	0.35	0.2	6.75	1.27	0.51	1.16	0.44	0.90

*, ** and *** Significant at P < 0.05, 0.01 and 0.001 levels, respectively.

depicted the diverse nature of ecosystems and genotype \times environment interaction on phenotype expression. Significance of environment (linear) component for all the studied traits, when tested against pooled deviation, suggested that the genotypes behaved linearly for most of the traits (Table 5).

Stability parameters

Selection of high yielding and stable genotypes under diverse environments is the first aim in any breeding program. According to Eberhart and Russell (1966)¹⁸ model of stability, a stable genotype is one that exhibit high mean yield, regression co-efficient

(bi) near unity and deviation from regression near to zero. Therefore Genotypes, HKR 11-509, HKR 11-447 and Pusa 1884-3-9-175, for grain yield per plant, number of tillers per plant and number of spikelets per panicle; Pusa Basmati 1121 for biological yield per plant and harvest index; Taraori basmati for percent filled spikelets; Pusa Sugandh 2 and SJR-70-3-2 for thousand grain weight; Pusa Basmati 1121, HKR 11-447 and Pusa 1884-3-9-175 for panicle length; Haryana Basmati 1 and Pusa 1884-3-9-175 for panicle weight; Pusa Sugandh 3 and Pusa Sugandh 5 for days to 50% flowering and days to maturity were found suitable for better environment (Table 6).

Table 6 — Stability parameters for studied traits of Basmati rice genotypes tested across the environments.

Genotypes	Parameter	DF	DM	PH	NTPP	PL	PW	NSPP	PFS	TGW	BYPP	GYPP	HI
Basmati 370	Mean	99.21	142.83	137.52	11.01	27.93	2.039	97.25	82.95	23.13	41.90	12.53	29.78
	Bi	1.35***	1.52***	1.21***	0.78***	0.99***	0.973***	1.14***	0.13	0.64	1.02***	0.83**	0.60***
	S2di	3.83***	3.48***	0.59	-0.21	0.27	0.000	8.57	1.00	-0.04	7.79***	-0.05	0.80
CSR-30	Mean	99.85	141.92	127.19	14.43	28.77	1.757	82.27	85.60	25.18	42.92	15.73	36.63
	Bi	0.93***	0.94***	0.92***	0.61***	0.20	0.224***	0.59***	0.73	1.34***	0.57	0.59**	0.54
	S2di	1.10	1.40	-1.40	0.16	1.23***	0.000	8.59	7.66***	-0.01	5.44***	0.57**	1.02
CSR TPB-1	Mean	107.19	138.19	96.17	9.62	26.82	2.231	72.00	76.37	23.76	35.48	11.34	31.62
	Bi	0.88***	0.89***	0.99***	0.81***	0.74	1.754***	0.51***	0.44	2.13***	0.94***	0.95**	1.17***
	S2di	4.75***	4.40***	0.58	0.13	0.77***	0.014***	7.17	0.53	-0.21	6.19***	0.37	-0.17
Haryana Basmati 1	Mean	99.92	130.63	115.17	12.02	28.37	2.480	110.63	83.98	23.43	40.87	13.80	33.10
	Bi	1.10***	1.44***	1.01***	1.63***	1.87***	2.058***	1.61***	0.79***	0.32	1.21***	1.66**	2.25***
	S2di	4.11***	2.85***	-2.27	0.10	0.25	0.001	8.73	1.00	-0.32	9.44***	0.47	2.24***
Haryana Mahak 1	Mean	96.88	137.92	135.52	12.29	28.51	2.423	105.38	81.39	26.21	43.86	13.60	30.97
	Bi	1.18***	1.17***	0.86***	0.49***	0.69	0.657***	1.01***	0.32	1.61***	0.65***	0.41**	0.28
	S2di	2.84***	1.83	-3.11	0.16	0.85***	0.000	31.14***	1.21	0.03	5.12***	0.41	1.35
HKR -11-509	Mean	109.38	139.65	130.08	14.48	29.16	2.075	102.35	81.89	25.48	45.59	15.99	34.93
	Bi	0.81***	0.83***	1.09***	1.15***	0.94***	0.992***	1.05***	0.89	0.74***	1.04***	1.04**	0.92***
	S2di	3.70***	2.61***	-2.73	0.05	-0.09	0.004***	8.10	4.09***	-0.34	4.46***	-0.15	0.35
HKR 03-408	Mean	102.15	142.13	138.73	10.75	27.95	1.869	76.42	83.70	24.38	39.29	12.22	31.01
	Bi	1.06***	1.09***	0.84***	0.96***	0.92	0.844***	0.88***	0.17	0.72	1.45***	0.91**	0.46
	S2di	2.08***	1.88	-0.56	-0.11	0.51	0.002	7.33	5.27***	-0.21	7.49***	0.05	1.37
HKR 08-417	Mean	96.56	126.56	116.79	11.65	28.32	1.985	81.15	84.54	24.77	37.62	13.17	34.53
	Bi	0.92***	0.93***	0.93***	1.37***	1.62***	0.587***	1.09***	1.69	0.68	1.33***	1.41**	1.81***
	S2di	0.38	-0.42	4.76	0.07	-0.01	0.004***	6.61	4.69***	-0.29	1.70	0.06	0.58
HKR 06-434	Mean	102.63	142.58	134.67	14.51	29.16	2.142	112.56	84.31	25.82	50.58	16.05	31.70
	Bi	1.14***	1.11***	0.76	0.83***	1.05***	0.742***	0.88***	1.45	0.65	0.77	0.89**	1.12***
	S2di	2.50***	2.23***	1.63	0.03	0.27	-0.001	8.56	11.62***	-0.17	10.67***	0.30	3.70***
HKR 06-443	Mean	94.98	125.04	132.83	11.94	28.36	1.785	87.75	81.71	28.95	40.50	13.49	33.16
	Bi	0.71***	0.80***	1.07***	0.99***	1.20***	0.571***	1.15***	1.00	0.56***	1.02***	1.00**	1.37***
	S2di	1.42	0.63	1.17	-0.06	-0.17	0.000	9.48	8.89***	-0.41	4.23***	0.07	2.62***
HKR 06-487	Mean	99.27	129.31	119.50	13.31	28.73	1.916	84.60	82.38	24.89	40.90	14.87	36.29
	Bi	1.00***	0.95***	1.20***	0.86***	0.99***	0.423***	0.66***	0.29	-0.12	0.71	0.75**	0.39
	S2di	1.70***	1.02	6.16	0.15	-0.11	0.006***	23.20***	6.48***	0.83***	12.71***	0.64**	0.64
HKR 08-425	Mean	94.10	124.40	122.15	15.07	29.55	2.169	110.02	78.59	24.78	45.01	16.80	37.11
	Bi	1.54***	1.40***	1.41***	1.10***	1.04***	0.936***	0.85***	1.34	0.29	1.34***	1.25**	0.91***
	S2di	4.18***	3.64***	5.44	1.14	0.18	0.002	7.68	2.76***	-0.11	6.58***	1.44**	0.75
HKR 11-447	Mean	109.56	140.50	121.98	15.00	29.33	2.289	102.23	82.65	25.31	45.07	16.39	36.19
	Bi	0.94***	0.90***	0.70	1.38***	1.27***	1.141***	1.18***	0.51	1.75***	0.98***	1.33**	1.86***
	S2di	1.49***	1.08	1.51	-0.30	0.11	0.002	9.21	3.09***	-0.18	5.31***	-0.07	0.47

