



# AMMI biplot analysis for grain yield of basmati lines (*Oryza sativa* L.) in North Western Himalayan Hill regions

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## Abstract

Thirty basmati and non-basmati rice genotypes were evaluated in five different locations representing varied agroclimatic zones in Himachal Pradesh during *kharif* 2017 and 2018 for stability of grain yield. Additive main effect and multiplicative interaction and stability model were employed to study the G×E interaction. ANOVA revealed significant differences among genotypes and locations along with significant G × E interaction. Both linear and non-linear components contributed towards G × E interaction. The mean grain yield per plant varied from 11.32-19.49 g among the genotypes with the general mean of 15.83g. Genotype HPR 2693 was identified to have higher mean grain yield per plant than general mean and was stable across the locations. AMMI analysis revealed that the first two significant IPCA scores together explained 77.18% of the total interaction variance. Biplot graphical analysis showed Dhaulakuan to be the less interacting and stable location. Genotype HPR 2693 scored zero for both IPCA1, IPCA2 and also lowest ASV score along with higher average grain yield per plant and therefore could be considered as stable across locations. Pusa-1121, one of the highly prized basmati was also found stable but the average yield per plant over all the location was low and hence could be identified for specific location. Genotypes HPR 2863, HPR 2612, HPR 2667, PB-1509, HPR 2858 showed specific adaptation to Malan while HPR 2761, HPR 2749, HPR 2746, HPR 2720, HPR 2862 and HPR 2880 exhibited specific adaptation at Palampur. These genotypes could be utilized for direct cultivation as well as for improvements of other cultivars.

**Key words:** G × E interaction, adaptability, stability, rice, AMMI analysis

## Introduction

India is the second largest rice-growing country in the world, however, the productivity is low. Rice is cultivated on about 43.99 m ha with a production of 116.42 m.t. (Anonymous 2018). Himachal Pradesh

(HP) occupies an area of 73.69 thousand hectares with production of 129.88 thousand tonnes and productivity 1.76 t/ha (Anonymous 2016). Basmati rice occupies an area of 7000 ha with a production of 30,000 tonnes and productivity of 4.29 t/ha in Himachal Pradesh (Anonymous 2017). India is endowed with a huge varietal diversity of rice spread across diverse growing ecologies and the Indo-Gangetic region holds a distinction of being home to the highly prized Basmati rice. Basmati rice has incredible grain with good cooking quality, pleasant aroma, excellent taste etc. Himachal Pradesh along with six other states of Punjab, Haryana, Delhi, Jammu & Kashmir, Uttar Pradesh and Uttarakhand has been granted Geographical Indication for basmati. However, cultivation in the state is confined to low and mid-hills areas below 1000 m altitude. The traditional varieties are tall, prone to lodging, photo-thermo sensitive and low yielding. In areas above 1000 m altitude, grain yield of traditional basmati varieties is low due to late maturity coupled with unripening of grains. There is need to develop/identify genotypes/varieties having high grain yield and consistent performance over all locations.

Multi-location testing of genotypes provides an opportunity to the plant breeders to identify the adaptability of a genotype to a particular environment and also stability of the genotype over different environments. Stability in grain yield is one of the most desirable traits of a genotype to be released as a variety for commercial cultivation. The developed varieties are wished to adapt to a wide range of target environments. Hence, pattern of response of genotypes is studied by the plant breeders for testing genotypes in different environments to assess the genotype x environment (G × E) interaction. For precise

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identification of high yielding genotype(s), both yield and stability must be considered simultaneously (Sara et al. 2019). To estimate the level of interaction of genotypes to environments and to eliminate as much as possible the unexplainable and extraneous variability contained in the data, several statistical techniques have been developed to describe G x E interaction and measure the stability of genotypes. Detailed study on current statistics used to test and measure genotype stability has given by Lin et al. (1986), Piepho (1999) and Laxmi and Gupta (2000). Since, G x E interaction is naturally multivariate, the Additive Main effects and Multiplicative Interaction (AMMI) model offers appropriate statistical analysis of the G x E interaction. The AMMI method presents information on main and interaction effects in addition to a biplot and is specifically efficient for illustrating adaptive responses (Annicchiarico 1997). It is suggested as a replacement to the joint regression analysis for most of the breeding programmes. AMMI interaction analysis is referred to as double centered principal component analysis. The AMMI model combines ANOVA for the genotype and environment main effects with principal components analysis of GEI (Zobel et al. 1988; Gauch and Zobel, 1996). The biplot analysis of G x E interaction depicts the best way for visualizing the interaction patterns between genotypes and environments and to determine the possible existence of different environment groups in a region where a set of genotypes are grown. Stability analysis helps the researcher to understand the crop as an integrated system with interconnected components, and also helps reveal the trait profiles of the genotypes, which are important for identifying superior cultivars and parents.

