

Research Article



Genotype × Environment Interaction for Yield and Associated Traits in Rice

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Abstract | This study was conducted to assess genotype by environment interaction (GEI) for yield and yield related traits in rice. The genetic material comprised 87 rice $F_{5:7}$ recombinant inbred lines (RILs) along with three check cultivars namely Pakhal, Kashmir Basmati and Fakhr-e-Malakand. The genetic material was planted in alpha lattice design using three replications across different locations namely Peshawar, Swat, Manshera and Charsadda of the Khyber Pakhtunkhwa province of Pakistan during 2017. Pooled analysis of variance indicated significant ($p \leq 0.01$) differences among the environments, genotypes and GEI for spikelets panicle⁻¹, grains panicle⁻¹, 1000-grain weight and grain yield. Across four locations, AUP-30 showed the highest number of spikelets panicle⁻¹ (242.5), grains panicle⁻¹ (228.6) and maximum 1000-grain weight (29.0 g). Rice RILs AUP-3, AUP-30 and AUP-29 manifested the higher grain yield of 4.3, 4.2 and 4.1 tonnes ha⁻¹ across locations, respectively. On the basis of individual locations, rice RILs AUP-3, AUP-29, AUP-30 and AUP-40 displayed the highest grain yield of 4.8, 4.6, 5.4 and 3.9 tonnes ha⁻¹ at Peshawar, Swat, Mansehra and Charsadda, respectively. Grain yield displayed significantly positive correlation with spikelets panicle⁻¹, grains panicle⁻¹ and 1000-grain weight. The study indicated differential behavior of the rice RILs for different traits across different environments. Rice RILs AUP-3, AUP-30 and AUP-29 excelled in performance for yield and yield attributes across locations while AUP-3, AUP-29, AUP-30 and AUP-29 displayed adaptation to specific environments of Peshawar, Swat, Mansehra and Charsadda, respectively.

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Introduction

Rice (*Oryza sativa* L.) is one of the principal cereal crops worldwide and has been used as a major source of food since prehistoric times. The enhancement of world's rice production depends on the development of new cultivars with high yield and stable performance across diverse environments (Akter et al., 2014).

The selection of superior genotypes on the basis of

yield *per se* at a single location doesn't serve as an effective criterion during the development of crop cultivars. Yield is a complex quantitative character and is greatly influenced by environmental fluctuations. A better understanding of genotype × environment interaction plays a vital role in the identification of stable genotypes for onward use as commercial cultivars (Shrestha et al., 2012). The interaction aspect of the genotypes with environment is quite complex and is highly variable across locations. Identification and development of rice genotypes

with wider adaptation across different production regions is, therefore, one of the major objectives of crop breeding programs. Multi- location trials are conducted to identify the consistently performing genotypes in different agro-ecological zones. The adaptation of a genotype over varied environments is usually assessed by the level of its interaction with different environments under which it is cultivated. The genotype having high yield across environments with a low degree of variation for yield over varied environments is considered to be relatively the more adapted/stable one (Ashraf et al., 2003). The stable performance of genotypes at different sites could be on account of genetic constitution, environmental factors associated with specific locations and the interaction between the genetic make-up and locations (Blanche and Lins, 2009). The performance of rice genotypes for yield and other production traits are mostly location specific but still in rice breeding programs there are the chances of the development of the genotypes which have the potential to produce high yield across different agro-ecological zones. The present study was performed to evaluate the newly developed rice recombinant inbred lines (RILs) over varied locations for grain yield and the associated production traits and to identify the promising RILs for commercial cultivation.

Materials and Methods

The research was conducted at four locations namely, The University of Agriculture-Peshawar, Agriculture Research Institute Mingora-Swat, Agriculture Research Station Baffa-Mansehra and Bacha Khan University-Charsadda of the Kyber Pakhtunkhwa Province -Pakistan during 2017 rice growing season. The genetic material comprised 87 rice $F_{5:7}$ recombinant inbred lines (RILs) along with three check cultivars Pakhal, Kashmir Basmati (K-Bas) and Fakhr-e-Malakand (F-MLD). The details of the rice RILs used in the study has been presented in Table 1. It is worth-mentioning that the rice RILs have been developed by the Rice Breeding Program, Department of Plant Breeding and Genetics, The University of Agriculture Peshawar. At each location, the rice RILs and check cultivars were planted using alpha lattice design with three replications. Each replication consisted of six blocks with each block comprising 15 RILs. Each genotype was planted in a four-row plot with row length of 3 meter and row-row distance of 30 cm. Data were recorded on spikelet

panicle⁻¹, grains panicle⁻¹, 1000-grain weight (g) and grain yield (tonnes ha⁻¹). Data were subjected to the analysis of variance separately for each environment (location) and combined over environments using Statistical Analysis System (SAS) package. Means were separated using least significant difference test to discriminate the genotypes at 5% level of probability.

