Original Research Article

Genotype by Environment Interaction of Grain Quality Traits of Basmati Rice

Aparajita Dwivedi[1*], Bharat Taindu Jain[2] and Ashok Kumar Sarial[1]

[1]Department of Genetics and Plant Breeding, College of Agriculture, CSK Himachal Pradesh Agricultural University, Palampur-176062 (H.P.), India
[2]CCS Haryana Agriculture University, Hisar-125004, Haryana, India

*Corresponding author

A B S T R A C T

Keywords

AMMI Model, Eberhart-Russell model, G × E interaction, Interaction, Stable

A set of thirty rice genotypes including basmati and non-basmati rice collected from Rice and Wheat Research centre (RWRC), Malan were evaluated at five different locations of Himachal Pradesh during *Kharif*-2017. The objective of this study was to examine the influence of G × E interaction on grain quality traits of basmati and non-basmati rice genotypes through Eberhart-Russell model and AMMI model. Results of the trial revealed that grain quality were influenced by environmental factors. All the basmati genotypes showed higher kernel length and kernel LB ratio than non-basmati regardless of the location. However kernel breadth was more affected by the interaction effect. Pusa-1121, a highly exported basmati rice of the country, recorded the highest mean kernel length, kernel LB ratio and found stable across the locations, followed by Lakhamandal. Other stable genotypes were PB-1509, HPR2858, HPR 2863, HPR 2667, HPR 2693, HPR 2861, HPR 2852, HPR 2855, HPR 2747, HPR 2862 HPR 2761 and HPR 2864. AMMI biplot analysis for kernel length (mm) and kernel LB ratio depicted that the relative variability due to genotypes was more than due environments. Dhaulakuan and Malan locations were categorised as favourable environment. The specific adaptation was observed for genotype Vasumati in Palampur; HPR 2863 in Una; HPR 2858 in Malan and Basmati-370 in Dhaulakuan.

Introduction

India is one of the top exporters of rice, both basmati and non-basmati rice, and the annual Indian rice exports hover around 10-13 million MT. During the year 2018-19, India exported 11.9 million MT of rice, out of which Basmati rice exports accounted for 4.4 million MT while non-basmati rice exports were 7.5 million MT (Anonymous 2019). Basmati rice is an unique product of Indo-Gangetic planes which is responsible for its distinctive quality traits and characteristic aroma. Basmati rice shares 30-40% of rice exports to almost 132 countries every year. India is largest rice growing country in the world, however, its productivity per unit area is low. Himachal Pradesh is one among other states which has got GI for basmati rice. Total Basmati paddy acreages during kharif 2019 are estimated at 19.39 lakh ha within a limited geographic region comprising parts of Punjab, Haryana, West Uttar Pradesh, Uttarakhand, Delhi, two districts of Jammu & Kashmir (Jammu and Kathua) and to a

limited extent in Himachal Pradesh. Haryana is a leading state in basmati cultivation with an area of 6.33 lakh ha and production of 25.02 lakh tones followed by Punjab having an area of 5.46 lakh ha and production of 21.02 thousand tones. Himachal Pradesh occupies an area of 7.1 thousand ha with a production 29.8 thousand tonnes (Anonymous, 2019). The basmati cultivation in Himachal Pradesh is only confined to areas below 1000 m altitude while in the area above 1000 m altitude, grain yield is low due to late maturity coupled with unripening of grains. The prevailing low temperature conditions in the mid hill zone are expected to be suitable for accumulation of stronger aroma in the basmati rice compared to lower altitudes. Genotypes with wide adaptability as well as good grain quality, which can perform consistently well over a range of environments is required. A stable genotype is the one giving consistent performance irrespective of any changes in environmental conditions (Becker and Leon 1988). Stability which refers to consistent performance under diverse environment while failure to performance consistently is Genotype × Environment Interaction (GEI). A number of stability analyses models are used to determine the contribution of G × E interaction (GEI) as well to identify genotypes which perform superior under several environments (Genard 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); Eberhart and Russell (1966) are based on two parameter regression coefficient and deviation from regression. 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).