Keeping the above in view, the present study was under taken to assess the extent of G x E interaction and to select the stable genotypes for grain yield of rice over and across the locations of HP.

### Materials and methods

The materials comprised of thirty rice genotypes including advanced breeding lines (ABL) of basmati and aromatic rice collected from Rice and Wheat Research centre (RWRC), Malan (Table 1). Field trials were conducted over five locations namely, Dhaulakuan (E1), Una (E2), Palampur (E3), Malan (E4) and Sundernagar (E5) during *kharif* 2017 and *kharif* 2018 (Table 2). The experiment was laid out in randomised block design (RBD) with three replications in five environments. Seeds were sown in nursery beds, and 25 days old seedlings were transplanted

**Table 1.** List of genotypes

S.No.	Variety	Parentage/Source
<b>Basmati genotypes</b>		
1	Pusa-1121	Pusa-751-87-7-1/IR8
2	Hasansarai	Introduction from Iranian Basmati
3	Vasumati	PR 109/Pakastani Basmati
4	Lakhamandal	Selection from local basmati collections from Lakhamandal village of Dehradun
5	Basmati-370	Pure line selection from Dehraduni basmati landraces
6	PB-1509	Improved version of Pusa 1121 derived from cross Pusa1301/Pusa1121
7	T-23	Traditional basmati selection from Kala Sukhdas
8	Kasturi	Basmati 370/CR 88-17-1-5
9	HPR 2612	Hassansarai/T 23//IR 66295-36-2
<b>Basmati type advanced breeding lines (ABL)</b>		
10	HPR 2323	HPU 741x PR 72
11	HPR 2692	Hasansarai/T23//IR67011
12	HPR 2693	Hasansarai/T23//TR66295-36-2
13	HPR2746	Hasansarai/T23//IR670
14	HPR 2747	Hasansarai/T23//IR66295
15	HPR 2749	Hasansarai/T23//IR66295-36-2
16	HPR 2761	Hasansarai/Kasturi
17	HPR 2763	Hasansarai/Kasturi
18	HPR 2852	Hasansarai/T23//IR66295-36-2
19	HPR 2855	Hasansarai /T23//IR66295-36-2
20	HPR 2858	Kalizhini/HPR 2143//HPR 2143
21	HPR 2667	Palampur Purple/Kasturi
22	HPR 2861	Palampur purple/Kasturi
23	HPR 2862	Palampur Purple/Kasturi
24	HPR 2863	Palampur Purple/Kasturi
25	HPR 2864	Palampur Purple/Kasturi
<b>Non-basmati</b>		
26	Sharbati	<i>Indica</i> rice with long slender grains
27	PR-121	Non-basmati <i>indica</i> rice derived from cross PR116///PR108/IRRI76/PR106-2
28	HPR 2880	HPU 2216 /Tetep
29	HPR 2795	Pure line selection from Sukara red
30	HPR 2720	Pure line selection from IC 455333I

with single seedling per hill in all the field trials. The plot size consisted of three rows of 15 plants each with plant to plant and row to row spacing 15 and 20 cms, respectively. All recommended package of practices were followed to raise the crop in irrigated conditions. Observations were recorded on five

**Table 2.** List of environments (Different locations)

Location	Description
E1	Hill Agricultural Research and Extension Centre (HAREC), Dhaulakuan(30°042' N and 75°052' E & 468 m amsl)
E2	Krishi Vigyan Kendra (KVK), Una(31°282' 6.42 2 N & 76°162' 14.792 2 E and 369 m amsl)
E3	Chaudhary Sarwan Kumar Himachal Pradesh Krishi Vishvavidyalaya (CSKHPKV), Palampur (32°802' N & 76°332' E and 1290.8 m amsl)
E4	Rice and Wheat Research Centre (RWRC), Malan(32°12' N & 76°12' E and 950 m amsl)
E5	Krishi Vigyan Kendra (KVK), Sundernagar (22.7739° N & 71.6673° E and 861 m amsl)

randomly selected plants in each plot for grain yield per plant (GYP). 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 the genotypes were tested over locations using stability models viz., (1) Eberhart and Russel (1966), (2) Additive Main effects and Multiplicative Interaction (AMMI) (Gauch 1988). Data were subjected to statistical analysis using Windostat Version 9.2 (Indostat services, Hyderabad, India). The AMMI model was used to analyze data for G × E interaction and for classification of genotypes and environments.

