Research Article



Effect of Genotype × Environment Interaction on Grain Yield Determinants in Bread Wheat

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Abstract | Knowledge of genotype by environment interaction (GEI) is essential for identifying environment-specific and widely adapted genotypes. Multi-environment trials were conducted to evaluate the magnitude of genotype (G), environment (E) and GEI effects on yield and yield components of wheat. Eightyone wheat genotypes were evaluated under nine environments within Khyber Pakhtunkhwa, Pakistan during 2013/14, 2014/15 and 2015/16 cropping seasons. Combined analyses of variance for G and GEI were significant for almost all traits. Significant GEI suggested that the performance of genotypes was not consistent across environments, revealing strong influence of environments. Generally, GEI explained major portion of total variation and thus had larger effect than G and E on the expression of phenotype for all traits. Average over nine environments, genotype G-79 exhibited maximum values for tillers m⁻² (181 tillers); grains spike⁻¹ (71 grains); grain yield (4862 kg ha⁻¹) and thus appeared as leading genotype for yield and production traits. Similarly, G-79 had higher grain yield in all test environments except E-03 i.e. E-01 (4537 kg ha⁻¹); E-02 (4840 kg ha⁻¹); E-04 (5035 kg ha⁻¹); E-05 (4976 kg ha⁻¹); E-06 (4797 kg ha⁻¹); E-07 (5024 kg ha⁻¹); E-08 (4767 kg ha⁻¹); E-09 (4886 kg ha⁻¹) signifying it as high yielding and widely adaptable genotype. However, G-08 with higher grain yield in E-01 (5272 kg ha⁻¹) and E-07 (4840 kg ha⁻¹), G-37 in E-04 (5106 kg ha⁻¹) and E-08 (4906 kg ha⁻¹), G-41 in E-05 (5034 kg ha⁻¹) and E-06 (5272 kg ha⁻¹), G-9 in E-02 (4975 kg ha⁻¹) and G-49 in E-03 (5271 kg ha⁻¹), established their specific adaptability in respective environments. Among environments, E-01, E-02, E-03, E-06 and E-07 were identified as highly productive environments in terms of grain yield. Correlation analysis revealed significant positive association of grain yield with tillers m^{-2} ($r_{a} = 0.72^{**}$), grains spike⁻¹ ($r_{g} = 0.41^{**}$) and 1000-grain weight ($r_{g} = 0.30^{**}$). Based on mean yield performance, G-79 was found as high yielding genotype and thus could be recommended for commercialization in Khyber Pakhtunkhwa.

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Keywords | Genotype, Environment, GEI, Yield determinants, Correlation analysis

Introduction

Wheat is the primary food source of people in Pakistan. At national level, wheat was grown on 9.2 million hectares which produced 25.1 million tons with an average yield of 2.7 ton ha⁻¹, while in Khyber Pakhtunkhwa, it was grown on 0.73 million hectares which produced 1.2 million tons with an average yield 1.7 ton ha⁻¹ (Pak. Beurau Stat. 2014-15). The average national wheat yield of Pakistan is far below than agro-technologically advanced countries of the world. In Khyber Pakhtunkhwa province the situation is even worse where yield is lower than the national average yield. Factors for lower grain yield



include lack of irrigation water, inadequate rainfall, heat stress, unavailability of high yielding cultivars and absence of quality seed. Demand for wheat being a staple food crop, would rise with the increase in population. Wheat production could be increased either by developing high yielding cultivars or growing more area under cultivation. The choice for wheat cultivation on larger area is partial; however, development of high yielding wheat cultivars with wider adaptability would play significant role.

Cultivars performance largely depends on their genetic makeup (G), environment (E) and their interaction (GEI). Fluctuating response of genotypes across test environments is an usual phenomenon, known as GEI (Akcura et al., 2009; Karimizadeh et al., 2012b; Mohammadi et al., 2012). Yield potential of a cultivar is the result of its performance over locations and years. Therefore, stability analysis of genotypes is required in the presence of GEI to ascertain high yielding and relatively stable genotypes. For several test environments, the GEI governs the credentials of the most stable genotypes that are suitable for specific environment (Annicchiarico, 2002). Thus, the genotypes possessing genetic homeostasis are essential to increase average yield.