Materials and Methods

A set of thirty rice genotypes (Table 1) including basmati and non-basmati rice collected from Rice and Wheat Research centre (RWRC), Malan were evaluated at five different locations (Table 2) namely Dhaulakuan (E1), Una (E2), Palampur (E3), Malan (E4) and Sundernagar (E5) during *Kharif* 2017 June-October. The randomized block design (RBD) was laid out with three replications. The 25 days old seedlings were transplanted, with single seedling per hill in all the field trials. The plot size consisted of three rows of 15 plants each with a spacing of 15 x 20 cm. Observations were recorded on five randomly selected plants in each plot for grain quality traits. Analysis of variance (ANOVA) was computed for the individual environment and significance of the trait was tested against the error sum of squares. The performance of genotypes was tested over locations using stability models viz, (1) Eberhart and Russel (1966), (2) Additive Main effects and Multiplicative Interaction (AMMI) (Gauch 1988). Data for quality traits were analyzed using Pbtool software.

Results and Discussions

Analysis of variance (ANOVA)

Analysis of variance (ANOVA) for the individual environment indicated the significance of the trait across all the locations indicated the variability present amongst genotypes. The perusal of the analysis (Table 3) as per Eberhart and Russel model (1966) showed that the variance due to genotypes was significant for kernel length, kernel breadth and kernel length-breadth ratio. This indicated that there is difference amongst genotypes for the kernel traits irrsespective of the location. Similar results for the kernel traits reported by Jain et al., (2019). Interaction component was found to

be highly significant for kernel traits indicating that the environment had influenced the trait to a considerate level. In a similar study, Dwivedi *et al.,* (2020) found that interaction was significant for grain yield in basmati rice which indicated the effect of this component on the yield of the rice. Variance due to environments was significant ($p < 0.05$) for all characters except kernel length-breadth ratio. The mean sum of squares due to GE interaction and combined environment and GE interaction component of variance when tested against pooled error was significant for kernel length, kernel breadth, and kernel length-breadth ratio indicated that environment play significant role influencing the trait.

Further, partitioning of combined environment and genotype x environment variance into linear and non-linear components when tested against pooled deviation showed that environment linear was highly significant for all the characters. GE (linear) was significant for the traits head rice recovery %, kernel length and kernel length-breadth ratio. However, pooled deviation (non-linear component) when tested against pooled error was significant for all the traits studied except hulling percent, milling percent and head rice recovery percent. In a similar study by Anandan et al., (2009), ANOVA across environment indicated variances due to genotypes, environments and G × E interaction was found highly significant ($P < 0.01$) for kernel length and kernel LB ratio but was non-significant for kernel breadth.

Average kernel length of genotypes ranged between 5.74 to 8.60 mm with an overall population mean of 7.24 mm. Pusa-1121 recorded highest mean kernel length (8.60 mm) followed by Lakhamandal (8.56 mm). The stability analysis revealed that two genotypes had significant regression

