



HERITABILITY, SELECTION RESPONSE AND CORRELATION FOR YIELD AND YIELD COMPONENTS IN IRRIGATED WHEAT

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ABSTRACT

Eighteen wheat genotypes along with two check cultivars (Pirsabak-2004 and Bathoor) were evaluated at three locations of Khyber Pakhtunkhwa. Analysis of variance across three locations revealed significant differences among wheat genotypes and locations for tillers m⁻², spike length, grains spike⁻¹, 1000-grain weight and grain yield. Genotype × location interaction was also significant ($P \leq 0.05$) for all studied traits indicating differential performance of genotypes over the three locations. Ranking of wheat genotypes for major yield components varied over three locations. Maximum tillers m⁻² were produced by genotype WG-08036 at AUP (421 tillers m⁻²), WG-08019 at NIFA (354 tillers m⁻²) and CT-08055 and WL-08109 at CCRI (287 tillers m⁻²). Genotypes SRN-55, SRN-28 and CT-0905 were high grain yielder at AUP (7222 kg ha⁻¹), NIFA (4756 kg ha⁻¹) and CCRI (5859 kg ha⁻¹). Moderate broad sense heritability estimates ($h^2_{B.S} = 0.40-0.70$) were observed for spike length, 1000-grain weight and grain yield, whereas, low broad sense heritability ($h^2 \leq 0.40$) were recorded for tillers m⁻² and grains spike⁻¹ over the three test locations. Grain yield exhibited significantly positive genetic correlation with tillers m⁻² ($r_G = 0.32$, $P < 0.01$) and grains spike⁻¹ ($r_G = 0.35$, $P < 0.01$) while strong positive phenotypic correlation was observed with 1000-grain weight ($r_P = 0.44$, $P < 0.05$).

Keywords: wheat, genetic correlation, heritability, selection response.

INTRODUCTION

Bread wheat (*Triticum aestivum* L.) has got a very unique position among the cereal crops as it is cultivated throughout the world over a wide range of environments. World's wheat production was 665.8 million tons during 2009-10, while in Pakistan, 23.8 million tons wheat was produced in year 2009-10 (MINFAL- 2009). There is a large gap between yield potential of modern wheat cultivars and farmer's yield, indicating that crop yield can be improved by using better crop husbandry. High yielding wheat cultivars with improved traits are being continuously developed throughout the world using conventional mutation and biotechnological approaches (Khalil *et al.*, 2010). Newly developed genetic material is evaluated in segregating generations (F2-F6), and lines possessing desired traits are selected for further evaluation in multi-year and location trials. The selected promising lines are then tested at different locations to ascertain genotype × environment interaction effects and their stability and adaptability over environments. The genotype × location and genotype × year interactions measure the consistency of performance of genotypes at different locations and in different years, respectively (Fehr, 1993). The lack of statistically significant interactions involving genotypes simplifies the nature of testing (at several locations/years) required for cultivar development and also simplifies cultivar selection by producer. As such, the lack of significant interaction of genotype with location, year or location × year indicates that evaluation at one location during one year would be sufficient to identify genotypes with superior genetic potential.

Heritability, a measure of phenotypic variance attributable to genetic causes, has the task of predicting crop breeding (Songsri *et al.*, 2008). The heritability of the character determines the extent that is passed from one generation to the next, and is more valuable tool when used in conjunction with other parameters in the prediction of genetic gain that follows in the selection for the character (Afiah *et al.* 2000; Baloch *et al.* 2003). The highest estimates of heritability, the simpler the selection procedure (Khan *et al.*, 2008). It has emphasized that heritability alone is not enough to make enough improvement to overall selection in advanced generations unless accompanied by substantial amount of genetic advance. The utility of heritability therefore increases when used to calculate genetic advance, which indicates the degree of a character gain obtained under particular selection pressure (Shukla *et al.*, 2004).