(Contd.)

Table 6 — Stability parameters for studied traits of Basmati rice genotypes tested across the environments. (Contd.)

Genotypes	Parameter	DF	DM	PH	NTPP	PL	PW	NSPP	PFS	TGW	BYPP	GYPP	HI
HKR 98-476	Mean	97.00	127.96	128.48	12.79	29.09	1.853	87.02	85.86	24.84	43.92	13.89	31.70
	Bi	0.91***	0.94***	1.00***	0.45***	0.38	0.334***	0.52	-0.11	0.62	0.04	0.31	0.84***
	S2di	1.86***	1.08	0.06	0.00	0.43	0.003	16.28***	0.32	-0.30	17.53***	0.58**	0.58
HUBR-16	Mean	97.10	97.10	102.73	12.93	28.81	3.055	92.81	84.47	26.28	39.25	14.43	36.37
	Bi	1.43***	1.43***	0.74	1.36***	1.48***	2.685***	0.80***	0.45	1.53	1.43***	1.41**	1.51***
	S2di	4.24***	4.24***	1.23	0.15	0.03	0.003	9.39	2.30***	0.31	2.47***	0.29	2.21***
Improved Pusa Basmati 1	Mean	94.17	126.19	101.19	14.14	29.29	2.269	99.33	80.28	25.74	42.34	15.59	36.65
	Bi	1.35***	1.33***	0.99***	1.21***	1.15***	0.972***	1.50***	1.30	0.97***	1.43***	1.28**	1.13***
	S2di	2.43***	2.11***	-3.02	0.02	0.09	0.001	13.12***	3.52***	-0.36	5.85***	0.23	0.17
PAU-6297-1	Mean	92.94	125.17	104.42	12.68	28.13	2.024	89.83	87.33	26.13	43.91	13.81	31.46
	Bi	1.00***	0.92***	1.26***	0.52***	0.46	1.044***	0.55***	1.18	0.56	-0.05	0.26**	0.60
	S2di	5.45***	4.15***	-2.59	-0.23	0.56	0.002	10.50	7.13***	0.18	2.13***	0.05	1.37
Pusa 1475-03-42-45-119-1	Mean	87.29	118.06	86.83	11.86	28.07	2.147	83.58	80.60	24.87	39.45	13.61	34.35
	Bi	0.69***	0.81***	0.80	0.87***	0.75***	0.697***	1.04***	2.67***	1.97***	0.91***	0.85**	0.94***
	S2di	2.77***	2.16***	14.58***	-0.30	-0.11	0.001	8.07	2.16***	0.20	1.37	0.02	0.77
Pusa 1637-2-8-20-5	Mean	91.21	121.21	101.50	14.92	29.63	2.390	108.60	83.25	25.64	44.27	16.83	38.01
	Bi	1.05***	1.01***	0.83***	0.77***	0.68	0.508***	1.06***	0.19	0.46	0.46	0.77**	1.02***
	S2di	2.76***	2.62***	-2.22	0.77	0.17	0.043***	31.81***	7.41***	0.16	13.69***	0.69**	2.76***
Pusa 1656-10-705	Mean	89.56	119.56	103.75	14.49	29.53	2.372	114.92	85.87	27.15	42.25	16.35	38.63
	Bi	0.40	0.38	1.18***	0.57***	0.59	1.361***	1.10***	1.73	0.96***	0.62***	0.84**	1.15***
	S2di	3.34***	3.06***	-1.23	-0.14	0.63***	0.009***	5.71	7.41***	-0.29	3.11***	0.06	2.32***
Pusa 1734-8-3-85	Mean	104.48	135.60	104.63	16.48	29.95	2.404	113.29	80.10	26.62	48.77	18.15	37.12
	Bi	1.06***	1.25***	1.39***	0.85***	0.50	0.270***	1.01***	0.61	1.54***	0.63	0.86**	1.00***
	S2di	2.84***	2.44***	4.77	0.39	0.26	0.007***	36.55***	11.09***	0.14	6.83***	0.98**	-0.23
Pusa 1826-12-271-4	Mean	100.38	130.50	98.56	13.45	29.06	2.278	95.25	82.80	25.50	43.12	15.06	34.83
	Bi	0.86***	0.84***	0.86***	0.72***	0.76***	1.347***	1.01***	1.68	0.81***	0.60	0.81**	1.10***
	S2di	1.59***	1.66	1.11	-0.19	0.03	0.007***	13.97***	4.8***	-0.32	6.26***	0.24	0.29