coefficient and five had significant deviation from regression. Genotype Vasumati had $b_i < 1$ and $S^{-2}di = 0$, mean kernel length greater than population mean, was below average stable, Basmati-370 was unpredictable. Fourteen genotypes were found to have $b_i = 1$ and $S^{-2}d_i = 0$ and mean greater than population mean i.e., Pusa-1121, Lakhamandal, PB-1509, HPR2858, HPR 2863, HPR 2667, HPR 2693, HPR 2861, HPR 2852, HPR 2855, HPR 2747, HPR 2862 HPR 2761 and HPR 2864. Likewise average kernel breadth of genotypes ranged between 1.61 to 1.87 mm with an overall population mean of 1.73 mm. HPR 2747 recorded minimum mean kernel breadth. The stability analysis revealed that one genotypes had significant regression coefficient (bi) and sixteen had significant deviation from regression (S^2d_i). Genotypes PR-121 had both linear and non-linear component significant and hence, unpredictable. Fourteen genotypes were found to have $b_i = 1$ and $S^{-2}d_i = 0$, of these 14, 10 genotypes i.e., PB-1509, HPR 2749, HPR 2746, HPR 2863, HPR 2852, HPR 2763, HPR 2855, Kasturi, HPR 2747 and HPR 2761 also had mean kernel breadth less than population mean. Genotype Vasumati, Basmati-370, HPR 2612 and HPR 2720 had mean kernel breadth greater than population mean. Finally average kernel length-breadth ratio of genotypes ranged between 3.22 to 5.22 with an overall population mean of 4.22. Genotype HPR 2720 recorded minimum mean kernel length-breadth ratio (3.22) while Pusa-1121 (5.22) recorded the maximum. Two genotypes had significant regression coefficient (b_i) and two had significant deviation from regression (S^2d_i). Thirteen genotypes Pusa-1121, Lakhamandal, PR-121, PB-1509, HPR 2749. HPR 2863, HPR 2667, HPR 2861, HPR 2747, HPR 2852, HPR 2761, HPR 2692 and HPR 2855 showed higher kernel length-breadth ratio.

AMMI analysis

Total mean sum of squares was attributed to different sources in varying proportion e.g. environmental effects genotypic and GE interaction effects (Table 4). Contribution of genotype to total sum of squares was very large in case of kernel length and kernel length-breadth ratio, this indicated that genotypes differed among themselves for these traits. Analysis revealed that environments were not diverse for this trait but genotypes were the major source of variation occurred for this trait. This distinctively implied that Basmati and non basmati genotypes differed among themselves irrespective of the environments. Kernel breadth revealed large G×E interaction mean sum of squares indicated that differences among the genotypes were substantial across the environments while moderate genotype mean sum of squares indicated that genotypes also differed among themselves.

AMMI 1 and AMMI 2 biplot analysis for kernel length (mm) depicted that the relative variability due to genotypes was more than the variability due environments as indicated by the distribution as well as position occupied by the thirty genotypes and five environments on biplot display (Fig.1a). On contrary, Singh et al., (1998) reported that, length of kernels were influenced by the field in which crop was grown. Genotypes or environments on right hand side of the mean line showed higher kernel length than those on the left hand side. Genotype Vasumati, HPR 2693 and HPR 2864 had high mean kernel length and positive IPCA score; HPR 2862, HPR 2852, HPR 2761, HPR 2855, HPR 2861, Basmati-370, HPR 2667, PR-121 and HPR 2863 had high mean and negative IPCA score; HPR 2746, Kasturi, HPR 2323, HPR 2763 and Hasansarai had low mean and positive IPCA scores; HPR 2795, HPR 2612, Sharbati and HPR 2749 had low mean and

negative IPCA score. Long kernels are desired attributes of basmati genotypes. Genotype HPR 2692, PB-1509, Lakhamandal, Pusa-1121, HPR 2747 had IPCA score approaching to zero, hence showed wide adaptability for this trait. Vasumati and HPR 2858 had high IPCA score, hence were unstable and showed specific adaptation. The environments as depicted in the biplot were not variable as they are falling almost on a perpendicular line. Dhaulakuan (E1) and Malan (E4) were categorised as favourable environment while Palampur (E3), Sundernagar (E5) and Una (E2) were unfavourable environment. Genotypes with high mean and negative interaction were best adapted to Dhaulakuan and Malan (favourable environment). The AMMI2 biplot was generated using genotypes and environments scores of the first two IPCA and presented as Fig. 1b to demonstrate the relative magnitude of the G × E for specific genotypes and environments. In this biplot, the environmental scores were joined to the origin by side lines. Sites with short spokes did not exert strong interactive forces. Those with long spokes exerted strong interaction. The environment Una (E2) and Sundernagar (E5) had short spoke and they did not exert strong interactive force while environment Dhaulakuan (E1), Palampur (E3) and Malan (E4) having long spoke exerted strong interaction. Genotypes Pusa-1121, PB-1509, HPR 2852, HPR 2612 and HPR 2880 were near the origin hence non-sensitive to environmental interactive forces and therefore showed wide stability whereas genotypes which fell away from the origin showed specific adaptation viz., HPR 2858, Basmati-370, Kasturi and HPR 2746. Basmati-370 was specifically adapted to Dhaulakuan; Vasumati to Palampur; HPR 2864, HPR 2763 to Sundernagar; HPR 2852 to Malan and HPR 2863 to Una. Dhaulakuan and Malan were favourable location for kernel length.