Wheat production can boost up through cultivars having broader genetic base and better performance under various agro-climatic conditions. In wheat, genetic improvement is slow process in nature however, the selective process of man can speed it up through appropriate management of environmental factors. Improvement gets complicated when a trait is environment-driven and selection gets more complex (Mohammad, 2011).Keeping in view the importance of GEI in reference to its application for identifying stable genotypes, the present experiment was conducted using 81 recombinant inbred lines (RIL's) including two check cultivars *viz.* Janbaz and Atta-Habib. The experiment was planted across nine environments to; i) assess GEI effects on grain yield and its components, ii) identify high yielding and stable genotypes for grain yield, and iii) compute genetic correlation coefficients among yield and yield components in wheat.

Materials and Methods

To interpret genotype by environment interaction (GEI) for grain yield and associated traits, eighty one (81) wheat genotypes were tested over 9 environments of Khyber Pakhtunkhwa, Pakistan during 2013/14, 2014/15 and 2015/2016. Detailed description of the experimental sites, history of breeding material, experimental designs and statistical analysis are given under separate heading as under;

Description of experimental sites

Eighty-one genotypes including 79 $\mathrm{F}_{5:8}$ RILs and two check cultivars "Janbaz" and "Atta-Habib" were evaluated in nine environments during 2013/14, 2014/15 and 2015/16. During 2013/14, the experimental materials were planted at single location i.e. The University of Agriculture Peshawar (E-01) for evaluation and seed multiplication, whereas, the experiments were planted during 2014/15 and 2015/16 at The University of Agriculture Peshawar (E-02 and E-03, respectively), Cereal Crops Research Institute, Pirsabak Nowshehra (E-04 and E-05, respectively), Agricultural Research Station, Charsadda (E-06 and E-07, respectively) and Agricultural Research Station, Swabi (E-08 and E-09, respectively). Hereafter, these will be referred as E-01, E-02, E-03, E-04, E-05, E-06, E-07, E-08, and E-09. Agro-metrological features of test sites/environments including temperature, rainfall etc. are given in Table 1.

Environments	Growing season	Geographical	Positon	Altitude	Average rain-	Temperature (°c)	
		Latitude	Longitude	(m.a.s.l)	fall (mm)	Min.	Max.
E-01	2014 (AUP)	34.0150° N	71.5805° E	359	238	20.1	34.8
E-02	2015 (AUP)	do	do	do	415	19.5	35.4
E-03	2016 (AUP)	do	do	do	189	17.8	38.2
E-04	2015 (CCRI)	34.0159° N	71.9755° E	288	220	10.1	28.6
E-05	2016 (CCRI)	do	do	do	112	16.3	35.9
E-06	2015 (ARSS)	34.1442° N	72.3785° E	321	263	18.0	36.7
E-07	2016 (ARSS)	do	do	do	312	14.5	32.1
E-08	2015 (ARSC)	34.1494° N	71.7428° E	381	460	10.4	28.5
E-09	2016 (ARSC)	do	do	do	392	17.4	36.2

Table 1: Description of nine environments used for evaluation of 81 wheat during 2014–2016 cropping season.

Source: Meteorological Department, Khyber Pakhtunkhwa, Pakistan.



Code

G-01

G-02

G-03

G-04

Breeding history of plant material

Pedigree

Seventy-nine $F_{5:8}$ RILs were originally developed in the department of Plant Breeding and Genetics during 2002/03 (Table 2). The segregating populations were advanced in bulk till F_4 generation. In F_5

Table 2: List of wheat RILs with pedigree.