Pusa 1884-3-9-175	Mean	92.67	123.60	98.13	13.82	28.85	2.217	99.63	78.40	25.08	43.46	15.25	34.73
	Bi	1.03***	1.01***	1.36***	1.32***	1.33***	1.433***	1.03***	0.92	1.82***	1.08***	1.37**	1.37***
	S2di	4.36***	4.72***	-0.75	-0.09	0.42	0.002	-0.44	10.46***	-0.40	6.65***	0.08	2.52***
Pusa 1884-9-12-14	Mean	96.15	128.23	106.60	10.88	27.71	1.758	75.98	86.64	24.40	38.96	12.18	31.01
	Bi	1.02***	0.96***	1.35***	0.96***	0.65	1.225***	0.60***	1.55	1.73***	1.02***	0.93**	0.89***
	S2di	5.73***	5.13***	-1.77	0.41	0.78***	0.005***	8.30	4.22***	-0.04	7.99***	0.24	-0.15
Pusa 6295-2	Mean	102.77	132.83	87.81	14.62	28.67	2.022	94.44	87.85	27.76	44.95	15.77	35.02
	Bi	0.81	0.80***	0.88***	0.71***	0.53	0.993***	0.96***	0.20	1.68	0.76***	0.60**	0.40
	S2di	5.72***	5.00***	0.14	-0.13	2.14***	0.006***	9.32	6.04***	2.21***	1.25	0.11	0.64
Pusa Basmati 1	Mean	92.54	123.60	104.71	16.20	30.26	2.704	133.10	82.36	24.89	47.13	18.54	39.23
	Bi	0.87***	0.83***	0.95***	1.06***	1.51***	0.742***	1.11***	0.51	0.35	1.45***	1.31**	0.66
	S2di	4.40***	4.19***	0.75	1.73***	-0.04	0.053***	44.52***	1.29	-0.08	26.39***	2.44**	1.43
Pusa Basmati 1121	Mean	95.46	125.40	134.88	15.87	29.59	1.949	88.58	82.37	29.22	45.18	16.73	36.62
	Bi	0.82***	0.85***	1.26***	1.98***	1.59***	0.736***	1.19***	2.42***	0.37	2.05***	1.83**	1.14***
	S2di	1.28	1.12	1.80	-0.20	-0.16	0.002	3.18	2.38***	-0.42	1.80	0.38	0.27
Pusa Basmati 1509	Mean	84.83	115.35	91.50	15.37	29.51	2.532	104.29	83.59	28.27	42.78	16.81	39.18
	Bi	1.11***	1.16***	0.79	0.89***	1.03	0.877***	0.75***	2.85***	0.88***	0.81***	0.90**	0.86***
	S2di	4.30***	4.20***	5.29	0.18	0.64***	0.007***	15.93***	7.69***	-0.27	6.89***	0.35	0.60
Pusa Sugandh 2	Mean	91.60	123.69	103.85	13.07	28.79	2.960	99.65	81.89	27.84	40.10	14.35	35.64
	Bi	0.92***	0.90***	0.72	0.84***	1.06***	1.785***	1.08***	-1.19	1.70***	0.88***	0.86**	1.00***
	S2di	5.12***	4.48***	4.45	-0.25	0.00	0.039***	2.31	10.44***	0.08	1.90***	0.10	0.94
Pusa Sugandh 3	Mean	96.44	126.40	109.73	14.48	29.43	2.281	112.88	81.14	25.09	41.98	16.05	38.15
	Bi	1.02***	1.00***	0.72***	1.09***	1.02***	1.131***	1.11***	0.87	0.94***	1.24***	1.00**	0.72***
	S2di	0.88	0.42	0.44	-0.29	0.20	0.014***	11.23***	14.79***	-0.31	2.15***	0.14	1.25
Pusa Sugandh 5	Mean	90.40	121.33	103.10	15.48	29.47	2.914	141.13	81.11	30.23	44.26	16.87	38.08
	Bi	1.26***	1.20***	0.97***	1.01***	1.02***	0.933***	1.43***	2.08***	1.51	1.12***	0.95**	0.91***
	S2di	1.05	1.10	-0.54	-0.24	0.29	0.002	12.00***	1.87	0.41	3.45***	0.17	1.87***
Pusa Sugandh 6	Mean	95.27	125.21	89.13	15.42	29.39	2.331	112.27	78.17	26.04	44.93	16.72	37.04
	Bi	0.52	0.58	0.89***	1.54***	1.52***	0.615***	1.59***	0.69	0.61	1.88***	1.56**	1.15***
	S2di	4.87***	4.43***	-1.18	0.16	0.35	0.002	10.93***	3.48***	0.11	5.45***	0.34	1.00