AMMI1 (Fig. 2a) and AMMI 2 (Fig. 2b) biplot analysis for kernel breadth depicted that genotype T-23, HPR 2720 and HPR 2880 had high mean and their IPCA1 score was near zero, so considered stable for kernel breadth. Genotype PB-1509, Sharbati and HPR 2763 had low mean kernel breadth and their IPCA1 score was near zero, so considered stable for kernel breadth and desirable. The environment Una (E2) and Sundernagar (E5) had high positive interaction while Dhaulakuan (E1), Palampur (E3) and Malan (E4) had high negative interaction. For kernel breadth Sundernagar and Palampur were favourable as they fell on the left side of mean axis but also unstable due to large IPCA1 score. Malan (E4) was the less interactive environment. Dhaulakuan (E1) and Una (E2) fell on right side and hence unfavourable because less kernel breadth is the desirable attribute of basmati rice. Genotype HPR 2667 and HPR 2858 were best adapted in Una (E2), Basmati-370 at Dhaulakuan (E1); PR-121 and HPR 2323 in Palampur; and PR-121 and Lakhamandal in Sundernagar. Malan (E4) was stable location among all. Xia et al., (2014) reported significant difference for kernel length and breadth over locations.

Similarly, for kernel length-breadth ratio also the relative variability due to genotypes was more than the variability due environments. Genotypes Basmati-370, HPR 2863, HPR 2747, HPR 2749 and HPR 2861 had high mean and positive IPCA score. HPR 2862, HPR 2855, PB-1509, HPR 2692, HOR 2667, HPR 2761 and Lakhamandal had high mean and negative IPCA score. Genotype HPR 2720, HPR 2880, HPR 2612, T-23, HPR 2746, Basmati-370 and Kasturi had low mean and positive interaction while HPR 2795, Sharbati, Hasanasarai, HPR 2693, HPR 2864, HPR 2763 and Vasumati had low mean and negative interaction. More kernel length-breadth ratio is desirable attribute of basmati genotypes. Genotype HPR 2852, HPR 2761,

HPR 2749 and Pusa-1121 showed wide adaptability for the trait, of these Pusa-1121 was the stable most. Non-basmati genotypes were on the left-hand side of the mean showed less kernel length-breadth ratio than basmati. Basmati-370 and Vasumati had high positive and negative IPCA score so were unstable and specifically adapted in Dhaulakuan and Sundernagar, respectively. The environments were not diverse for this trait as depicted by their position on the biplot. Una (E2) and Malan (E4) were less interacting environment. Dhaulakuan (E1) and Sundernagar (E5) were favourable environment. Vasumati, Lakhamandal, PR-121, HPR 2855 and Basmati-370 were unstable and had specific adaptation. Lakhamandal and Vasumati were adapted to Palampur; Basmati-370 at Dhaulakuan (E1); Pusa-1121, HPR 2692 and HPR 2855to Una; HPR 2747, HPR 2852 and HPR 2612 to Malan and PR-121 to Sundernagar. Genotype HPR 2855, HPR 2747, HPR 2693, Pusa-1121, PR-121, HPR 2763, HPR 2864, Vasumati, Lakhamandal, Kasturi, Basmati-370, HPR 2747 were unstable due to their position away from the origin. Rest genotypes were stable i.e., HPR 2323, HPR 2749, Hasansarai, HPR 2667, PB-1509, Sharbati, T-23, HPR 2746, HPR 2852, HPR 2693, HPR 2862 and HPR 2858. The environment Dhaulakuan and Sundernagar were categorized as favourable.