Results and Discussion

Pooled analysis of variance of the rice genotypes for spikelets panicle⁻¹, grains panicle⁻¹, 1000-grain weight and grain yield has been presented in Table 2. The summarized versions of mean data of rice genotypes for the studied traits have been presented in Table 3 while correlation co-efficient among the studied traits have been given in Table 4. The detailed means across locations and at each experimental site have been presented from Supplementary Table 1 to Supplementary Table 5.

Spikelets panicle⁻¹

Pooled analysis of variance revealed significant ($p \leq 0.01$) variation among the environments, genotypes and genotype by environment interaction (GEI) for spikelets panicle⁻¹ (Table 2). The significance of GEI depicted that the genotypes showed differential behavior in different environments. Means for spikelets panicle⁻¹ among the studied genotypes across all the environments ranged between 140.1 and 242.5. Rice recombinant inbred line AUP-30 showed the superiority for spikelets panicle⁻¹ (242.5) across all the studied agro-ecological zones while AUP-55 gave the lowest number of spikelets panicle⁻¹ (140.1). In the specific environments, AUP-3 displayed maximum spikelets panicle⁻¹ (265.0) at Peshawar while AUP-29 displayed the highest number of spikelets panicle⁻¹ (281) at Swat. Similarly, AUP-30 produced the highest number of spikelets panicle⁻¹ (265) at Mansehra while AUP-40 had maximum (208) value for this trait at Charsadda (Table 3). These results are in agreement with the findings of Rashmi et al. (2017) and Ajmera et al. (2017). Rashmi et al. (2017) evaluated twenty-two advanced rice breeding lines across three different experimental sites and observed significant genotype x environment interaction for spikelets panicle⁻¹. In their study, the rice genotype JK2 15-1 showed maximum spikelets panicle⁻¹ (143.8). Ajmera et al. (2017) studied thirty-seven rice genotypes including two checks at three different locations and observed significant differences for environments, genotypes and genotype x environment interaction.

Table 1: List of the rice genotypes used in the study.

