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Evaluation of bread wheat genotypes for variability and association among yield and yield related traits

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Abstract

Ten wheat (*Triticum aestivum*L.) genotypes were evaluated for genetic variability for yield and association between different plant characters at Mountain Agricultural Research Station (MARC) Chilas during 2014-15.Analysis of variance revealed highly significant variation among different wheat genotypes for all traits studied. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) ranged from days to 50 % maturity (GCV=1.83, PCV=2.33) to grain weight yield per plot (GCV=18.48, PCV=18.59).PCV value for higher than GCV for all traits and narrow difference were found between GCV and PCV for most of traits. High heritability coupled with high genetic advance was estimated for traits like yield per hectare, total grain yield per plot, straw weight per plot and harvest index indicated these traits are under additive gene control and simple selection is effective for improvement of these traits. Yield per hectare showed positive and highly significant correlation with grain yield per plot ($r = 0.989^{**}$), 100 seeds weight ($r = 0.489^{**}$) and harvest index ($r = 0.648^{**}$).

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Introduction

Wheat (*Triticum aestivum*L.) is the leading grain crop of the world both in area and production (Deyong, 2011). About 20 percent of food calories for the world population is provided by wheat (FAOSTAT, 2015). In the world wheat occupied an area of 218.46 million hectares with annual production of 749.3 million tones and average production of 2900 kg ha^{-1}. In Pakistan, it contributes 2.1 % to GDP area under wheat cultivation was 9180 million hectares during 2014-15 with a production of 25.478 million tons and average production of 2775 kg per hectare (PBS, 2016).

Use of better yielding and widely adaptable varieties is important for enhancement of wheat production. Thus development of disease resistant and high yielding wheat genotypes has always been a most important goal of wheat breeding programs. Extensive investigation of wheat genotypes under different environments is an important practice for screening desirable genotypes (Nawaz *et al.,* 2013; Shafi *et al.,* 2013). Development of high yielding cultivars which is an important approach to maintain production draws attention of wheat breeders. Indirect selection of yield related characters is an effective approach in plant breeding. (Golabady and Arzani, 2003).

Grain yield is the main trait of a grain crop, it is a difficult polygenic trait which is affected by number of yield contributing traits and external environment. So selection for desirable genotypes should not only be based on yield, the other yield contributing traits should also be considered. Information about mutual relationship between yield and yield traits is compulsory (Majumder *et al.*, 2008; Akhtar and Chowdhary, 2006; Dehghani *et al.,* 2008).

The selection of better genotypes becomes difficult if the development is made for a poly-genetically traits like grain yield. Since, effective selection of genetically better genotypes requires sufficient phenotypic variation and high heritability for the desired trait (Hailegiorgis *et al.,* 2011).

Successful breeding program depends on the existence of genetic variability in the population. Estimates of heritability provide information about transmition of specific trait to the next generations. Knowledge of heritability leads a plant breeder for making effective selections. Information about heritability guides us to calculate performance and response to selection of trait in successive generations. Coefficients of variability, heritability and genetic gain have been used to evaluate the nature and amount of genetic variation in wheat population. The success of a breeding program depends upon the magnitude of genetic variations present in the breeding material. Information about heritability guides us to calculate performance and response to selection of trait in successive generations. High heritability coupled with high genetic advance is good indicated that a specific trait can be improved through selection (Haq *et al.* 2008). Therefore, information of heritability and genetic advance present in various yield traits is a pre-requisite for successful crop improvement exercise (Ullah *et al.,*2006; Rahman *et al.,* 2016). So selection for desirable genotypes should not only be based on yield, the other yield contributing traits should also be considered. Information about mutual relationship between yield and yield traits is compulsory. It is necessary to know the association of different traits with yield and among them. Association of various traits with grain yield can be better understand through Correlation studies. (Zafar *et al.,* 2012; Kalimullah *et al.*, 2015) It is essential identify the nature and degree of relationship among plant character to enhance crops yields (Singh and Dewivedi, 2002).

In current research study different genotypes were used to create information of variability, heritability, genetic advance and association for yield and its related traits and their uses for selection of superior genotypes of wheat. So the present research was conducted to estimate the genetic variability, heritability, genetic advance and correlation of yield and yield related characters for selection desirable wheat genotypes.

Materials and methods

Breeding material

The present research was conducted at Mountain Agricultural Research Station (MARC) Chilas Diamer during cropping season 2014-15. The experimental material was comprised often wheat genotypes viz. Uqab, Pir seaback 2013, NARC 2011, 129, 142,146, Pakistan-2013, Shahakar 2013, Galaxy and NARC 2009 which were planted in randomized complete block design with three replications. Plot size was 5×1.8m with a row to row distance of 30 cm and plant to plant distance of 15cm.Sowing was don eat 5 December 2014. All agronomic and cultural practices were carried out uniformly for all genotypes throughout cropping season.

Parameters studied

The data was recorded for 8 morphological traits days to 50% heading, days 50 % to maturity, number of grains spike^{-1}, plant height (cm), grain yield plot^{-1}(g), straw yieldplot^{-1}(g), 100 grain weight (g) and yield ha^{-1}(kg). Ten plants were selected randomly from each treatment in each replication to record the data for plant height (cm) and number of grains per spike. Total grain and straw yield (kg) per plot was recorded to take grain and straw yield per hectare.

Statistical analysis

Obtained Data was subject to analysis of variance using Microsoft Excel (2007) following method used by Steel and Torrie, (1980) and Means were split using LSD at 0.05 % probability level. Correlation coefficient among yield and yield related characters was estimated via software IBM-SPSS ver 22.0 Correlation was studied following the method of Singh and Chaudhery (1997).