AMMI model helps us in identifying the average as well as specific adaptation of the genotypes which is not the feature in earlier model. So rather than forcing a genotype to perform well in a particular environment we can identify its suitable environment to obtain its maximum performance (Dwivedi et al, 2020). Kernel trait is an important parameter of basmati rice and pertaining to this trait, in this study we have found the genotypes which is stable across locations and also specific adaptation of certain genotypes (Fig. 3 and Table 1–4).

Table.1 List of genotypes

Basmati

1	Pusa-1121	11	HPR 2692	21	HPR 2667
2	Hasansarai	12	HPR 2693	22	HPR 2861
3	Vasumati	13	HPR2746	23	HPR 2862
4	Lakhamandal	14	HPR 2747	24	HPR 2863
5	Basmati-370	15	HPR 2749	25	HPR 2864
6	PB-1509	16	HPR 2761	**Non-basmati**	
7	T-23	17	HPR 2763	26	Sharbati
8	Kasturi	18	HPR 2852	27	PR-121
9	HPR 2612	19	HPR 2855	28	HPR 2880
10	HPR 2323	20	HPR 2858	29	HPR 2795
				30	HPR 2720

Table.2 List of environments (Different locations)

| Location	Description
E1	Hill Agricultural Research and Extension Centre (HAREC), Dhaulakuan, (30°04′ N and 75°05′E & 468 m amsl)
E2	Krishi Vigyan Kendra (KVK), Una, (31°28′6.4″N &76°16′14.79″E and 369 m amsl)
E3	Chaudhary Sarwan Kumar Himachal Pradesh Krishi Vishvavidyalaya (CSKHPKV), Palampur (32°80′ N & 76°33′ E and 1290.8 m amsl)
E4	Rice and Wheat Research Centre (RWRC), Malan, ($32^01′$N &$76^01′$E and 950 m amsl)
E5	Krishi Vigyan Kendra (KVK), Sundernagar, (22.7739° N & 71.6673° E and 861 m amsl)

Table.3 Pooled analysis of variance over 5 environments for different traits in rice (Eberhart and Russell, 1966 model)

Source	DF	Hulling %	Milling (%)	Head rice recovery (%)	Kernel Length(mm)	Kernel Breadth (mm)	Kernel LB Ratio
Genotype (G)	29	14.48	15.55	23.92	2.14**	0.02**	1.10**
Environment (E)	4	76.36**	77.64**	101.04**	1.003**	0.03**	0.056
G × E	116	13.08	15.21	18.12	0.16**	0.008**	0.098**
E + G × E	120	15.19	17.29	20.89	0.19**	0.009**	0.097**
E (Linear)	1	305.45**	310.55**	404.13**	4.01**	0.15**	0.224*
G × E (L)	29	17.14	13.63	26.71*	0.22**	0.01	0.083**
Pooled Deviation	90	11.33	15.22	14.75	0.14**	0.007**	0.099**
Pooled Error	290	14.69	16.91	18.19	0.03	0.002	0.027