Grain yield is a polygenic trait and is a product of expressions of many genes. Grain yield is governed by several metric traits like tillers per unit area, spike length, grains per spike and grain weight, and there is usually positive directed correlation between them. Several research studies have been carried out on relationship of various yield components with grain yield and its related traits (Yousaf *et al.*, 2008). It has been reported that selection on the basis of such correlation studies can lead to better selection of genotypes with appropriate grain yield. It is also effective to select genotypes on the basis of performance of yield associated traits (Majid *et al.*, 2007). The objectives of the present study were (i) to investigate genotype × location interaction for morphological and yield related traits in wheat under irrigated conditions, (ii)



to estimate heritability and selection response for yield components in wheat at three locations of Khyber Pakhtunkhwa (Peshawar, NIFA and Pirsabak) and (iii) to determine relationship among various traits of wheat at genetic and phenotypic level.

MATERIALS AND METHODS

Micro plot trails (MPT) consisting of 18 wheat genotypes and two commercial check cultivars were evaluated at three locations viz. (i) Agricultural University Peshawar (AUP), (ii) Nuclear Institute for Food and Agriculture (NIFA) and (iii) Cereal Crop Research Institute (CCRI), Pirsabak (Nowshera). The MPT were used as independent experiment under irrigated condition at each location in a randomized complete block design with three replications. The 18 wheat lines were CT-09056, WG-08018, CT-08055, WG-08036, WL-0912-1, SRN-47, WL-08109, SRN-65, WL-0912-4, WG-08032, SRN-55, WG-08099, SRN-37, SRN-28, CT-0905, WG-08019, CT-09128 and CT-09115, while Bathoor and Pirsabak-2004 were the two check cultivars. The experiments were planted during mid-November 2011 at each test location. A plot for each genotype consisted of 5m long four rows with row-to-row distance of 0.30m. Recommended dose of fertilizer, irrigation and other cultural practices essential for crop management were applied at each test location. At proper maturity, data were recorded for tillers m^{-2} , spike length, grains $spike^{-1}$, 1000-grain weight and grain yield.

Statistical analyses

Data were analyzed across three test locations using mixed effects model to ascertain genotype \times location interaction effect for each trait (Annicchiarico, 2002). The mean squares pertaining to genotype \times location interaction was used as an error term to test the significance of locations and genotypes main effect, while significance of genotype \times location interaction was determined by using mean squares of pool error. Since, genotype \times location interaction effect was significant for most of the traits,

data were also analyzed independently for each location to compute genetic and environmental variances required for estimation of broad sense heritability and selection response of traits (Singh and Chaudhery, 1997). A similar selection intensity of 20% assumed at each location, wherein $i = 1.40$ in formula of selection response (Fehr, 1993). Genetic and Phenotypic correlation among traits were also computed by pooling data over the three locations as proposed by Annicchiarico (2002).