## Results and discussion

### Pooled analysis of variance

The ANOVA showed that mean squares due to genotypes were highly significant for grain yield per plant (GYP) in all environments in both the years (Supplementary Table S1). The significance of genotypes mean squares indicated that genotypes differed among themselves and there existed a considerable variability irrespective of the effect of environments on the GYP. Similar results were obtained by Jain et al. 2018. The perusal of the Table 3 for analysis as per Eberhart and Russell (1966) showed that the variance due to genotypes,

environments and G×E interaction was significant. Pandya et al. (2015) also reported significant G×E interaction for grain yield per plant IPAC2.

Significant G×E interaction implied that GYP was significantly affected by the locations. Combined environment and G×E interaction component of variance when tested against pooled error was also found significant. Further, partitioning of combined environment and genotype × environment variance into linear and non-linear components when tested against pooled deviation also showed that environment linear was highly significant for all the characters while G × E (linear) was found to be non-significant. However, pooled deviation (non-linear component) when tested against pooled error was significant.

Grain yield is the most important trait in any crop. Grain yield, being a quantitative trait is highly influenced by the environment. So a breeder should identify a variety which is less influenced by environments i.e., a stable one. Stability is the consistent performance of a genotype over locations and any deviation in the performance is termed as genotype-environment interaction. Also some genotypes which perform poor in one environment may perform better in a different environment. This is known as specific adaptation. So if we could identify genotypes stable over the locations or across specific location. GYP recorded on the 5 plants basis per replication ranged from 11.32 g-19.49 g. Mean GYP for all the thirty genotypes are presented in Supplementary Table S2. Genotype HPR 2323 recorded highest grain yield per plant at Una along with highest mean grain yield per plant over locations. Sixteen genotypes out of 20 recorded more GYP than average (15.83 g) and nine out of these 16 even had more average GYP than recommended check (HPR2612). Stability analysis as per Eberhart and Russell (1966) (Table 4) for grain yield revealed that none of the genotype had significant regression coefficient and nine genotypes had non-significant deviation from regression, therefore, 21 genotypes were predictable. Seven genotypes HPR 2693, HPR 2852, HPR 2862, HPR 2692, HPR 2864, HPR 2795

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

Source	Genotype	Environment	G × E	E + G × E	E (Linear)	G × E (L)	Pooled deviation	Pooled error
DF	29	4	116	120	1	29	90	290
GYP	22.08*	358.41**	14.00**	25.71**	1,433.61**	9.25	15.37**	7.15

\* = significant at 5% level of significance, \*\* = significant at 1% level of significance

**Table 4.** Stability parameters for grain yield per plant of rice genotypes tested across five locations

Genotypes	Mean	$b_i$	$S^2_{di}$
Pusa 1121	15.49	2.13	-1.34
Hasansarai	11.96	0.39	3.03
Vasumati	18.32	0.63	24.28*
Lakhamandal	16.68	0.09	23.37*
Basmati-370	15.55	1.43	-0.44
PR-121	17.96	0.97	29.23*
PB-1509	13.39	1.54	-1.36
Sharbati	12.83	1.13	3.71
T-23	15.46	0.92	16.06
HPR 2858	14.51	1.30	1.83
HPR 2323	19.49	0.99	35.42*
HPR 2667	11.32	0.60	3.63
HPR 2693	17.40	0.76	-0.82
HPR 2749	14.06	0.44	9.09
HPR2746	15.95	0.69	30.62*
HPR 2861	18.50	1.62	30.57*
HPR 2863	15.57	1.66	14.04
HPR 2852	16.56	1.15	4.48
HPR 2763	14.66	0.65	16.03
HPR 2747	14.92	0.68	18.97*
HPR 2862	17.93	0.91	7.90
HPR 2761	14.28	0.97	29.69*
HPR 2692	19.30	1.59	15.01
HPR 2864	16.34	0.91	5.07
HPR 2855	13.89	0.86	8.50
Kasturi	15.14	1.13	7.03
HPR 2612	17.05	1.21	25.17*
HPR 2880	14.65	0.84	7.24
HPR 2795	18.46	1.26	10.59
HPR 2720	17.31	0.56	13.11
<b>Range</b>	11.32-19.49		
<b>Mean</b>	15.83		
<b>Standard error</b>		0.567	