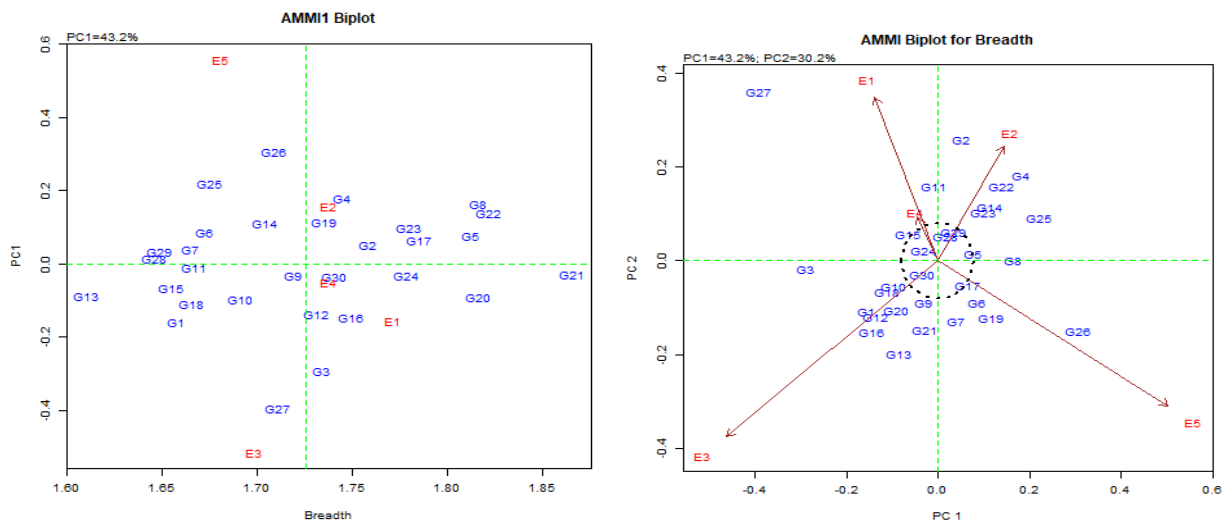**Table.4** AMMI analysis for grain quality traits in rice across different environments

Source	DF	Kernel-length (mm)		Kernel-breadth (mm)		Kernel-LB Ratio	
		MSS	% explained	MSS	% explained	MSS	% explained
Trials	149	0.57		0.011		0.29	
Genotypes	29	2.14**	73.22	0.020**	35.69	1.102**	73.38
Environments	4	1.003**	4.73	0.039**	9.29	0.056	0.51
G x E interaction	116	0.161**	22.03	0.008**	55.00	0.098**	26.10
PCA 1	32	0.229**	39.5	0.012**	43.20	0.131**	37
PCA II	30	0.204**	32.9	0.009	30.21	0.131**	34.7
PCA III	28	0.116**	17.5	0.004	14.25	0.071	17.6
Residual	26	0.073	10.2	0.004	12.33	0.05	10.7