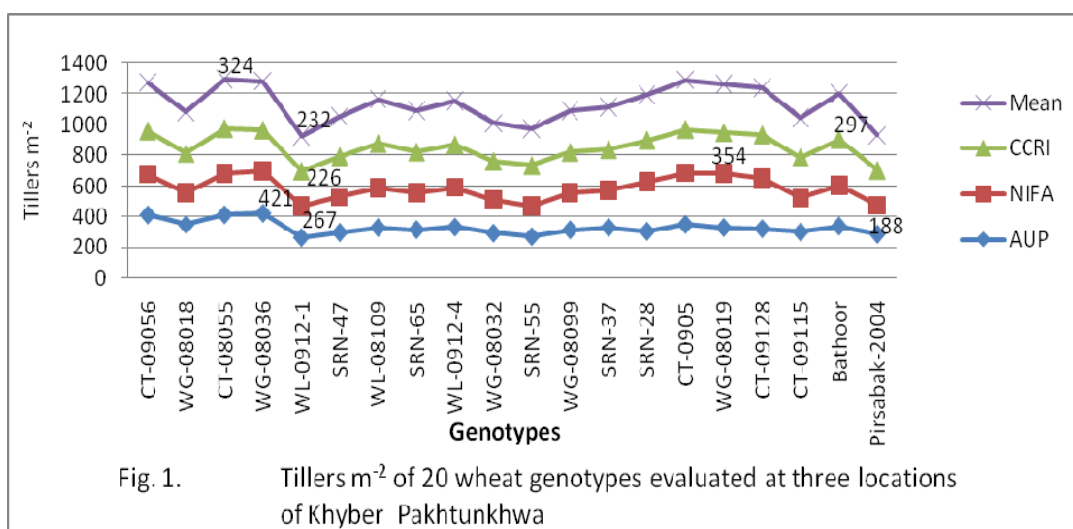
RESULTS AND DISCUSSIONS

Tillers m^{-2}

Analysis of variance over three locations revealed highly significant differences ($P \leq 0.01$) among locations, genotypes and genotype \times location interaction (Table-1). The significant genotype \times location interaction indicates that genotypes differed in production of tillers over the three locations. Tillers m^{-2} is an important yield contributing trait and leads to increased biological and grain yield (Farroq *et al.*, 2010). Mean tillers m^{-2} ranged from 267 to 421 at AUP for genotypes WL-0912-1 and CT-09056, 188 to 354 at NIFA for check cultivar Pirsabak-2004 and genotype WG-08019 and 225 to 297 at CCRI for genotype WG-08018 and check cultivar Bathoor, respectively (Figure-1). Averaged across three locations, genotype CT-08055 produced maximum tillers m^{-2} (324) while genotype WL-0912-1 produced minimum (232) tillers m^{-2} (Figure-1). Low broad sense heritability (0.37) was observed for tillers m^{-2} at AUP whereas moderate heritability (0.52) was recorded at NIFA (Table-2). These results are in accordance with those of Khan (2000), and Wajid *et al.* (2004) who also reported low to medium narrow and broad sense heritability for tillers in wheat. At CCRI, heritability was not determined due to zero genetic variance. Tillers m^{-2} exhibited positive and highly significant genetic correlation with all parameters except 1000-grain weight while it showed positive and significant phenotypic correlation with spike length and 1000-grain weight (Table-3).

Table-1. Mean squares for yield and yield related traits of 20 wheat genotypes.

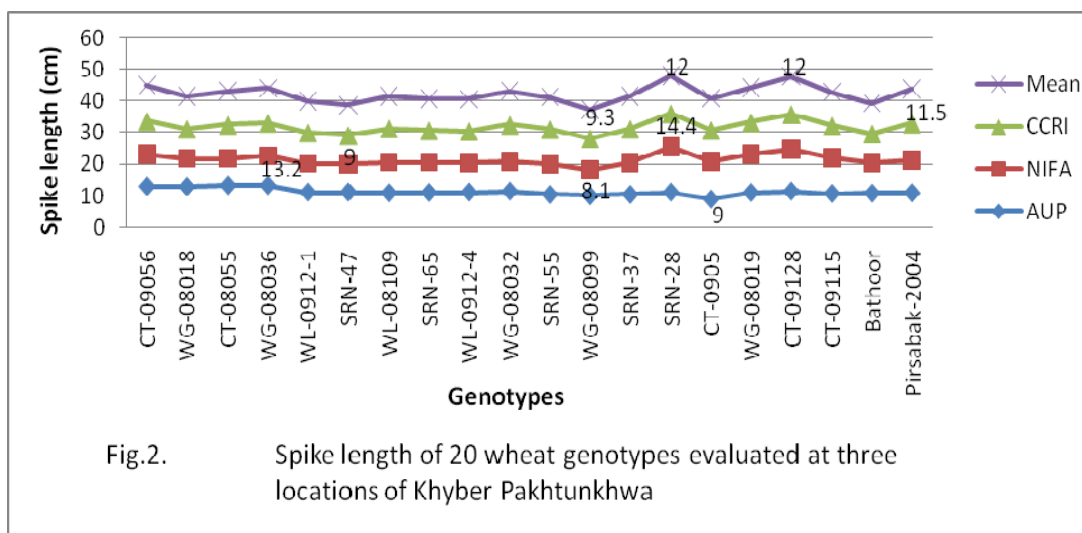
Source	DF	Tillers m^{-2}	Spike length	Grains $spike^{-1}$	1000-grain weight	Grain yield
Loc	2	34611.0**	19.48**	6185.6**	2025.7**	30405687.2**
Rwp w/n Loc	6	-	-	-	-	-
Genotype	19	8144.2**	4.3**	171.9*	65.9*	1362685.2**
Gentype x Loc	38	2757.2*	4.3**	151.8*	52.4*	653975.8**
Error	114	1680.2	1.4	97.9	34.8	249283.6
CV %		14.43	11.25	19.23	14.06	10.1