\* = significant at 5% level of significance

and HPR 2720 out of 21 recorded high mean were found stable. Unlike AMMI analysis the Eberhart and Russell (1966) model fails to show specific adaptation of the genotypes with respect to environments.

The AMMI analysis showed that there were significant differences among the genotypes, the environments (locations) and G × E interaction (Table 4). The analysis revealed that total mean sum of

squares was attributed to different sources in varying proportion i.e., Environmental effects 32.48%, genotypic 17.19% and genotype × environment interaction effects 44.33%. High contribution of environmental mean sum of square indicated that differences among the environmental means were very high while high G×E interaction mean sum of squares indicated that differences among genotypes was substantial across the environments. Further the G × E interaction component of variation was partitioned and explained in three interaction principal component axes (IPCA) to capture the entire total pattern contained in the G×E interaction. The first two IPCA axes, IPCA1 and IPCA2 together contributed 77.18% of the total interaction variance. The noise in the G × E interaction can be estimated by the interaction df times the error mean square, namely  $116 \times 6.59 = 764.44$ . The G × E sum of squares is  $116 \times 14 = 1624$ , of which IPCA1 captured  $32 \times 25.40 = 812.8$ . Since signal is captured preferentially in the early components but noise selectively in the late components. Of the two significant IPCA axes much of the interaction variance was explained by the first IPCA (49.21%) followed by the 2nd IPCA axes (27.97%) (Table 5). This implied that the interaction of

**Table 5.** AMMI analysis for grain yield per plant (g) in rice across different locations

Source	DF	MSS	% variation explained
Trials	149	25.00	
Genotypes	29	22.08*	17.19
Environments	4	358.40**	38.48
GxE Interaction	116	14.00**	44.33
PCA I	32	25.40**	49.21
PCA II	30	15.40	27.97
PCA III	28	7.35	12.46
Residual	26	6.59	10.37

\*,\*\* = significant at 5%,1% level of significance, respectively ; AMMI = Additive main effects and multiplicative interaction

the 30 rice genotypes with five environments were predicted by the first two components of genotypes and environments.

Persaud et al. (2019) observed that resistance for Sheath Blight was slightly influenced by the G × E interaction and identified genotypes that showed stable resistance in all environments and suggested to be used for breeding resistance for the disease in rice.

Haile et al. (2007) observed similar type of result in which the maximum interaction variation for durum wheat protein content was explained by IPCA1 and noise probably dominated IPCA2-5. AMMI stability value (ASV) was calculated for each genotype according to the relative contributions of the principal component axis scores (IPCA1 and IPCA2) to the interaction sum of squares as per Purchase et al. (2000). Yield stability index (YSI) was also calculated (Table 6) using the sum of the ranking based on yield and ranking based on the AMMI stability value. YSI incorporates both mean yield and stability in a single criterion. Low values of both parameters show desirable

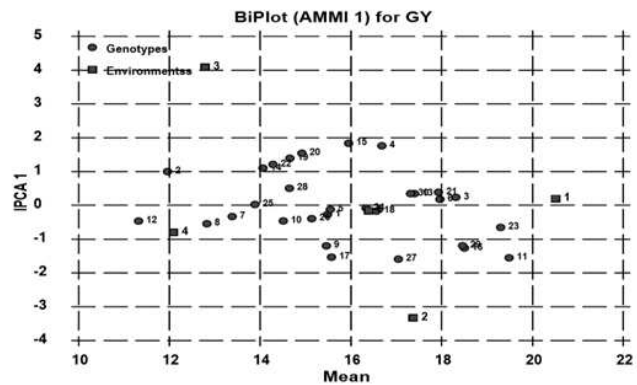
**Table 6.** Ranking of thirty rice genotypes based on grain yield, AMMI stability value (ASV) and yield stability index (YSI)