Fig.1a AMMI biplot of kernel length main effects and G×E interaction of rice genotypes in five environments; **Fig.1b** AMMI-2 biplot for kernel length showing IPCA scores of rice genotype (G) plotted across Environment (E)
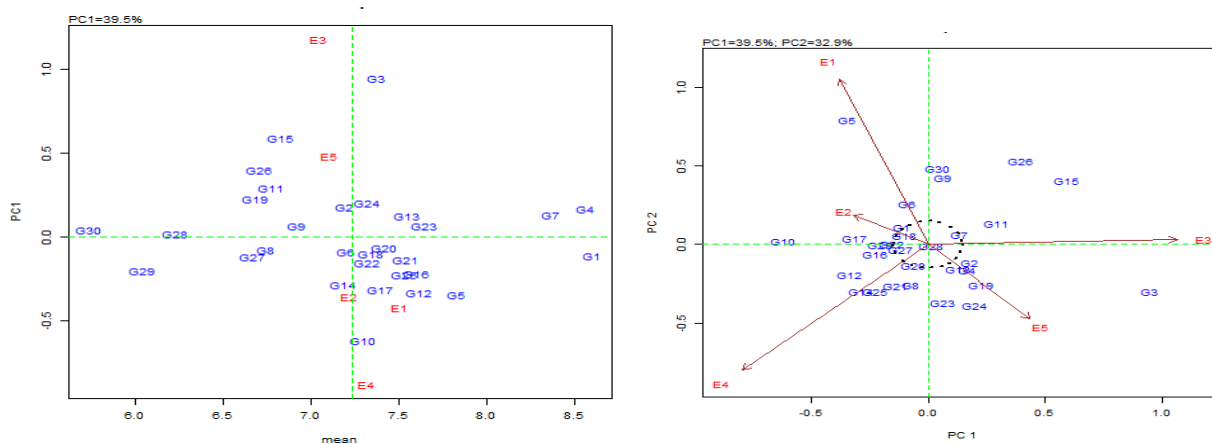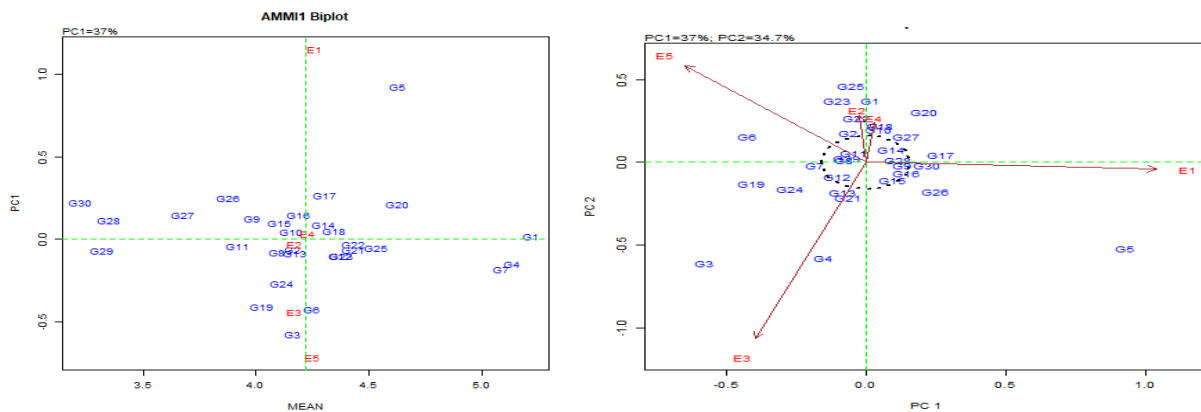

Legend 1:Pusa Basmati 1121, 2:Hasansarai, 3:Vasumati, 4:Lakhamandal, 5:Basmati-370, 6:PR-121, 7:PB-1509, 8: Sharbati, 9:T-23, 10:HPR 2858, 11:HPR 2323, 12:HPR 2667, 13:HPR 2693, 14:HPR 2749, 15:HPR 2746, 16: HPR 2861, 17: HPR2863, 18:HPR 2852, 19:HPR 2763, 20:HPR2747, 21: HPR2862, 22:HPR 2761, 23: HPR2692, 24: HPR2864, 25: HPR2855, 26: Kasturi, 27: HPR 2612, 28: HPR2880, 29: HPR2795, 30: HPR 2720, E1:Dhaulakuan E2:Una, E3:Palampur, E4: Malan, E5: Sundernagar

Fig.2a AMMI biplot of Kernel breadth main effects and G x E interaction of rice genotypes in five environments; **Fig.2b** AMMI-2 biplot for Kernel breadth showing IPCA scores of rice genotype (G) ploted across Environment (E)

Legend 1: Pusa Basmati 1121, 2:HPR 2858, 3:HPR 2323, 4: HPR 2667, 5.HPR 2693, 6: HPR 2749, 7: HPR 2746, 8:HPR 2861, 9: HPR 2863, 10: HPR 2852, 11: HPR 2763, 12: Hasansarai, 13:HPR 2747, 14: HPR 2862, 15: HPR 2761, 16: HPR 2692, 17: HPR 2864, 18: HPR2855, 19: Kasturi, 20: HPR 2612, 21: HPR 2880, 22: HPR 2795, 23: Vasumati, 24: HPR 2720, 25: Lakhamandal, 26: Basmati-370, 27:PR-121, 28: PB-1509, 29: Sharbati, 30: T-23; E1:Dhaulakuan E2:Una, E3:Palampur, E4: Malan, E5: Sundernagar