Spike length

Analysis of variance across three locations showed highly significant ($P \leq 0.01$) differences among locations and genotypes for spike length (Table-1). Genotype \times location interaction was significant indicating that genotypes differed for spike length over three locations. Spike length is an important yield contributing trait and has a direct contribution to grains $spike^{-1}$ and grain yield (Fischer and Byerlee, 1991). The results of the present study are supported by the findings of Khalil *et al.* (2006) who have reported significant differences among wheat genotypes for spike length. Across three locations, genotype WG-08099 had the minimum spike length (9 cm), while the maximum spike length (12 cm) was recorded for genotype SRN-28 (Table-4). Moderate broad sense heritability (0.55) along with a selection response of

1.01cm was recorded for spike length (Table-2). Low heritability were observed at AUP (0.28) and CCRI (0.18) with expected selection response of 0.50 and 0.25cm, respectively, showing that at these two locations selection for this trait will be less effective. Spike length exhibited positive and highly significant ($P \leq 0.01$) genetic correlation with all parameters except grain yield. Anwar *et al.* (2009) and Shah *et al.* (1988) have also reported positive genetic association of spike length with grains $spike^{-1}$. It also showed significantly positive ($P \leq 0.01$) phenotypic correlation grains $spike^{-1}$ ($r_p = 0.79$, $P \leq 0.01$) and 1000-grain weight ($r_p = 0.71$, $P \leq 0.01$) (Table-12). Singh *et al.* (1995) and Akram *et al.* (2008) who have also reported significantly positive phenotypic association of spike length with grains $spike^{-1}$, 1000-grain weight and other yield related traits in wheat.



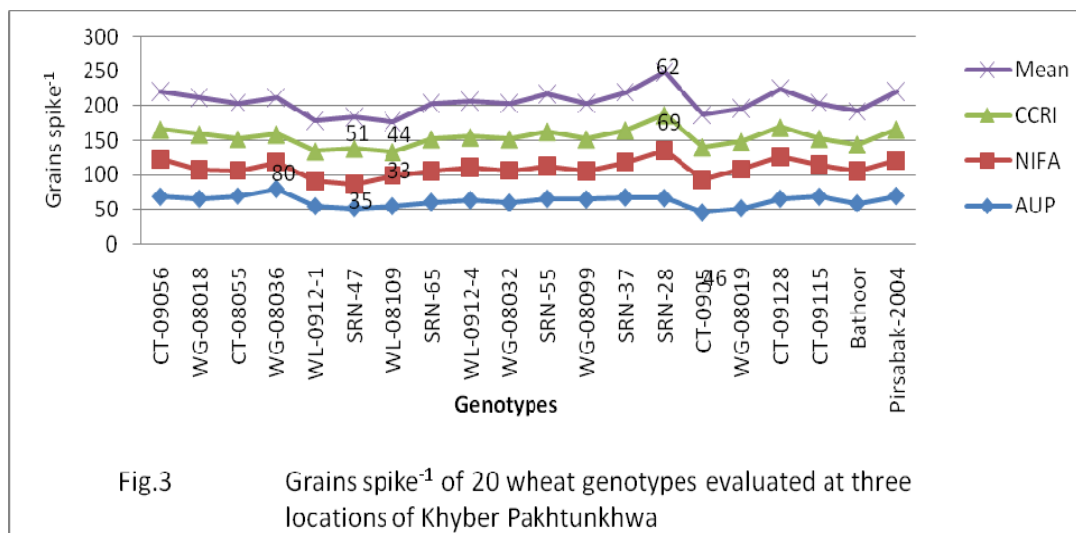
**Table-2.** Genetic (Vg) and environmental (Ve) variances, heritability (h²) and selection response (Re) for yield and yield components traits in irrigated wheat.