Takbir × Khatakwal-3-1

Takbir × Khatakwal-3-5

Takbir × Khatakwal-3-7

Takbir × Khatakwal-3-8

00.		0.0	
G-05	Takbir × Khatakwal-3-9	G-46	Tatara × Ghaznavi 98-31-1
G-06	Takbir × Khatakwal-3-16	G-47	Tatara × Ghaznavi 98-31-2
G-07	Takbir × Khatakwal-3-18	G-48	Tatara × Ghaznavi 98-31-4
G-08	Tatara × Inqilab-4-3	G-49	Tatara × Ghaznavi 98-31-7
G-09	Tatara × Inqilab-4-6	G-50	Ghaznavi 98 × Khatakwal -33-5
G-10	Tatara × Inqilab-4-9	G-51	Ghaznavi 98 × Khatakwal -33-7
G-11	Tatara × Inqilab-4-10	G-52	Ghaznavi 98 × Khatakwal -33-10
G-12	Tatara × Inqilab-4-11	G-53	Ghaznavi 98 × Khatakwal -33-15
G-13	Tatara × Inqilab-4-13	G-54	Tatara × Ghaznavi 98-37-15
G-14	Tatara × Inqilab-4-16	G-55	Tatara × Margala-43-2
G-15	Wafaq × Ghaznavi 98	G-56	Tatara × Margala-43-4
G-16	Wafaq × Ghaznavi 98	G-57	Tatara × Margala-43-11
G-17	Wafaq × Ghaznavi 98	G-58	Tatara × Margala-43-12
G-18	Tatara × Takbir-9-8	G-59	Tatara × Inqilab -45-10
G-19	Tatara × Takbir-9-10	G-60	Takbir × Inqilab -45-12
G-20	Tatara × Takbir-9-12	G-61	Tatara × Ghaznavi 98-48-2
G-21	Tatara × Takbir-9-813	G-62	Tatara × Ghaznavi 98-48-3
G-22	Tatara × Inqilab-18-15	G-63	Tatara × Ghaznavi 98-48-13
G-23	Tatara × Inqilab-18-19	G-64	Tatara × Ghaznavi 98-48-15
G-24	Tatara × Inqilab-18-20	G-65	Tatara × Ghaznavi 98-48-19
G-25	Tatara × Takbir-19-3	G-66	Wafaq × Ghaznavi 98-49-2
G-26	Tatara × Takbir-19-4	G-67	Wafaq × Ghaznavi 98-49-4
G-27	Tatara × Takbir-19-8	G-68	Wafaq × Ghaznavi 98-49-5
G-28	Tatara × Takbir-19-11	G-69	Wafaq × Ghaznavi 98-49-6
G-29	Tatara × Takbir-19-16	G-70	Wafaq × Ghaznavi 98-49-9
G-30	Tatara × Takbir-19-18	G-71	Wafaq × Ghaznavi 98-49-10
G-31	Tatara × Ghaznavi 98-22-1	G-72	Wafaq × Ghaznavi 98-49-12
G-32	Tatara × Ghaznavi 98-22-2	G-73	Wafaq × Ghaznavi 98-49-13
G-33	Tatara × Ghaznavi 98-22-6	G-74	Wafaq × Ghaznavi 98-49-15
G-34	Tatara × Ghaznavi 98-22-8	G-75	Wafaq × Ghaznavi 98-49-16
G-35	Tatara × Ghaznavi 98-22-9	G-76	Wafaq × Ghaznavi 98-49-19
G-36	Tatara × Ghaznavi 98-22-12	G-77	Wafaq × Ghaznavi 98-49-20
G-37	Tatara × Ghaznavi 98-22-13	G-78	Tatara × Takbir-19-17
G-38	Tatara × Ghaznavi 98-22-19	G-79	Tatara × Takbir-19-18
G-39	Tatara × Ghaznavi 98-22-20	Check	Janbaz
G-40	Tatara × Inqilab-26-4	Check	Atta-Habib
G-41	Tatara × Inqilab-26-6		
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Code

G-42

G-43

G-44

G-45

Pedigree

Tatara x Inqilab-26-7

Tatara × Inqilab-26-11

Tatara × Inqilab-26-15

Tatara × Inqilab-26-20

generation, single heads were selected from the bulk populations based on agronomic fitness and disease resistance. The $F_{5:6}$ heads were raised as head-to-row for seed multiplication and disease screening against stripe rust in particular. However, lines were found





segregating for stripe rust resistance. Therefore, twenty heads were hand harvested and planted as head-torow during 2012/13. The heavy infestation of stripe and leaf rusts fungi offered opportunity for screening $F_{5:7}$ RILs. For the current study, 79 $F_{5:8}$ RILs were selected for further evaluation in multi-location trials over years.

Experimental design and procedure

Eighty-one genotypes including 79 $F_{5:8}$ RILs and two check cultivars Janbaz and Atta-Habib were field-tested in nine environments during 2013/14, 2014/15 and 2015/16. List of genotypes with parentage is given in Table 2. Experimental materials were planted in 9×9 alpha lattice design with two replicates at each environment. Each plot had 6 rows of 5-meter length and a row-to-row space of 30 cm. Standard dose of nitrogen (120 kg ha⁻¹) and phosphorous (80 kg ha⁻¹) was applied. Uniform cultural practices required for wheat crop were followed throughout the growing season.