(Contd.)

Table 6 — Stability parameters for studied traits of Basmati rice genotypes tested across the environments. (Contd.)

Genotypes	Parameter	DF	DM	PH	NTPP	PL	PW	NSPP	PFS	TGW	BYPP	GYPP	HI
SJR-70-3-2	Mean	96.29	126.33	109.38	14.99	29.01	2.274	104.65	77.59	26.05	46.68	16.43	35.28
	Bi	0.79***	0.79***	1.13***	1.41***	1.51***	1.003***	1.34***	1.24	1.32***	0.71	1.33**	2.25***
	S2di	2.35***	2.09***	-0.96	-0.04	0.38	0.004***	11.83***	11.55***	-0.19	20.39***	0.28	2.68***
Super Basmati	Mean	104.42	134.48	120.46	12.22	28.32	1.577	90.90	80.80	24.12	42.89	13.88	32.19
	Bi	0.95***	0.96***	0.84***	1.25***	1.18***	1.679***	1.04***	0.47	1.33***	1.82***	1.29**	0.41
	S2di	3.01***		0.83	-0.14	0.35	0.021***	7.13	4.84***	-0.11	7.55***	0.01	2.79***
Taraori Basmati	Mean	100.88	143.27	144.02	11.47	28.13	1.800	81.02	89.41	24.61	41.83	12.82	30.52
	Bi	1.32***	0.91***	0.81***	1.04***	1.16***	0.706***	0.93***	1.76***	0.10	1.49***	1.06**	0.44
	S2di	4.79***	4.05***	0.52	0.00	0.09	0.007***	9.25	1.30	-0.45	12.65***	0.07	2.96***
UPR-3886-9-1-1	Mean	89.79	120.71	107.90	13.41	28.68	2.261	93.19	81.36	24.28	40.30	14.77	36.62
	Bi	1.24***	1.19***	1.30***	0.61***	0.63	1.019***	0.64	2.21	0.93***	0.57	0.59**	0.83***
	S2di	1.55***	1.57	8.77***	1.28***	0.78***	0.003	29.18***	9.02***	-0.29	12.88***	1.20**	0.28

Table 7 — AMMI analysis for various traits in rice across different environments.

Source	df	DF	DM	PH	NTPP	PL	PW	NSPP	PFS	TGW	BYPP	GYPP	HI
Trials	575	46.63	74.15	267.70	8.64	1.93	0.16	318.10	16.38	3.43	33.11	8.74	14.98
Genotypes	35	55.247*	1002.72*	4159.95*	47.43*	7.97*	1.88*	3739.35*	138.63*	42.49*	151.48*	49.33*	119.95*
Environments	15	345.46*	353.48*	349.70*	170.67*	28.17*	1.14*	2602.66*	48.32*	12.00*	521.69*	170.80*	180.87*
G×E interaction	525	4.37**	4.27**	5.88**	1.43**	0.78**	0.02**	24.74**	7.32**	0.58*	11.26**	1.40**	3.25**
PCA I	49	11.74*	12.55*	27.10*	6.43*	2.73*	0.094*	79.50*	16.52*	1.97*	47.31*	7.12*	14.82*
PCA II	47	9.76*	8.05*	8.63*	3.22*	1.44*	0.060*	59.13*	19.28*	1.47*	33.42*	3.16*	6.02*
PCA III	45	6.30*	6.31*	7.30*	2.15*	1.10*	0.025*	26.55*	10.88*	1.14*	17.15*	1.65*	5.28*
Pooled Error	1150	0.89	1.22	4.42	0.84	0.36	0.002	7.41	1.37	0.56	1.25	0.48	0.96

*, ** and *** Significant at $p < 0.05$, 0.01 and 0.001 levels, respectively.

Table 8 — Percentage of contribution in the total explanation of the trait variance.