Traits	Location	Vg	Ve	h ²	Re
Tillers m ⁻² (no.)	AUP	1183.80	2031.10	0.37	23.23
	NIFA	1806.20	1654.80	0.52	29.72
	CCRI	Not calculated due to non-significant <i>F</i> -test			
Spike length (cm)	AUP	0.62	1.56	0.28	0.50
	NIFA	2.10	1.74	0.55	1.01
	CCRI	0.21	0.94	0.18	0.25
Grains spike ⁻¹ (no.)	AUP	22.09	124.04	0.15	2.36
	NIFA	42.50	82.86	0.34	4.32
	CCRI	Not calculated due to non-significant <i>F</i> -test			
1000-grain weight (g)	AUP	Not calculated due to non-significant <i>F</i> -test			
	NIFA	27.37	10.91	0.71	3.31
	CCRI	Not calculated due to non-significant <i>F</i> -test			
Grain yield (kg ha ⁻¹)	AUP	317551.00	403606.00	0.44	391.64
	NIFA	Not calculated due to non-significant <i>F</i> -test			
	CCRI	327711.40	182828.80	0.64	384.25

Grains spike⁻¹

Analysis of data for grains spike⁻¹ over the three locations revealed highly significant ($P \leq 0.01$) differences among locations. Differences among genotypes and genotype \times location interaction were also significant (Table-1). Grains spike⁻¹ is an important yield contributing trait and has a direct effect on grain yield (Ashfaq *et al.*, 2003). These results are in accordance with those of Shoran *et al.* (2000) who also reported significant differences among wheat genotypes for grains spike⁻¹. Grains spike⁻¹ of 20 wheat genotypes ranged from 46 to 80 for genotypes CT-0905 and WG-08036 at AUP, 35 to 69 for genotypes SRN-35 and SRN-28 at NIFA and 33 to 51 for genotypes WL-08109 and WG-08018 at CCRI (Figure-

3). Averaged over three locations, number of grains spike⁻¹ ranged from 44 to 62 for genotypes WL-08109 and SRN-28, respectively followed by CT-09128 (56) and check cultivar Pirsabak-2004 (Figure-3). Low heritability (0.15) was observed for grains spike⁻¹ at AUP because genetic variance was lower in magnitude (22.09) than environmental variance (124.04). Likewise, at NIFA genetic variance (42.50) was lower than environmental variance (82.96) resulting in low heritability (0.34) (Table-2). The obtained results are in line with those of Sharma *et al.* (1995), Ansari *et al.* (2004) and Eid (2009) who also reported low heritability for grains spike⁻¹ in wheat. The expected selection responses for AUP and NIFA were observed as 2.36 and 4.32, respectively (Table-2).





Grain spike⁻¹ showed significantly positive genetic correlation with tillers m⁻², ($r_G=0.47$, $P \leq 0.01$), spike length ($r_G=0.53$, $P \leq 0.01$) and grain yield ($r_G=0.35$, $P \leq 0.01$) (Table-3). Grains spike⁻¹ also showed positive and significant phenotypic correlation with spike length ($r_p=0.79$, $P \leq 0.01$) and 1000-grain weight ($r_p=0.47$, $P \leq$

0.05) (Table-3). These results are in conformity with the findings of Budak and Yildirim (1995, 1999), and Shoran *et al.* (2000) who also observed positive phenotypic correlation of grains spike⁻¹ with spike length and other yield contributing traits.