Genotype	Mean	Rank (A)	ASV	Rank (B)	YSI=A+B
Pusa 1121	15.49	17	0.2754	3	20
Hasansarai	11.96	29	-0.99669	16	45
Vasumati	18.32	5	-0.23515	17	22
Lakhamandal	16.68	11	-1.76085	30	41
Basmati-370	15.55	16	0.12603	2	18
PR-121	17.96	6	-0.17245	19	25
PB-1509	13.39	27	0.3315	5	32
Sharbati	12.83	28	0.54627	11	39
T-23	15.46	18	1.20161	21	39
HPR 2858	14.51	23	0.46239	6	29
HPR 2323	19.49	1	1.55485	27	28
HPR 2667	11.32	12	0.46725	7	19
HPR 2693	17.4	8	-0.34839	4	12
HPR 2749	14.06	25	-1.10016	18	43
HPR2746	15.95	14	-1.83591	29	43
HPR 2861	18.5	3	1.26029	24	27
HPR 2863	15.57	15	1.53598	25	40
HPR 2852	16.56	12	0.17451	8	20
HPR 2763	14.66	21	-1.38993	22	43
HPR 2747	14.92	20	-1.54021	26	46
HPR 2862	17.93	7	-0.38564	13	20
HPR 2761	14.28	24	-1.21296	23	47
HPR 2692	19.3	2	0.6525	15	17
HPR 2864	16.34	13	0.08328	9	22
HPR 2855	13.89	26	-0.02618	1	27
Kasturi	15.14	19	0.39706	12	31
HPR 2612	17.05	10	1.59303	28	38
HPR 2880	14.65	22	-0.50412	10	32
HPR 2795	18.46	4	1.19555	20	24
HPR 2720	17.31	9	-0.34887	14	23

A: Rank based on mean grain yield; B: Rank based on ASV

genotypes with high mean yield and stability (Bose et al. 2014).

Genotype HPR 2693, HPR 2692, HPR 2855, HPR 2667 and Pusa 1121 scored low YSI and hence considered as stable and desirable one while HPR 2862 had highest YSI and hence undesirable. AMMI1 biplot analysis (Fig. 1) revealed that genotype HPR 2746 and Lakhamandal had the highest positive IPCA score as well as highest AMMI stability value (ASV). They also recorded high GYP than average but were



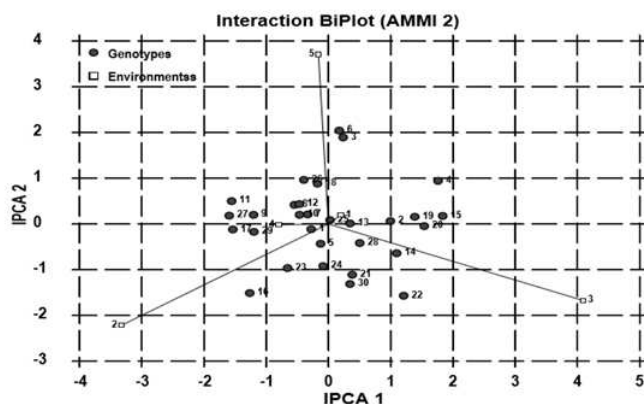
**Fig. 1.** AMMI1 biplot of grain yield per plant main effects and GXE interaction of 30 rice genotypes across five environments, E1 = Dhaulakuan, E2 = Una, E3 = Palampur, E4 = Malan, E5 = Sundernagar

highly interacting and unstable and could be recommended for specific location. Genotype HPR 2667 had the lowest mean GYP with negative IPCA scores. The highest grain yield per plant (29.41g) was recorded at Una followed by Sundernagar (26.70g) and Dhaulakuan (26.20) whereas the lowest was observed at Palampur (5.93g) followed by Malan (7.13g). AMMI1 biplot clearly revealed that Dhaulakuan, Sundernagar and Una are favourable environment for grain yield which can be indicated by its positive value of environmental index (Supplementary Table S2) as well as due to its position on the righthand side of the mean abscissa, while in contrast with negative value of environmental index and left side location whereas Malan and Palampur were found to be unfavourable. The location Una had highest negative IPCA score and hence was unstable or we can say a highly interactive environment. Dhaulakuan and Sundernagar showed IPCA scores near zero compared to the other locations indicating these to be non-interactive and stable locations. In terms of average GYP of genotypes Dhaulakuan was the best location followed by Una and Sundernagar. Genotype HPR 2855, Basmati-370,