Source	DF	DM	PH	NTPP	PL	PW	NSPP	PFS	TGW	BYPP	GYPP	HI
Genotypes	72.11	82.31	94.59	33.41	25.09	71.49	71.55	51.52	75.7	27.85	34.35	48.72
Environments	19.33	12.44	3.41	51.52	37.99	18.55	21.35	7.70	9.15	41.11	50.97	31.49
G×E interaction	8.56	5.26	2.00	15.07	36.92	9.96	7.10	40.79	15.14	31.04	14.68	19.79
PCA I	24.50	27.9	43.40	42.10	32.60	50.40	29.90	23.60	32.10	39.20	47.30	42.60
PCA II	20.10	17.10	13.10	20.20	16.50	30.60	21.40	21.00	23.40	26.60	20.10	16.60
PCA III	12.40	12.30	10.60	12.90	12.10	12.10	9.20	12.70	17.00	13.10	10.00	13.90

Among the environments, the system of rice intensification (SRI K16, SRI U16, SRI K17, and SRI U17) was found to be most favorable production environment for number of tillers per plant, panicle length, panicle weight, number of spikelets per panicle, percent filled spikelets, thousand grain weight, biological yield per plant, grain yield per plant, and harvest index, while transplanted rice (TPR K16, TPR U16, TPR K17 and TPR U17) was the most favorable for days to 50% flowering, days to maturity and plant height. Genotypes Pusa Basmati 1509 and Pusa 1656-10 for grain yield per plant; Pusa 6295-2 for biological yield per plant were found suitable for the unfavorable environment. Direct seeded rice was observed as an adverse environment (Table 6).

Stability analysis based on AMMI Model

Bartlett's test indicated homogenous error variance for the studied traits in each of the sixteen environments and allowed to proceed further for

pooled analysis across the environments. The combined analysis (Table 7) of variance depicted that mean sum of squares due to genotypes, environments and genotype and environment were significant for all the traits. This suggested the existence of variability among the genotypes and environments. The AMMI analysis of variance (Table 7) for grain yield across the settings represented that 34.35% of the total variation was attributed to genotypic effects, 50.97% to the environmental impacts and 14.68% to genotype × environment interaction effects (Table 8). The existence of GEI was determined by the AMMI model, suggesting the considerable differences in genotypic response across the environments. The cumulative variance was about 77.40% for PCA I, PCA II and PCA III. This implies that the interaction of the 36 rice genotypes with sixteen environments was concluded by first three components of genotypes and environments.

AMMI biplot analysis

Based on AMMI biplot analysis, the elite genotypes namely, Improved Pusa Basmati 1, HKR 98-476 and HKR 08-417 were identified suitable for days to 50% flowering and days to maturity. Pusa Sugandh 5, Pusa Basmati 1 and Pusa Sugandh 3 were determined as top genotypes for the number of tillers per plant. Whereas, Pusa Sugandh 5, Pusa Basmati 1509 and Pusa 1734-8-3-85 were the top genotypes for the grain yield per plant (Fig. 1). While, in case of the identification of suitable environment for grain yield per plant, genotypes Improved Pusa Basmati 1, HKR 11-509 and Taraori Basmati were found ideal for TPR; HKR 03- 408, Pusa 1475-03-42-45-119-1 and Basmati 370 for CFC; Pusa 1884-3-9-175, Pusa Basmati-1, Pusa Basmati 6 and Pusa Basmati 1121 for SRI and HKR 98-476 and PAU-6297-1 for DSR (Fig. 1). For number of tillers per plant, genotypes Improved Pusa Basmati 1, Pusa 1884-3-9- 175 and HKR 11-509 were found suitable for TPR; Pusa Sugandh 2 and Pusa 1884-9-12-14 for CFC; Pusa Basmati 1121 and HKR 11-447 for SRI (Fig. 1). In the case of number of spikelets per panicle, Improved Pusa Basmati 1, Pusa Basmati 1121 and Basmati 370 were found suitable for TPR; Pusa Sugandh 2 and Pusa Basmati-1 for CFC; Haryana Basmati-1 and SJR-70-3-2 for SRI; and HKR 98-476, HKR 06-487 and PAU-6297-1 for DSR. For biological yield per

plant, genotypes Pusa 1637-2-8-20-5, Pusa Basmati 6 and HKR 03-408 were found suitable for TPR; Pusa 1884-9-12-14 and HKR 06-487 for CFC; HKR 06-417, Basmati 370 and Pusa Basmati 1121 for SRI and HKR 98-476 for DSR.

GGE Biplot

Relationship and representation of test environments

The GGE biplot in Figure 2a explained 85.4% of total variations, so this technique can be used for measuring the relationship among the environments. The straight lines that join the biplot origin are environment vectors and the angle between them is analogous to the correlation coefficient. The tester view is primarily used to find the test environments with positive or negative correlations. Environments with short angles between them were correlated positively and they furnish related information on genotypes (Fig. 2a). Thus the sixteen backgrounds were divided into five groups, group 1 (E5, E6, E7 and E8); group 2 (E1, E2, E4); group 3 (E3, E13, E14, E15), group 4 (E11, E12, E16) and group 5 (E9, E10) suggesting that these environments provide redundant information about the genotypes (Fig. 2a). In general getting similar information with fewer environments curtails the cost of evaluation and boost up the breeding competence.