S. No.	Cross combinations	RILs	S. No.	Cross combinations	RILs
1	Dokri-Basmati/DR-92	AUP-1	46	TN-1/Dilrosh	AUP-46
2	Dokri-Basmati/DR-92	AUP-2	47	IR-8/Shadab-31	AUP-47
3	Dokri-Basmati/DR-92	AUP-3	48	IR-8/Shadab-31	AUP-48
4	Dokri Basmati/Pakhal	AUP-4	49	IR-8/Shadab-31	AUP-49
5	Dokri Basmati/Pakhal	AUP-5	50	DR-82/Shadab-31	AUP-50
6	Dokri Basmati/Pakhal	AUP-6	51	DR-82/Shadab-31	AUP-51
7	DR-92/DR-83	AUP-7	52	DR-82/Shadab-31	AUP-52
8	DR-92/DR-83	AUP-8	53	Basmati-6129/Basmati-370	AUP-53
9	DR-92/Dokri-Basmati	AUP-9	54	Basmati-6129/Basmati-370	AUP-54
10	DR-92/Dokri-Basmati	AUP-10	55	Basmati-6129/Basmati-370	AUP-55
11	Pakhal/ Kashmir Basmati	AUP-11	56	Basmati-6129/Dokri Basmati	AUP-56
12	Pakhal/ Kashmir Basmati	AUP-12	57	Basmati-6129/Dokri Basmati	AUP-57
13	DR-83/ Dokri-Basmati	AUP-13	58	Basmati-2008/Kashmir Basmati	AUP-58
14	DR-83/ Dokri-Basmati	AUP-14	59	Basmati-2008/Kashmir Basmati	AUP-59
15	DR-83/DR-92	AUP-15	60	Basmati-2008/TN-1	AUP-60
16	DR-83/NIAB-IR-8	AUP-16	61	Basmati-2008/TN-1	AUP-61
17	DR-83/NIAB-IR-8	AUP-17	62	Basmati-2008/TN-1	AUP-62
18	IR-8/Sugdesi	AUP-18	63	Basmati-2008/Dilrosh	AUP-63
19	IR-8/Sugdesi	AUP-19	64	Basmati-2008/Dilrosh	AUP-64
20	IR-8/Sugdesi	AUP-20	65	Basmati-2008/Dilrosh	AUP-65
21	DR-83/Sugdesi	AUP-21	66	Dokri Basmati/Basmati-6129	AUP-66
22	DR-83/Sugdesi	AUP-22	67	Dokri Basmati/Basmati-6129	AUP-67
23	DR-83/Sugdesi	AUP-23	68	Dokri Basmati/Basmati-6129	AUP-68
24	NIAB-IRRI-8/IR-8	AUP-24	69	Dilrosh/Kashmir Basmati	AUP-69
25	NIAB-IRRI-8/IR-8	AUP-25	70	Dilrosh/Kashmir Basmati	AUP-70
26	IR-8/NIAB-IR-8	AUP-26	71	Dilrosh/Kashmir Basmati	AUP-71
27	IR-8/NIAB-IR-8	AUP-27	72	Kashmir Basmati/Dilrosh	AUP-72
28	IR-8/NIAB-IR-8	AUP-28	73	Dilrosh/TN-1	AUP-73
29	DR-82/IR-8	AUP-29	74	Dilrosh/TN-1	AUP-74
30	DR-82/IR-8	AUP-30	75	Dilrosh/TN-1	AUP-75
31	Dokri-Bas/DR-83	AUP-31	76	Dilrosh/TN-1	AUP-76
32	Dokri-Bas/DR-83	AUP-32	77	Kashmir Basmati/TN-1	AUP-77
33	Dokri-Bas/Sugdesi	AUP-33	78	Kashmir Basmati/TN-1	AUP-78
34	Sada/Mathra	AUP-34	79	TN-1/Kashmir Basmati	AUP-79
35	Sadahayat/Mathra	AUP-35	80	TN-1/Kashmir Basmati	AUP-80
36	Sadahayat/Khushbo	AUP-36	81	TN-1/Kashmir Basmati	AUP-81
37	Sadahayat/Khushbo	AUP-37	82	TN-1/Kashmir Basmati	AUP-82
38	Sathara/Sadahayat	AUP-38	83	Kangni-27/Kashmir Basmati	AUP-83
39	Sathara/Sadahayat	AUP-39	84	Kangni-27/Kashmir Basmati	AUP-84
40	Dilrosh/Kangni-27	AUP-40	85	Kashmir Basmati/Kangni-27	AUP-85
41	Kangni-27/TN-1	AUP-41	86	Kashmir Basmati/Kangni-27	AUP-86
42	Kangni-27/Dilrosh	AUP-42	87	Kashmir Basmati/Kangni-27	AUP-87
43	Kangni-27/Dilrosh	AUP-43	88	Pakhal	Pakhal
44	TN-1/Kangni-27	AUP-44	89	Kashmir Basmati	K-Bas
45	TN-1/Kangni-27	AUP-45	90	Fakhr-e-Malakand	F-MLD

Table 2: Mean squares of rice genotypes for yield and yield related traits across four locations (environments) during 2017.

SoV	Df	Spikelets panicle ⁻¹	Grains panicle ⁻¹	1000-grain weight	Grain yield
Env	3	344890.8**	393727.2	538.9**	176.1**
Rep(Env)	8	121.8	92.7	58.0	2.7
Blk(Env*Rep)	60	1019.9	870.1	9.0	11.0
Gen	89	2445.0**	1987.8	9.9**	100.7**
Gen*Env	267	1929.1**	1658.9	9.5**	8.7**
Error	652	905.9	774.6	11.9	12.8
Total	1079				
C.V		19.3	20.0	10.2	29.6

** = Highly significant at 1% probability level.

Table 3: Summarized means of rice genotypes for yield and yield related traits across four locations (environments) during 2017.

Locations		Parameters			
		Spikelets panicle ⁻¹	Grains panicle ⁻¹	1000-grain weight (g)	Grain yield (t ha ⁻¹)
Peshawar	Minimum	136.3(AUP-86)	129(AUP-86)	23.9 (AUP- 64)	2.6 (AUP- 64)
	Maximum	265(AUP-3)	253(AUP-3)	31.4(AUP- 3)	4.8 (AUP- 3)
	Mean	183.7	167.5	28.9	3.7
Swat	Minimum	134.3(AUP-60)	118.7(AUP-60)	25.0 (AUP- 64)	3.0 (AUP- 64)
	Maximum	281.3(AUP-29)	264(AUP-29)	31.0 (AUP- 29)	4.6 (AUP- 29)
	Mean	185.2	169.9	28.7	3.7
Mansehra	Minimum	142.7(AUP-8)	128.3(AUP-11)	26.0 (AUP- 37)	3.1 (AUP- 59)
	Maximum	265(AUP-30)	251(AUP-30)	33.2 (AUP- 25)	5.4 (AUP- 30)
	Mean	183.7	167.1	29.1	4.1
Charsadda	Minimum	111.5(AUP-8)	99.7(AUP-4)	19.3 (AUP- 31)	2.1 (AUP- 7)
	Maximum	208(AUP-40)	197.3(AUP-40)	28.0 (AUP- 40)	3.9 (AUP- 40)
	Mean	133.5	124.2	20.8	2.9
Across all environments	Minimum	140.1(AUP-55)	127.2(AUP-55)	24.5(AUP-64)	2.9(AUP-64)
	Maximum	242.5(AUP-30)	228.6(AUP-30)	29.0(AUP-30)	4.3(AUP-3)
	Mean	172.8	157.16	26.86	3.5