Traits measurement

Data were recorded on yield and yield components i.e. tillers⁻²,grains spike⁻¹and 1000-grain weight following the procedure described by Sayre et al. (1997).

Statistical analysis

Analysis of variance: Data recorded on various yield and yield associated traits were statistically analyzed across nine environments appropriate for alpha lattice design using SAS computer program (SAS, 2009). Upon significant differences, means were separated using LSD test at 5% level of probability.

Correlation analysis: Genetic correlations for various morphological and yield traits were computed following the procedure of Singh and Chaudhry (1997) using the following formula:

Genetic correlation
$$(r_G) = \frac{COV_{G(x_1x_2)}}{\sqrt{\delta^2_{G(x_1)}\delta^2_{G(x_2)}}}$$

Results and Discussion

Combined analysis of variance

Combined analysis of variance depicted highly significant differences among genotypes and genotype by environment interactions (GEI) for all traits. (Table 3). Significant GEI exhibited that the performance of genotypes was not stable across different environments and hence justified to proceed for further analysis of genotypes in individual environments. Mean performance of genotypes for various yield and associated traits are discussed below:

Mean Performance

Tillers⁻²: Productive tillers are considered as one of the important traits in wheat production. It has been estimated that approximately 30 to 50% of the grain yield in wheat comes from the main stem and 50 to 70% comes from the tillers under normal conditions (Elhani et al., 2007). Combined analysis of variance depicted significant differences (P≤0.01) among genotypes, environments and GEI for tillers m⁻². Percent variation due to GEI (45.1%) was four times more than the combined effect of environments (6.1%) and genotypes (6.6%), exhibiting that mean performance and ranking of genotypes were mainly due to their interaction with environments (Table 3). Averaged over nine environments, tillers m⁻² ranged from 128 to 180 tillers with the mean value of 153 tillers (Table 4). Maximum number of tillers was produced by G-79 (181 tillers), followed by genotypes G-08 (174 tillers) and G-41 (171 tillers), whereas minimum number of tillers were noted for G-67 (129 tillers). Among environments, tillers m⁻² ranged from 92 to 229 in E-01; 91 to 229 in E-02; 77 to 224 in E-03; 100 to 198 in E-04; 76 to 220 in E-05; 99 to 275 in E-06; 94 to 229 in E-07; 97 to 178 in E-08 and 92 to 210 in E-09. Genotype G-26 produced maximum tillers in E-01 (229 tillers), G-79 in E-02 (229 tillers), G-39 in E-03 (224 tillers), G-6 (198 tillers) in E-04, G-79 in E-05 (220 tillers), G-31 in E-06 (275 tillers),

Table 3: Pooled mean squares for various traits of 81 wheat genotypes across nine environments.

Traits	Environment (df=8)		Genotypes (df=80)		G × E (df=640)			Replica-	S-Block			
	SS	MS	%SS	SS	MS	%SS	SS	MS	%SS	tion (E) df=9)	(Rep(E)) (df=144)	(dt=576)
Tillers m ⁻²	102377.2	12797.1**	6.1	111369.9	1392.1**	6.6	763321.3	1192.7**	45.1	7599.1	978.4	680.9
Grains spike ⁻¹	504.8	63.1 [*]	0.4	21226.0	265.3**	18.7	54614.8	85.3**	48.1	63.1	51.7	28.4
1000-grain weight	1262.6	157.8**	2.2	5022.5	62.8**	8.8	23430.0	36.6**	41.1	40.0	44.5	30.3
Grain yield	68250000	8531091.8**	7.7	106800000	1334496.7**	12.1	455800000.0	712153.4**	51.7	2028789.2	298973.5	187534.1
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G-28 in E-07 (229 tillers) G-6 in E-08 and G-19 in E-09 (210 tillers). None of the genotypes completely dominated rest of the genotypes at all environments, showing site specific performance for tillers m^{-2} . En-

vironment E-06 (163 tillers) and E-09 (145 tillers) were declared as highly productive and less productive environments, respectively for of tillers m⁻² (Figure 1).

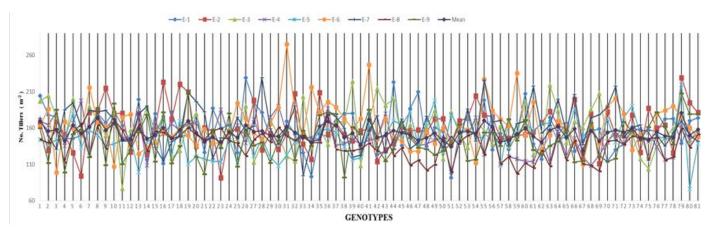


Figure 1: Mean values for tillers m^{-2} of 81 wheat genotypes over nine environments.