Discriminating ability and representativeness are the essential properties of a test environment²⁴. An ideal environment is denoted by a small circle. An ideal test environment is one having most extended vector (most discriminating) of all test environments and placed on AEC abscissa (most representative)²⁴. Fig. 2b shows that E2 is an ideal environment. Environment 2 has high PC1 score and small PC2 score. Test environment E2 is representative as well as discriminating so; it was a good test environment for selecting generally adapted genotypes (Figure 2b). The ranking of environments based on ideal environment were E2>E4>E1>E3>E13>E15>E14>E16>E12>E11>E5>E6>E7>E8>E9>E10. On other hand, E5 and E10 was the most discriminating environment but are non-representative (Fig. 2b). So these environments are suitable for the selection of specially adapted genotypes and inadequate for selection of genotypes for general adaptation. E2 and E4 were most representative. The discriminating ability of an Ideal environment concerned with the content of genotypes, but the presence of genotype × environment interaction convolute the selection of ideal environment²⁵. The test environments should

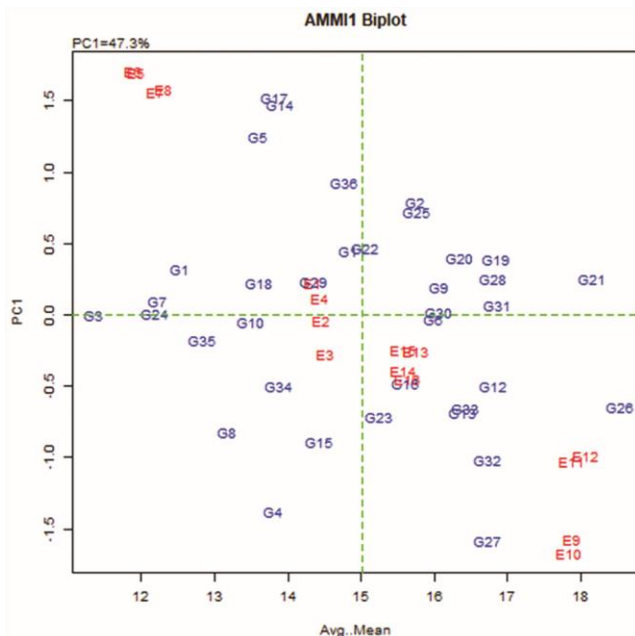


Fig. 1 — AMMI-1 model biplot for grain yield of Basmati rice genotypes across the environments.

have high PCA 1 scores to differentiate genotypes for genotypic effect and small PCA 2 scores to be more representative of the overall locations²⁶.

Genotype evaluation based on GGE Biplots

The genotypes ranking on basis of mean grain yield and stability for environments showed in Figure 3a. It noted that when PCA 1 in a GGE biplot approximates the mean performance,

PCA 2 must approximate the $G \times E$ correlated with each genotype, which is a measure of instability²⁵⁻²⁷. Therefore, genotypes G17 and G27 found a more variable and less stable performance than the other genotypes. Genotypes G16, G22 and G23 found more durable than the others (Fig. 3a).

The genotypes placed near the ‘ideal genotype’ are more desirable than others. Hence, G21 and G26 are

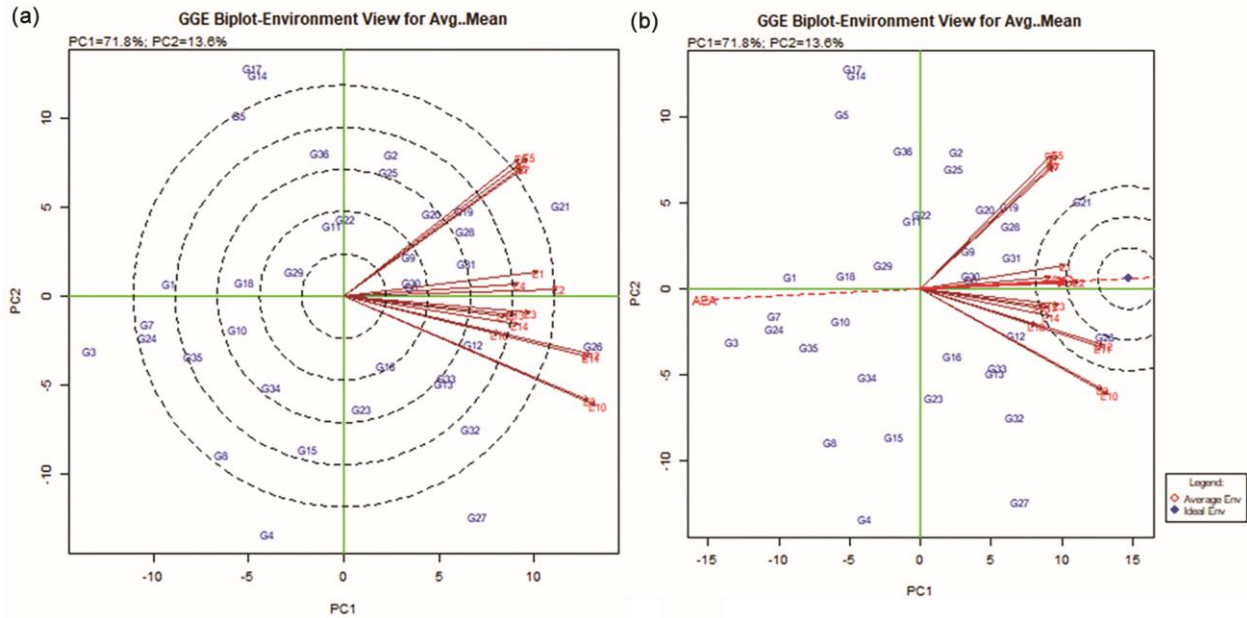


Fig. 2 — The environment view of GGE biplot. (a) Similarities among test environments in discriminating the genotypes; (b) Discrimination and representativeness view of the GGE biplot to show the discriminating ability and representativeness the test environments.