Table-3. Genetic (above diagonal) and Phenotypic (Below diagonal) correlation among various yield component traits in irrigated wheat.

	Tillere m ⁻²	Spike length	Grain spike ⁻¹	1000-grains weight	Grain yield
Tillers m ⁻²	-	0.40**	0.47**	-0.04 ^{NS}	0.32**
Spike length	0.55**	-	0.53**	0.15*	0.13 ^{NS}
Grain spike ⁻¹	0.31 ^{NS}	0.79**	-	-0.24**	0.35**
1000-grain weight	0.60**	0.71**	0.47*	-	-0.05 ^{NS}
Grain yield	0.07 ^{NS}	0.28 ^{NS}	0.25 ^{NS}	0.44*	-

1000-grain weight (g)

1000-grain weight is one of the most important yield contributing traits and is considered as potential selection criteria for yield under different environments. It is influenced by genetic as well as by environmental factors (Hamam *et al.*, 2009 and Hadjichristodoulou, 1990). Analysis of data for 1000-grain weight of 20 wheat genotypes across locations showed significant differences among the three test locations ($P \leq 0.01$) and genotypes ($P \leq 0.05$) (Table-1). Genotype \times location interaction was also significant indicating the differential performance of wheat genotypes for 1000-grain weight over three locations (Table-1). Our findings are in close agreement with those of Ansari *et al.* (1989.) and Tahir *et al.* (2009) who also reported significant differences among wheat genotypes for 1000-grain weight. 1000-grain weight of 20 wheat genotypes averaged over three locations ranged from 38.1 to 49.2g for genotype SRN-65 and CT-09128, respectively (Figure-4). At AUP genotype SRN-65 had the minimum 1000-grain weight (32.6g) whereas genotype

CT-08055 had the maximum (42.9 g). At NIFA, 1000-grain weight ranged from 32.8 to 50.7g for genotypes SRN-65 and CT-0905 while it ranged from 41.4 to 60.2g at CCRI for genotypes WL-0912-1 and CT-09128, respectively (Figure-4). 1000-grain weight is a vital yield component and is more or less stable character of wheat genotypes. However, under drought this trait is adversely affected tremendously and genotypes showing good grain weight under irrigated condition may not be able to produce grains of similar weight under drought stressed condition (Riaz, 2003). At NIFA, genetic variance (27.37) was higher in magnitude than the environmental variance (10.91) resulting in high heritability (0.71) and selection response (3.31g) for this trait (Table-2). It shows that selection at NIFA for this trait will be more effective than AUP and CCRI. These results are in close conformity with the previous work of Rebetzke and Richards (2000) and Mohsin *et al.* (2009) who also reported high heritability for 1000-grain weight. However, genetic variances for 1000-grain weight at AUP and CCRI were zero.