Table 4: Descriptive statistics of	f 81	1 guheat genotypes	for marious	traits across	nine enquironments
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	Parameter	Tiller ⁻²	Grains spike ⁻¹	1000-grain weight	Grain yield
Across nine envi- ronments	Range	128-180	50.7-70.7	33.4-44.3	2804-4862
	Desirable RIL	G-79	G-79	G-72	G-79
	Mean	153	60	38.3	3438
E-01	Range	91-229	42-83	29.1-51.7	1938-5272
	Desirable RIL	G-26	G-79	G-36	G-7,G-79
	Mean	157	60	39.2	3597
E-02	Range	91-229	42-83	29.1-51.7	1630-4975
	Desirable RIL	G-79	G-51	G-08	G-9,G-79
	Mean	161	60	39.2	3670
E-03	Range	77-224	46-85	25.1-65.9	1939-5071
	Desirable RIL	G-39,G-63	G-79	G-40	G-49
	Mean	158	60	39.9	3620
E-04	Range	100-198	42-83	27.6-55.7	1931-5106
	Desirable RIL	G-06	G-79	G-14	G-37,G-79
	Mean	148	60	37.2	3302
E-05	Range	76-220	43-85	28.0-56.0	1873-5035
	Desirable RIL	G-79	G-41	G-79	G-41,G-79
	Mean	147	60	37.2	3284
E-06	Range	99-275	47-76	27.3-51.4	2023-4920
	Desirable RIL	G-31,G-41	G-78,G-79	G-46	G-41,G-79
	Mean	163	61	37.4	3608
E-07	Range	94-229	47-76	31.4-49.8	1938-5024
	Desirable RIL	G-19,G-28	G-12,G-26	G-36,G-79	G-08,G-79
	Mean	161	61	38.1	3615
E-08	Range	97-178	43-76	27.6-51.1	1931-4906
	Desirable RIL	G-10,G-36	G-25,G-79	G-37	G-37,G-79
	Mean	137	59	37.9	3089
E-09	Range	92-210	47-73	32.9-50.5	2109-4886
	Desirable RIL	G-19,G-79	G-54	G-77,G-79	G-79
	Mean	145	59	38.8	3150

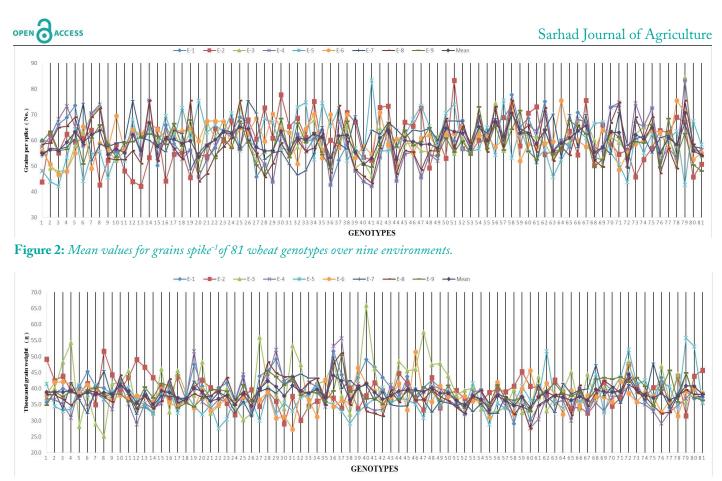


Figure 3: Mean values for 1000-grain weight of 81 wheat genotypes over nine environments.

Grains spike⁻¹: Pooled analysis of variance for grains spike⁻¹ unveiled significant differences ($P \le 0.01$) among genotypes, environment and GEI. The GEI explained 48.1% of the total variation, while genotypes and environments captured 18.7% and 0.4%, respectively. Significant differences among genotypes for grain spike⁻¹ provide room for selecting desirable genotype; however, selection should be environment specific due to significant GEI effect (Table 3). Mean over nine environments, grains spike⁻¹ ranged from 51 grains to 71 grains with a mean value of 60 grains (Table 4). Maximum number of grains spike⁻¹ was observed for G-79 (71 grains), followed by genotype G-58 and G-56, while minimum number of grains spike⁻¹ was noticed for G-40 (51 grains). G-79 produced maximum grains spike⁻¹ in all environments except E-06, E-07 and E-09, indicating its superiority and stability across environments. Within environments, grains spike⁻¹ ranged from 42 grains to 83 grains in E-01; 44 grains to 80 grains in E-02; 46 grains to 85 grains in E-03; 42 grains to 83 grains in E-04; 43 grains to 85 grains in E-05; 47 grains to 76 grains in E-06; 45 grains to 78 grains in E-07; 43 grains to 76 grains in E-08 and 47 grains to 73 grains in E-09 (Figure 2).