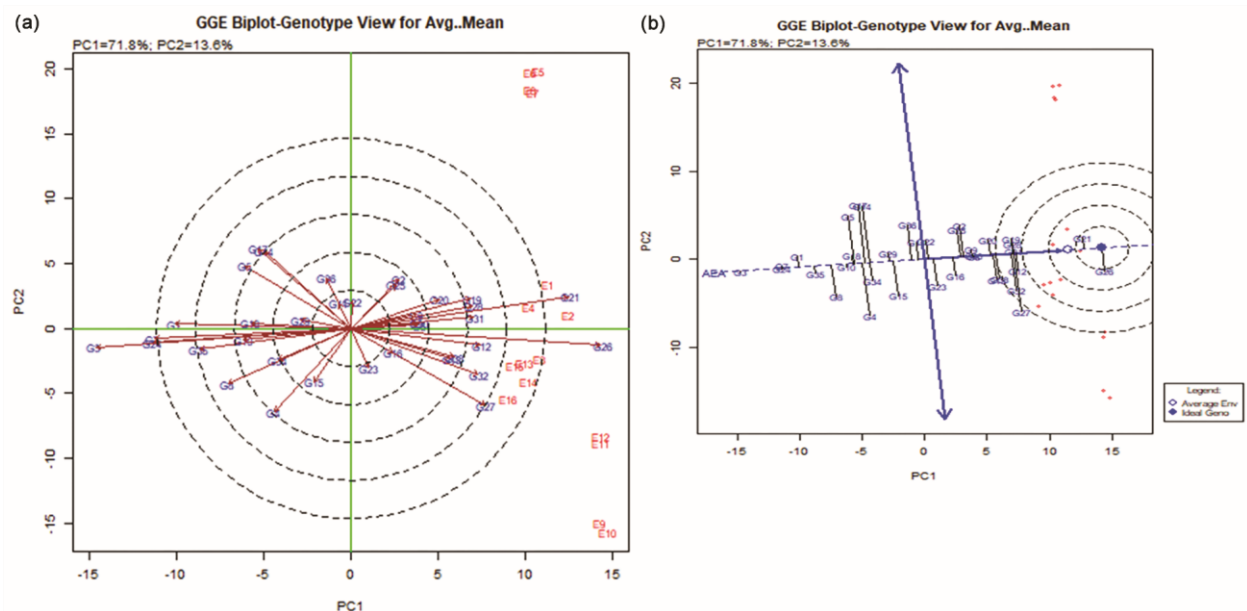


Fig. 3 — The genotype view of GGE biplot. (a) Ranking of genotypes based on the performance across the environments; (b) The average-environment coordination (AEC) view to rank genotypes relative to ideal genotypes.

closer to ideal genotype and therefore most desirable than other screened genotypes. (Fig. 3b). On other hand, the poor performing genotypes G3, G1, G7 and G24 were treated as abominable because they are located distantly from the Ideal genotype. Similarly, genotypes with short vector length are more stable and with longer vector length are least stable. Thus, the genotypes G4, G14 and G27 were least stable, whereas genotypes G1, G9, G10 and G21 were most stable genotypes. The stable genotype is desirable only when it is correlated with high mean yield. In this case G21 was observed as high yielding and stable genotype (Fig. 3b).

Polygon view of GGE biplot analysis of multi-environment trial data

Genotypic evaluation based on GGE biplot which-won-where pattern presents the individual genotypic adaptation to a specific environment (Fig. 4). Polygon is drawn on distantly located genotypes from the biplot origin in such a way that other genotypes were comes under the polygon. To each side of the polygon, perpendicular lines were drawn, starting from the biplot origin. There were five rays in Fig. 4 which divide the biplot into five sectors. The genotypes came into all five sectors, but all the tested environments fell into one sector. The vertex genotype in each sector represented the highest yielding genotype in the environment that fell within that particular sector. The genotypes G21, G26, G27,

G3, G4, G14 and G17 were the vertex genotypes. The genotypes, G2, G6, G9, G12, G13, G19, G20, G25, G28, G30, G31, G32, G33 fell into sector 1 with G21 and G26 were the vertex genotypes suggesting the high yielding genotypes for these 16 environments (Fig. 4).

Discussion

To improve rice most of the rice breeding programs are focused on the identification of novel genes from wild relatives of rice to improve the productivity of existing genotypes^{28,29}. But, the widespread cultivation of rice over different ecologies and increasing climatic variability demand the identification and cultivation of adaptable and stable genotypes^{30,31}. Keeping in the view, the present study was conducted to identify the stable and adaptable genotype for grain yield. In the absence of genotype to environment interaction, mean grain yield over the environment is generally used as a selection criterion to measure the genotypic performance³². In the present study, two multivariate approaches AMMI and GGE have been used. AMMI was observed as powerful technique to measure the genotype and environment interaction and to find stable and adaptable genotypes³³.