HPR 2864, HPR 2852, PR-121 and Vasumati exhibited IPCA score nearing zero and lowest ASV. Amongst these genotypes, HPR 2864, HPR 2852, PR-121 and Vasumati also had average grain yield per plant higher than the general mean (15.83g) could be considered stable. Although Genotype HPR 2855 and Basmati-370 recorded IPCA score and ASV equaled to zero but was poorly adapted due to low GYP than general mean. Large numbers of genotypes with negative IPCA score and high mean grain yield per plant were adapted to Una and genotypes with low GYP and higher negative IPCA1 scores to Malan. The results obtained were in harmony with Akter et al. (2014). Genotype with high positive or negative scores exhibited specific adaptability which is more precisely explained by AMMI2 biplot or interaction biplot analysis.

The AMMI2 biplot (Fig. 2) graphical analysis for IPCA1 and IPCA2 indicated that genotypes HPR 2693, HPR 2855, Pusa-1121, Basmati-370, HPR 2858, PB-1509, Sharbati and HPR 2667 exhibited nearly zero score for both IPCA1 and IPCA2 implying that these genotypes were less interacting with the locations. Among these genotypes, HPR 2693 was considered to be most stable as it had GYP more than general mean. Pusa-1121, one of the highly prized basmati was also found stable but the average yield per plant over all the location was low. It yielded more at Dhaulakuan and the reason could be the presence of optimum temperature during its grain filling stage at this location. The reason for low GYP at other locations may be due to the presence of low temperature at the grain filling stage. Genotypes exhibiting higher IPCA1 and IPCA2 scores were Lakhamandal, HPR 2323, HPR 2612, HPR 2863, HPR 2861, HPR 2720, HPR 2761,

HPR 2746 present at the outer boundary of the polygon indicating that they were more interacting with environment and must exhibit specific adaptation. In case of environments, location Una and Palampur exhibited highest IPCA1 and IPCA2 score. Sundernagar had IPCA1 score near zero but IPCA2 score was highest positive while in contrast Malan had zero IPCA2 score but high IPCA1 score. Among five locations, Dhaulakuan exhibited nearly zero score for both IPCA1 and IPCA2 stating it to be the less interacting and most stable location for GYP for all the genotypes. Indicated by AMMI1 biplot that Malan and Palampur were unfavourable location for GYP, but there were some genotypes identified as shown in AMMI2 biplot which exhibited specific adaptation and performed well even in these locations where the temperature drastically falls below 15-18°C at reproductive stage. Genotypes HPR 2863, HPR 2612, HPR 2667, PB-1509, HPR 2858 showed specific adaptation to Malan while HPR 2761, HPR 2749, HPR 2746, HPR 2720, HPR 2862 and HPR 2880 exhibited specific adaptation at Palampur. A non-basmati genotype PR-121 genotypes also showed interaction with Sundernagar and could be recommended for this location. Islam et al. (2014) also identified specific adaptation for five rice genotypes across different Haor areas of Bangladesh. Similar results were also reported by Das et al. (2018) in paddy genotypes under different agro-ecological zones of Odisha. AMMI2 biplot revealed that majority of the genotypes were stable at Dhaulakuan and Malan while specific adaptation of genotypes viz; HPR 2861, HPR 2692 and HPR 2864 at Una; HPR 2749 and HPR 2880 at Palampur and Vasumati and PR-121 at Sundernagar.



**Fig. 2. AMMI2 biplot of grain yield per plant showing IPCA scores genotypes and environments. E1 = Dhaulakuan, E2 = Una. E3 = Palampur. E4 = Malan, E5 = Sundernagar**

Results of the present work clearly showed the differences among locations in determining grain yield per plant. Dhaulakuan was considered to be most favourable locations represented a low elevation site and hence was suitable for grain yield per plant of genotypes. Sundernagar and Una were highly interacting environment and were suitable for specific genotypes while in contrast Palampur and Malan which were at higher elevation were unfavourable. The reason of low grain yield per plant at these two locations can be attributed to the drastic fall in the temperature below 18°C during grain filling stage which causes sterility of the spikelets. Satake et al. (1976) observed that low temperature in the range of 15-19°C during the reproductive stage impairs microspore development and causes the production of sterile pollen grains, resulting in poor grain filling and high spikelet sterility.