1000-grain weight: Combined analysis of variance March 2018 | Volume 34 | Issue 1 | Page 59 revealed significant differences (P \leq 0.01) among genotypes, environments and their interactions. The GEI explained maximum variation of 41.1% of total sum of squares, which is four times larger than both genotypes (8.8%) and environment (2.2%) (Table 3). Mean over nine environments, 1000-grain weight ranged from 33.4 to 44.3 g with a mean value of 38.3 g (Table 4).

Maximum 1000-grain weight was noted for G-72 (44.3 g), followed by G-36 and G-37, whereas minimum value was recorded for genotype G-55 (33.4 g). Among environments, 1000-grain weight ranged from 29.1 to 51.9 g in E-01; 27.1 to 50.2 g in E-02; 25.1 to 65.9 g in E-03; 27.6 to 55.7 g in E-04; 28.0 to 56.0 g in E-05; 27.3 to 51.4 g in E-06; 41.1 to 49.8 g in E-07; 27.6 to 51.1 g in E-08 and 32.9 to 50.5 g in E-09. Maximum 1000-grain weight was recorded for G-36 in E-01, G-08 in E-02 G-40 in E-03, G-14 in E-04, G-79 in E-05, G-46 in E-06, G-36 in E-07, G-37 in E-08 and G-37 in E-09. For 1000-grain weight, E-03 (39.9 g) and E-05 (37.2 g) were declared as highly productive and least productive environments, respectively (Figure 3).

Grain yield : Analysis of combined data exhibited

significant differences (P≤0.01) among genotypes, environments and GEI for grain yield. Although, environments and genotypes were significant but they capturedleast sum of squares of 2.2% and 8.8%, respectively. Correspondingly, GEI captured 51.7% of the total variation, exhibiting its role in mean performance and ranking of genotypes across environments (Table 3). Averaged over nine environments, grain yield ranged from 2804 to 4862 kg ha⁻¹ with mean value of 3438 kg ha⁻¹ (Table 4). Overall, 33 out of 81 genotypes had higher yielding than mean yield, while 21 out of 79 had higher yield than both check cultivars. Genotype G-79 produced maximum grain yield (4862 kg ha⁻¹), followed by G-08 (4195 kg ha⁻¹), G-56 (4030 kg ha⁻¹) and G-37 (4003 kg ha⁻¹), whereas minimum value for grain yield was noticed for G-40 (2804 kg ha⁻¹). Grain yield ranged from 2024 to 5272 kg ha⁻¹ in E-01; 1980 to 4975 kg ha⁻¹ in E-02; 1938 to 5102 kg ha⁻¹ in E-03;1995 to 5106 kg ha⁻¹ in E-04; 1931 to 5035 kg ha⁻¹in E-05; 1897 to 5100 kg ha⁻¹ in E-06; 1974 to 5024 kg ha⁻¹ in E-07; 1941 to 4906 kg ha⁻¹ in E-08 and 2110 to 4886 kg ha⁻¹ in E-09. Genotype G-8 (5272 kg ha⁻¹) produced maximum grain yield in E-01, G-9 (4975 kg ha⁻¹) in E-02, G-49 (5071 kg ha⁻¹) in E-03, G-79 (5106 kg ha⁻¹) in E-04, G-79 (5035 kg ha⁻¹) in E-05, G-79 (4920 kg ha⁻¹) in E-06, G-79 (5024 kg ha⁻¹) in E-07, G-79 (4906 kg ha⁻¹) in E-08 and G-79 (4886 kg ha⁻¹) in E-09. E-01 (5272 kg ha⁻¹) and E-09 (4886 kg ha⁻¹) appeared as high and least productive environments, respectively (Figure 4).