Fig.3a AMMI biplot of Kernel length-breadth ratio main effects and G x E interaction of rice genotypes in five environments; **Fig.3b** AMMI-2 biplot for Kernel length-breadth ratio showing IPCA scores of rice genotype (G) ploted across Environment (E)

Legend 1:Pusa Basmati 1121, 2:Hasansarai, 3:Vasumati, 4:Lakhamandal, 5:Basmati-370, 6:PR-121, 7:PB-1509, 8: Sharbati, 9:T-23, 10:HPR 2858, 11:HPR 2323, 12:HPR 2667, 13:HPR 2693, 14:HPR 2749, 15:HPR 2746, 16: HPR 2861, 17: HPR2863, 18:HPR 2852, 19:HPR 2763, 20:HPR2747, 21: HPR2862, 22:HPR 2761, 23: HPR2692, 24: HPR2864, 25: HPR2855, 26: Kasturi, 27: HPR 2612, 28: HPR2880, 29: HPR2795, 30: HPR 2720, E1:Dhaulakuan E2:Una, E3:Palampur, E4: Malan, E5: Sundernagar

437

References

Anandan, A., Sabesan, T., Eswaran, R., Rajiv, G., Muthalagan, N. and Suresh, R. (2009). Appraisal of Environmental Interaction on Quality Traits of Rice by Additive Main Effects and Multiplicative Interaction Analysis. Cereal Research Communications 37(1): 131–140.

Anonymous. 2019. Agricultural and Processed Food Products Export Development Authority of India (APEDA) *http://www.apeda.gov.in*

Becker, H.C., Leon, J. 1988. Stability analysis in plant breeding. Plant Breeding 101: 1-23.

Bernardo, R. 2002. Quantitative Traits in Plants. – Stemma Press, Bowsens Lanne, Woodbury, MN.

Dwivedi, A., Basandrai, D and Sarial, AK. 2020. AMMI biplot analysis for grain yield of of basmati lines (*Oryza sativa* L.) in North Western Himalayan Hill regions. Indian Journal of genetics and plant breeding. 80(2): 140-146.

Eberhart, S.A., Russell, W.A. 1966. Stability parameters for comparing varieties. – Crop Science 6: 36-40.

Gauch, H.G. 1988. Model selection and validation for yield trials with interaction. – Biometrics 44: 705-715.

Gauch, H.G. 1992. Statistical analysis of regional yield trials: AMMI analysis of factorial designs. – Elsevier Amsterdam, The Netherlands: 53-110.

Genard, M., Lescourret, F., Bevacqua, D., Boivin, T. 2017. Genotype-by-environment interactions emerge from simple assemblages of mathematical functions in ecological models. Frontiers in Ecology and Evolution https://doi.org/10.3389/fevo.2017.00013.

Jain, BT., Sarial, AK., and Kaushik, P. 2019. Understanding G × E interaction of elite basmati rice (*Oryza sativa* L.) genotypes under north Indian conditions using stability models. Applied Ecology and Environmental Research 17(3): 5863-5885.

Malosetti, M., Ribaut, JM., Van Eeuwijk, FA. 2013. The statistical analysis of multienvironment data: modeling genotype-by-environment interaction and its genetic basis. Frontiers in Physiology. https://doi.org/10.3389/fphys.2013.00044

Singh, RK., Singh, US., Khush, GS. 1998. Ind ian indigenous aromatic rices. Indian Farming 21: 1–6.

Xia, Y., Zhang, J., Fan, M., Liu, C., Yang, L., Li, M., Jiang, Y. and Xu, Z. 2014. Effect of environment on yield and quality of rice recombinant inbred lines. *Advanced Materials Research* 1010-1012: 33-37.