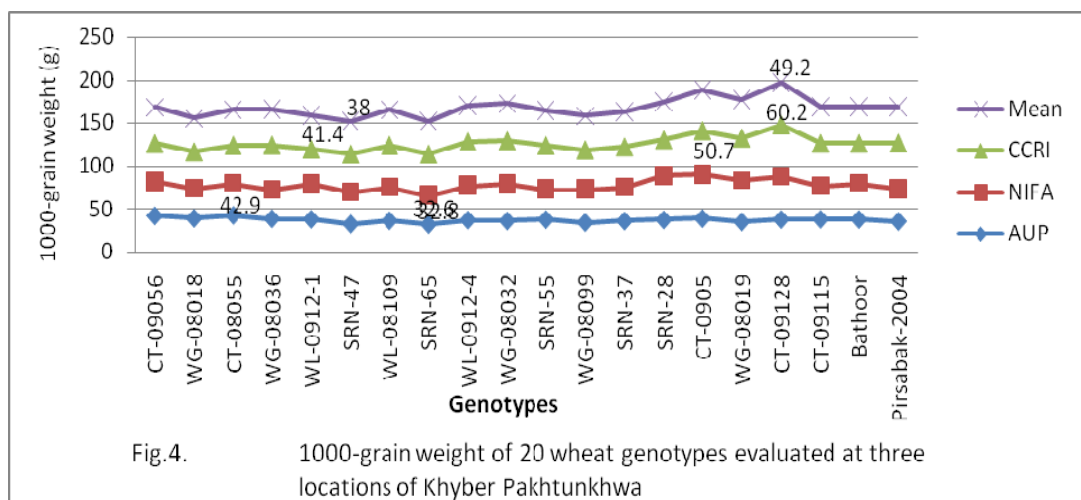


Fig.4. 1000-grain weight of 20 wheat genotypes evaluated at three locations of Khyber Pakhtunkhwa



1000-grain weight exhibited strong positive genetic correlation with spike length ($r_G = 0.15$, $P \leq 0.05$) while negatively correlated with grains spike⁻¹ ($r_G = -0.24$, $P \leq 0.01$). Furthermore, positive and significant phenotypic correlation was observed for 1000-grain weight with tillers m⁻² ($r_p = 0.60$, $P \leq 0.01$), spike length ($r_p = 0.71$, $P \leq 0.01$), grains spike⁻¹ ($r_p = 0.47$, $P \leq 0.05$) and grain yield ($r_p = 0.44$, $P \leq 0.05$) (Table-3). Our results are in close agreement with Mohsin *et al.* (2009) who also reported significant and positive correlation of 1000-grain weight with different yield and agronomic traits.

Grain yield (kg ha⁻¹)

The cumulative efforts of plant breeders for the improvement of different characters, in most cases, are concentrated for the improvement of grain yield. Analysis across the three locations showed highly significant differences ($P \leq 0.01$) among genotypes for grain yield

(Table-1). Differences among locations and genotype \times location interaction were also highly significant for grain yield (Table-1). Presence of significant genotype \times locations interaction showed that genotypes had differential performance for grain yield over the three locations. These results are in close agreement with the findings of Talebi *et al.* (2009) who observed significant differences in environments and genotype \times environment interaction for grain yield. Grain yield of 20 wheat genotypes ranged from 4000 to 7222, 3878 to 4756 and 3715 to 5859 kg ha⁻¹ at AUP, NIFA and CCRI, respectively (Figure-5). Averaged across three locations, CT-0905 was the top grain yield producing wheat genotype (5672 kg ha⁻¹) followed by SRN-55 with averaged yield of 5620 kg ha⁻¹. Seven of the 18-wheat lines included in the micro-plot trials produced more averaged yield than the best yielding check Pirsabak-2004.