They noted that the rice genotype RPHP 107 gave the maximum number of spikelets panicle⁻¹ (181.2).

Spikelets panicle⁻¹ exhibited significantly positive correlation with grains panicle⁻¹, 1000-grain weight and grain yield (Table 4) which indicated that the increase in number of spikelets panicle⁻¹ would have positive impact on yield and yield components. The results of the present study are in line with the findings of other researchers. Naseem et al. (2014) have also observed significant positive correlation of spikelets panicle⁻¹ with grains panicle⁻¹. Similarly, Ashfaq et al. (2012) and Reddy et al. (2013) have also reported significantly positive phenotypic correlation of spikelets panicle⁻¹ with yield and yield attributes.

Table 4: Phenotypic correlation among yield and yield related traits of rice genotypes across four locations (environments) during 2017.

	Spikelets panicle ⁻¹	Grain panicle ⁻¹	1000-grain weight	Grain yield
Spikelets panicle ⁻¹	-			
Grain panicle ⁻¹	0.97**	-		
1000 grain weight	0.48**	0.50**	-	
Grain yield	0.46**	0.48**	0.71**	-

Grains panicle⁻¹

Combined analysis of variance showed significant (p≤0.01) differences among the genotypes, environments and GEI for grains panicle⁻¹ (Table 2). Means for grains panicle⁻¹ among the studied

genotypes across all the environments ranged between 127.2 and 228.6. Rice RIL AUP-30 showed the superiority for grains panicle⁻¹ (228.6) across all the studied agro-ecological zones while AUP-55 gave the lowest number of grains panicle⁻¹. At Peshawar, the highest number of grains panicle⁻¹ (253) was revealed for AUP-3 while at Swat maximum value for grains panicle⁻¹ (264) was observed for AUP-29. AUP-30 produced maximum grains panicle⁻¹ (251) at Manshera while AUP-40 manifested the highest value for grains panicle⁻¹ (197) at Charsadda (Table 3). Significant GEI interaction for grain panicle⁻¹ implied the higher contribution of this yield component towards the differential response of the genotypes for grain yield across different environments. The results of the present study are compatible with the findings of [Luguterh and Dioggban \(2016\)](#) and [Dewi et al. \(2014\)](#). [Luguterh and Dioggban \(2016\)](#) evaluated 15 rice genotypes in complete randomized block design with three replications across four locations. The combined analysis of variance showed significant differences among the genotypes, environment and genotypes by environment interaction for different yield attributes. Similarly, [Dewi et al. \(2014\)](#) assessed ten advanced rice lines along with two check varieties using six environments for yield and yield related traits and observed differential response of the genotypes across different environments for grains panicle⁻¹.

Significantly positive phenotypic correlation of grains panicle⁻¹ was observed with spikelets panicle⁻¹, 1000-grain weight and grain yield in the present study (Table 4). These results depicted that increasing number of grains panicle⁻¹ would enhance 1000-grain weight and grain yield and this trait could therefore be used as indirect selection criteria for increasing grain yield. Similar results of positive correlation between grains panicle⁻¹ and grain yield were also observed by [Naseem et al. \(2014\)](#).