Similarly, GGE (Genotype plus genotype and environment interaction) is also a powerful tool to determine the genotypic stability for multi-environment trials. GGE biplot divides the $G + G \times E$ into principal components through singular value decomposition of environmentally centered yield²⁴. Many studies have used AMMI and GGE biplot technique for genotype evaluation, meg-environment evaluation and the identification of adaptable and stable genotypes in rice^{34,35}. To identify rice genotypes with broader adaptation, it is necessary to study the magnitude and pattern of GE interaction. Significant differences were observed for genotypes, environments and G and E interaction which suggest the effect of settings in the G and E interaction, genetic variability among the genotypes and possible scope for the selection for stable genotypes. In our work the ANOVA represented the percent contribution of environment (50.97%), genotype (34.35%) and genotype and environment interaction (14.68%) effects on phenotypic expression of grain yield. Grain yield was mainly contributed by the environment which suggested that the environments were divergent with significant differences among the environmental means. AMMI and GGE biplot

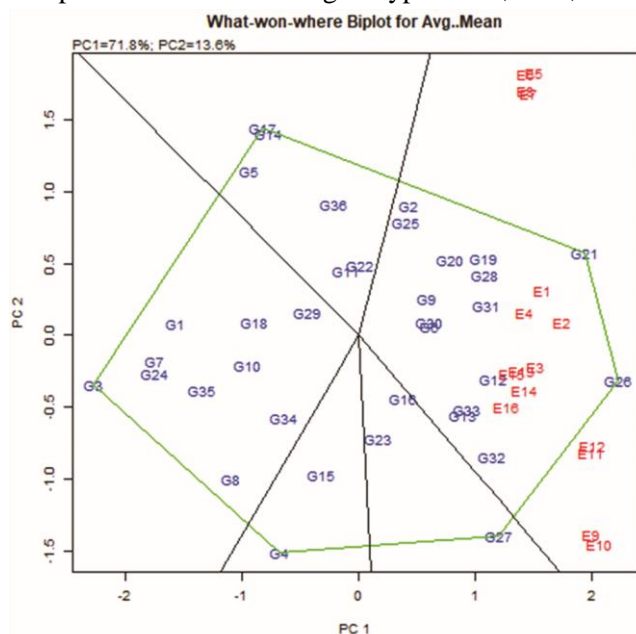


Fig. 4 — Polygon view of genotype- environment interaction across sixteen test environments.

technique was successfully used in rice for the evaluation of stability adaptability for grain yield by Sandhu *et al.*³⁶, Kumar *et al.*³⁷ and Jain *et al.*³³. In comparison to present study, Sharifi *et al.*³⁸ suggested that environment, genotype and genotype and environment interactions accounted for 29%, 30% and 41% of the total sum of squares of rice grain yield, respectively.

An ideal genotype is one having high mean yield and stable across the environment²². “Ideal” genotype is adjacent to the direction of the mean climate and its projection on AEC ordinate is near zero³⁹. A genotype near to ideal genotype is more favorable than that is far away⁴⁰. G21, G1, G9 and G10 were identified as stable genotypes. But stable genotype with high mean yield is considered to be desirable. In the present study, Genotype G21 was identified as high yielding and stable genotype. Comparable findings were also recorded by Jain *et al.*³³ described Basmati 370 as the most stable genotype for biological yield and Taraori Basmati for test grain weight. In the graphical analysis, the first PCA represents the genotype productivity and second PCA represents genotype stability. Thus an ideal genotype had a high PCA 1 value (high productivity) and near to zero PCA 2 value (more stable)²⁴. Based on the distance between any two environmental vector five groups were formed for sixteen environments, group 1 (E5, E6, E7 and E8); group 2 (E1, E2, E4); group 3 (E3, E13, E14, E15), group 4 (E11, E12, E16) and group 5 (E9, E10). The test environment should be both discriminating of the genotypes (have large PCA 1 score) and representative of mega environment (small PCA 2 score)⁴¹. E5 and E10 were the most discriminating and suitable for the selection of specially adapted genotypes and miserable for selection of genotypes for general adaptation and similar results were also reported by^{33,42}.

Grain yield, the end product of many processes of plants is highly influenced by the environmental conditions. Polygon outlook of a biplot is the best approach to visualise the genotypes and environments interaction patterns and to adequately interpret a biplot. Which-won-where pattern of multi-environment trials data is essential for examining the probable presence of contrasting mega-environments in a region^{40,43}. A mega-environment is a growing site with similar conditions that cause the almost identical performance of some genotypes⁴⁴. In the which-won-where view of the GGE biplot, the six environments

were divided into three sectors with different winning cultivars. Specifically, G21 and G26 were the highest yielding genotypes in most of the genotypes. Balakrishnan *et al.*⁴⁵ also studied G x E interaction of yield traits in introgression lines derived from *Oryza sativa* cv. Swarna/*Oryza nivara* and identified G3, G4 and G12 as specific adaptable genotypes for irrigated environment.

Conflict of Interests

Authors declare no conflict of interest

Author Contributions

Supervision by K R, R M, R K and P K; Data analysis by H K, P K, D K; Final draft, correction and writing by H K and P K

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