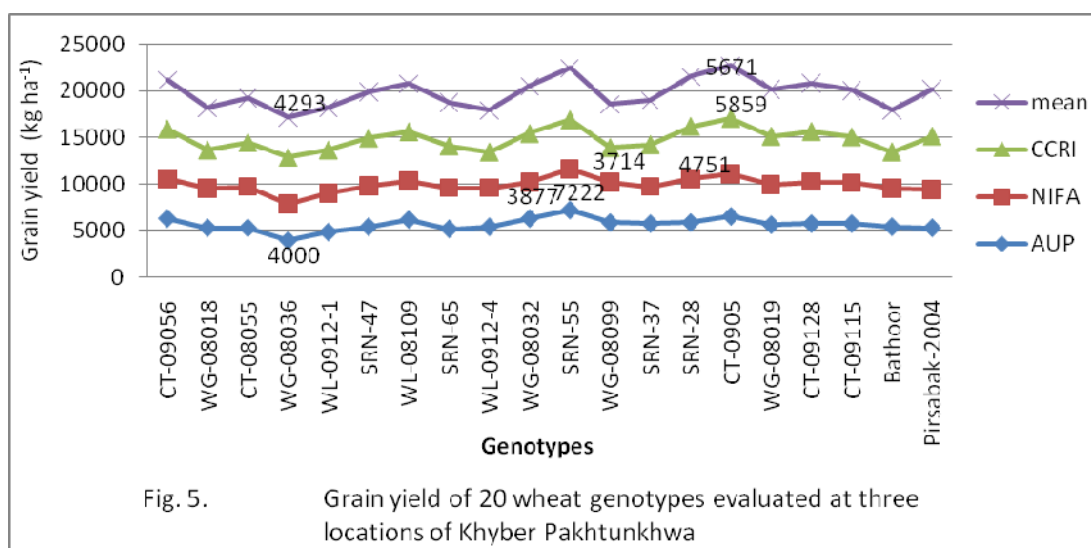


Fig. 5. Grain yield of 20 wheat genotypes evaluated at three locations of Khyber Pakhtunkhwa

Genetic variance for grain yield was greater than environmental variance at CCRI only (Table-2). Moderate broad sense heritability was recorded for grain yield at AUP (0.44) while high heritability (0.64) at CCRI. The expected selection response for grain yield was 392.6 and 384.3 kg ha⁻¹ at AUP and CCRI, respectively (Table-2). These results are supported by the findings of Kumar and Mishra (2004), Kumar *et al.* (2003) and Patal and Jain (2002) who also observed high heritability for grain yield. Grain yield is a complex trait and is made up of interaction between several yield components such as tillers m⁻², spike

length, grains spike⁻¹ and grain weight. (Sial *et al.*, 2005 and Anwar *et al.*, 2009). Grain yield exhibited significantly positive genetic correlation with tillers m⁻² ($r_G = 0.32$, $P < 0.01$) and grains spike⁻¹ ($r_G = 0.35$, $P < 0.01$) (Table-3). Tammam *et al.* (2000) and Narwal *et al.* (1999) also observed positive correlation of grain yield with biological yield and other yield contributing traits. Positive and significant phenotypic correlation of grain yield was observed 1000-grain weight ($r_p = 0.44$, $P < 0.05$) (Table-3).

**Table-4.** Mean of 4 top genotypes (Xs) and mean of check cultivars (Xc) at three test locations of Khyber Pakhtunkhwa.

Trait	Loc	Xs	Xc	Four top ranking genotypes
Tillers m ⁻² (no.)	AUP	399	313	WG-08036, CT-08055, CT-08056, CT-0905
	NIFA	336	227	WG-08019, CT-0905, CT-0912, SRN-28
	CCRI	283	261	WL-08019, CT-08055, CT-09128, CT-0905
	OVERALL	322	267	CT-08055, CT-0905, WG-08036, CT-09056
Spike length (cm)	AUP	13.0	10.8	CT-08055, WG-08036, CT-09056, WG-08018
	NIFA	13.0	10	SRN-28, CT-09128, WG08019, CT-0905.
	CCRI	11.1	10.3	WG-08032, CT-09128, SRH-55, SRN-37
	OVERALL	11.6	10.2	CT-09128, SRN-28, CT-09056, WG-08019
Grains spike ⁻¹ (no.)	AUP	72	64	WG-08036, CT-08055, CT-09056, CT-09115
	NIFA	61	49	CRN-28, CT-09128, WG08019, CT-09056
	CCRI	51	41	WG-08018, SRN-28, SRN-47, SRN-50
	OVERALL	57	48	SRN-28, CT-09128, SRN-37, SRN-55
1000-grain weight (g)	AUP	41.1	37.1	CT-08055, CT-09056, WG-08018, CT-0905
	NIFA	49.5	39	CT-0905, SRN-28, CT-09128, WG-08019
	CCRI	53.8	52	CT-09128, WG-08036, WL-0912-4, CT-0905
	OVERALL	44.6	39.3	CT-0905, WG-08019, CT-09128, SRN-28
Grain yield (kg ha ⁻¹)	AUP	6611	5388	SRN-55, CT-0905, WG-08032, CT-09056
	NIFA	4828	4144	SRN-28, CT-0905, CT-09128, SSRN-55
	CCRI	5484	4757	CT-0905, SRN-28, CT-09128, CT-09056
	OVERALL	5491	4763	CT-0905, SRN-55, SRN-28, CT-09056

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