Thousand-grain weight

Pooled analysis of variance exhibited significant ($p \leq 0.01$) differences among the genotypes and environments for 1000-grain weight. However, non-significant GEI was observed for this trait (Table 2). Means for 1000-grain weight among the studied genotypes across all the environments ranged between 24.5 and 29.0 g. Rice recombinant inbred line AUP-30 showed superiority for 1000-grain weight (29.0 g) across all the studied agro-ecological zones while line AUP-64 displayed the lowest 1000-grain weight

(24.5 g). On the basis of individual locations, AUP-30 showed the highest value for 1000-grain weight (31.4 g) at Peshawar while AUP-29 had maximum 1000-grain weight (31.0 g) at Swat., AUP-3 and AUP-40 manifested the highest value of 33.2 and 28.0 g at Mansehra and Charsadda, respectively (Table 3). Our results regarding the significant differences among the genotypes and environments for 1000-grain weight are in agreements with the findings of [Lakshmi et al. \(2014\)](#) and [Kulsum et al. \(2013\)](#). [Lakshmi et al. \(2014\)](#) studied genotype \times environment interaction for grain yield and associated traits using 13 rice genotypes across five environments and observed significant differences among the genotypes and environments for 1000-grain weight. Similarly, [Kulsum et al. \(2013\)](#) investigated genotype-environment interaction for yield and associated traits using 13 rice genotypes across five environments and noticed significant variation among the genotypes and environments for 1000-grain weight. Non-significant GEI for 1000-grain weight in the present study depicted relatively lesser environmental influence on expression of this trait.

Thousand-grain weight manifested significantly positive phenotypic correlation with grains panicle⁻¹ and grain yield (Table 4). These results are in line with the findings of different researchers like [Ogunbayo et al. \(2014\)](#) and [Lakshmi et al. \(2014\)](#) who also reported significantly positive correlation of 1000-grain weight with grains panicle⁻¹ and grain yield.

Grain yield

Combined analysis of variance exhibited significant ($p \leq 0.01$) differences among the environments, genotypes and GE interaction for grain yield (Table 2). Means for grain yield among the studied genotypes across all the environments ranged between 2.9 and 4.3 tonnes ha⁻¹. Rice recombinant inbred line AUP-3 showed superiority for grain yield (4.3 tonnes ha⁻¹) across all the studied agro-ecological zones (Table 3) followed by the lines AUP-30 and AUP-29 with grain yields of 4.2 and 4.1 tonnes ha⁻¹, respectively (Supplementary Table 1). AUP-64, however, gave the lowest grain yield of 2.9 tonnes ha⁻¹. On the basis of individual experimental sites, AUP-3 produced maximum grain yield of 4.8 tonnes ha⁻¹ at Peshawar while AUP-29 gave maximum grain yield of 4.6 tonnes ha⁻¹ at Swat. Rice lines AUP-30 and AUP-40 showed the highest grain yield of 5.4 and 3.9 tonnes ha⁻¹ at Mansehra and Charsadda, respectively (Table

3). The results of the present study are compatible with the findings of Ajmera et al. (2017). They studied the performance of 37 rice genotypes along with two checks across three different locations for grain yield and related traits and observed significant genotype by environment interaction for yield and yield associated traits. The study identified that the rice genotype RPHP 107 has superior performance for grain yield and associated traits in comparison with the other studied genotypes.

Grain yield exhibited significantly positive phenotypic correlation with yield attributes like spikelets panicle⁻¹, grains panicle⁻¹ and 1000-grain weight (Table 3). The study thus indicated the importance of these secondary traits towards the improvement of grain yield. Naseem et al. (2014) also reported significant positive correlation of grain yield with grains panicle⁻¹. Likewise, Ogunbayo et al. (2014) also observed significantly positive phenotypic correlation between grain yield and 1000-grain weight.

Conclusions and Recommendations

Pooled analysis of variance manifested significant differences among the genotypes, environments, and genotype × environment interaction for spikelets panicle⁻¹, grains panicle⁻¹ 1000-grain weight and grain yield. Across all the experimental locations, rice recombinant inbred lines AUP-3, AUP-30 and AUP-29 displayed superior performance for grain yield and related attributes. These lines thus showed relatively broad adaptation and stability across the tested environments. On the basis of individual locations, rice lines AUP-3, AUP-29, AUP-30 and AUP-40 excelled in performance for yield and associated traits at Peshawar, Swat, Manshera and Charsadda, respectively. These genotypes could, therefore, be recommended for commercial cultivation in the respective specific environments after additional testing. Grain yield manifested significantly positive phenotypic correlation with spikelets panicle⁻¹, grains panicle⁻¹ and 1000-grain weight and selection of the genotypes on the basis of these yield associated traits could improve grain yield in rice breeding programs.

Author's Contribution

Aziz Ur Rahman: Field layout, experimental execu-
June 2019 | Volume 35 | Issue 2 | Page 537

tion, data collection reviewed and wrote the manuscript.

Syed Mehar Ali Shah: Overall research supervision, designing of experiment, provision of research material, data interpretation, discussion, write-up and editing.

Supplementary Material

There is supplementary material associated with this article. Access the material online at: <http://dx.doi.org/10.17582/journal.sja/2019/35.2.532.538>

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