Correlation analysis: Correlation coefficients among yield and yield associated traits were computed based on mean data of 81 genotypes over nine environments. Correlation analysis depicted that grain yield had strong positive association with tillers m⁻² ($r_g = 0.72^{**}$), grains spike⁻¹ ($r_g = 0.41^{**}$) and 1000-grain weight ($r_g = 0.41^{**}$)

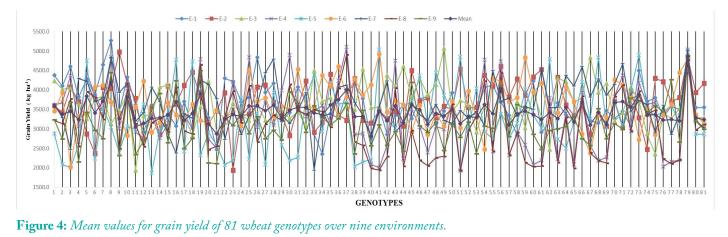
0.30^{**}). Positive relationship of these aforementioned traits with grain yield indicated that these traits had major contribution towards grain yield in wheat (Table 5). Therefore, these traits needs due weightage in selecting wheat genotypes for higher grain yield.

Table 5: Genetic correlation coefficient among yield and yield components of 81 wheat genotypes across nine environments.

Traits	Tiller ⁻²	Grains spike ⁻¹	1000-grain weight	Grain yield
Tiller ⁻²	-	-0.11 ^{ns}	0.20 ^{ns}	0.72**
Grains spike ⁻¹		-	-0.50**	0.41**
1000-grain weight			-	0.30**
Grain yield				-

Pooled analysis of variance revealed significant differences among genotypes, environment and their interaction for tillers m⁻², grains spike⁻¹, 1000-grain weight and grain yield. Previously, Elhani et al. (2007), Ali et al. (2008), Shankarrao et al. (2010), Mohammadi et al. (2012), Mehari et al. (2015), and Ebrahimnejad and Rameeh (2016) also reported similar results in wheat. Contrarily, Khan et al. (2010) and Motamedi et al. (2013) reported non-significant differences among genotypes, environments and their interaction for tillers m⁻² and for 1000-grain weight in wheat. Contradictory findings in this regard may be due to difference in genetic makeup of genotypes tested, environmental conditions or both.

In every plant breeding program the integral component is to develop high yielding line/cultivar which determines future of the crop and its growers (Muflin, 2000). For plant breeder there are many challenges to get besides, maintain high productivity and effective practice is to subjecting potential lines to a series of



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diverse environmental conditions to identify the best stable yielding genotypes (Kaya et al., 2002; Roozeboom et al., 2004; Loffler et al., 2005). Favorable conditions during flowering and pollination result in higher number of fertile tillers⁻² and grains spike⁻¹(Agoston and Pepo, 2005). Tillers m⁻², grains spike⁻¹ and 1000-grain weight are very important and direct contributing traits towards grain yield in wheat, therefore stability of these traits leads to grain yield stability (Dreccer et al., 2008). G-79 produced maximum number oftillers m⁻²and grains spike⁻¹ in almost all environments. Through tillers m⁻², grains spike⁻¹and 1000-grain weight considerable genetic progress for higher yield was achieved (Sayre et al., 1997).

Correlation analysis revealed that grain yield had positive associations with tillers plant⁻¹, number of grain spike⁻¹and 1000-grain weight. Mohsen et al. (2012) also reported that grain yield had positive correlations with above mentioned traits and suggested that plant breeders should consider these traits in breeding wheat for grain yield improvement.

Conclusions

Significant genetic differences among genotypes for yield and yield components exhibited the existence of sufficient variability to have an effective selection. Similarly, significant genotype by environment interactions (GEI) indicated inconsistent performance of genotypes across environments for almost all traits. The GEI captured major part of sum of squares exhibiting its greater effects in the phenotypic expression of all traits. Correlation analysis revealed significant positive associations of grain yield with tillers m⁻², grains spike⁻¹ and 1000-grain weight indicating that these traits had major contribution towards grain yield in wheat. Genotype G-79 exhibited maximum tillers m⁻², grains spike⁻¹ and grain yield across all environments, and was thus identified as high yielding genotype for commercialization in Khyber Pakhtunkhwa.

Author's Contributions

This research article is an integral part of doctoral study of the first author MAUK. MAUK and FM) formulated the research. MAUK performed the experiments and wrote the first draft of the manuscript. FM made critical corrections in the first draft. Both authors read and approved the final manuscript.

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