Ghadirnezhad and Fallah (2014) recorded similar type of result of poor grain filling at low temperature during ripening stage.

#### Authors' contribution

Conceptualization of research (AKS, DB); Designing of the experiments (AKS, DB, AD); Contribution of experimental materials (AD, DB); Execution of field/lab experiments and data collection (AD, DB); Analysis of data and interpretation (AKS, DB, AD); Preparation of manuscript (AKS, DB, AD).

#### Declaration

The authors declare no conflict of interest.

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**Supplementary Table S1.** Analysis of variance (ANOVA) for grain yield of rice at different environments

Environments	Source of variation	DF	Grain yield per plant(g)
E1	Replications	2	1.55
	Treatments	29	18.18**
	Error	58	1.09
E2	Replications	2	47.53
	Treatments	29	80.00**
	Error	58	10.12
E3	Replications	2	3.72
	Treatments	29	60.78**
	Error	58	5.86
E4	Replications	2	1.70
	Treatments	29	22.05**
	Error	58	5.24
E5	Replications	2	9.04
	Treatments	29	56.09**
	Error	58	13.42

\*, \*\* significant at 5% and 1% level of significance respectively; E1 = Dhaulakuan, E2 = Una, E3 = Palampur, E4 = Malan, E5 = Sundernagar



**Supplementary Table S2.** Mean performance of 30 genotypes for grain yield per plant (g) at five locations

Genotypes	Environments					Mean
	E1	E2	E3	E4	E5	
Pusa 1121	26.20	18.03	10.14	7.13	15.93	15.49
Hasansarai	15.00	10.17	13.37	9.00	12.27	11.96
Vasumati	20.73	24.34	20.20	13.37	12.93	18.31
Lakhamandal	18.87	15.11	23.19	11.93	14.33	16.69
Basmati-370	23.13	15.97	10.49	11.23	16.90	15.54
PR-121	22.93	24.09	19.18	12.27	11.34	17.96
PB-1509	20.93	16.39	8.74	8.13	12.74	13.39
Sharbati	18.67	16.00	7.53	11.03	10.90	12.83
T-23	18.53	20.37	7.63	15.90	14.85	15.46
HPR 2858	21.47	16.93	9.00	11.93	13.23	14.51
HPR 2323	18.80	29.41	12.71	15.73	20.78	19.49
HPR 2667	13.67	14.59	7.17	11.15	10.04	11.32
HPR 2693	22.20	17.02	15.46	15.07	17.26	17.40
HPR 2749	17.80	10.00	14.47	11.47	16.58	14.06
HPR2746	21.40	12.68	21.00	8.47	16.20	15.95
HPR 2861	21.53	22.92	8.93	12.43	26.70	18.50
HPR 2863	21.00	22.16	5.93	11.90	16.87	15.57
HPR 2852	22.80	20.11	13.73	12.93	13.23	16.56
HPR 2763	18.87	12.91	18.11	8.13	15.27	14.66
HPR 2747	20.20	11.61	18.20	8.93	15.66	14.92
HPR 2862	22.47	15.61	14.64	14.42	22.52	17.93
HPR 2761	20.53	8.28	13.37	8.93	20.29	14.28
HPR 2692	23.00	23.39	13.21	11.27	25.64	19.30
HPR 2864	20.67	15.44	11.22	14.47	19.88	16.34
HPR 2855	20.67	13.06	9.67	14.12	11.93	13.89
Kasturi	19.20	21.03	12.52	10.02	12.93	15.14
HPR 2612	21.53	22.92	7.19	17.47	16.12	17.05
HPR 2880	21.33	11.72	11.85	13.35	14.97	14.64
HPR 2795	22.20	23.67	10.40	15.98	20.03	18.46
HPR 2720	18.87	15.22	14.33	14.63	23.52	17.31
Mean	20.51	17.37	12.79	12.09	16.39	15.83
C.D	1.71	5.21	3.97	3.75	15.83	
C.V	5.09	18.32	18.93	18.94	22.35	
Ij	4.68	1.54	-3.04	-3.74	0.56	

E1 = Dhaulakuan, E2 = Una, E3 = Palampur, E4 = Malan, E5 = Sundernagar, C.D = Critical difference, C.V = Coefficient of variation; Ij = Environmental index