Results and discussion

Analysis of variance

Analysis of variance revealed that all genotypes were significantly differed from each other presented in table 1, means values for genotypes are presented in table 2. Gashaw *et al.* (2010) and Thanna *et al.* (2011) also reported significant variation among different wheat genotypes for different yield traits. Maximum days to 50% heading was showed by line 146 (125 days) and minimum days was taken by Shahakar 2013 and line 129 (119 days). Wheat genotype Pakistan-2013 showed maximum day to 50% maturity (166days) while genotype 146 showed minimum days (155 days). Maximum plant height was noted in Uqab (86.3 cm) and Shahakar 2013 showed minimum plant height (67.7 cm).

Table 1. Mean squares for different traits.

Characters	Reps	Genotypes	Error	CV%
Days 50 % heading	2.033	26.577**	1.477	0.99
Days 50 % maturity	10.3	32.207**	5.485	1.44
Plant height	0.933	129.07**	7.303	3.75
Number of grain spike^{-1}	7.408	49.080**	7.215	6.42
Straw yield plot^{-1}	101.733	819565**	347.104	0.54
100 Grain weight	0.005	0.258**	0.004	1.84
Grain yield plot^{-1}	379.6	487184**	2055.56	2.08
Yield hectare^{-1}	468.653	601461.7**	2537.754	2.08
Harvest index	0.049	70.893**	0.320	1.46

*= significant at 0.05 and ** = 0.01 probability level.

The highest number of grains spike-1were found in genotype 146 (49.8 grains) while lowest number of grains spike^{-1} were counted for genotype Galaxy (36.4 grains).Highest grain yield plot^{-1} was measured for genotype 129 (3.1 kg) and the lowest grain yield was produced by Pirsabak2013 (1.8 kg). Maximum straw yield per plot was found in NARC 2011 (4.1 kg) and the minimum straw yield plot^{-1} was produced by Genotype Galaxy (2.9 kg). Highest 100 grain weight recorded for Genotype Galaxy (4.1g) ant the lowest

100 grain weight registered in genotype (3.1 g). Maximum yield ha^{-1} was produced by 129 (3485.6 kg) and Pirsabak 2013 produced minimum yield ha^{-1}(1966.7 kg). Highest harvest index was recorded for 146 (46.5%) and minimum harvest index was measured in Pirsabak 2013 (32.5%). Similar ranges for different traits in wheat were reported earlier by Kaddem *et al.,* (2014); Thanna *et al.* (2011); Peymaninia *et al.* (2012); Farooq and Cheema (2014) and Zafar *et al.* (2015).

Table 2. Table of means values for different characters.

Genotypes	DH	DM	PH	NG	GYP	SYP	GW	YH	HI
Uqab	123	164	86.3	42.4	1.9	3.2	3.4	2148.1	37.4
Pirsabak-2013	117	161	66.7	40.9	1.8	3.7	3.1	1966.7	32.4
NARC2011	120	159	72.3	41.3	2.2	4.1	3.2	2481.5	35.2
129	119	164	70	43.8	3.1	4.0	3.8	3485.6	44.04
142	124	165	75.3	46.6	2.2	3.4	3.6	2444.4	39.2
146	125	155	70.3	49.8	2.1	3.9	3.5	2370.4	35.4
Pakistan-2013	122	166	77.3	39.5	2.5	2.8	3.6	2759.3	46.6
Shahakar-2013	119	162	62.7	38.7	2.2	2.7	3.7	2400.0	44.8
Galaxy	121.3	162.7	67.7	36.64	1.8	2.8	4.1	2000.0	39.1
Means	126	165	71	38.2	1.9	3.7	3.8	2118.5	34.0

DH = Bays to 50 % heading, DM = days to 50 % maturity, Ph= Plant height (cm),NG = Number of grains spike^{-1},GYP = Grain yield plot^{-1}, SYP = Straw yield plot^{-1}, GW = 100 grain weight (g), YH = yield hectare^{-1} and HI = Harvest index.

Components of genetic variability

Estimates of genotypic and phenotypic variance ranges from (0.08) for 100 grain wheat to (199641.3 and202179.1) for yield ha^{-1} presented in table 4. Phenotypic variance was higher than genotypic variance for all traits under consideration. Higher value of phenotypic variance indicated influence of external environment on the traits. Values of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were estimated and presented in table 3. GCV and PCV ranged from (GCV = 1.83 and PCV= 2.33) for days to 50% maturity to (18.48 and18.6) for yield ha^{-1}. Moderated GCV and PCV was estimated for traits viz. yield ha^{-1}(18.48, 18.6), yield plot^{-1} (18.48, 18.59), straw yield plot^{-1}(15.23, 15.24) and harvest index (GCV = 12.49, PCV=12.58) indicated these traits are under control of additive genes and modified selection would be effective for improvement of these traits. Low GCV and PCV were estimated for characters like days to 50% maturity (1.83 and 2.33), days to 50% heading (2.37and2.57), 100 grain weight (8.06 and 8.27), plant height (8.85 and 9.61) and number of grains spike^{-1} (8.94 and11) revealed that these characters are controlled by non-additive genes. Current results are at par with findings of Ashfaq *et al.,* (2014); Kumar *et al.,* (2014); Gashaw *et al.,* (2010); Thanna *et al.*, (2011) and Haq *et al.,* (2016).

Heritability

High heritability was estimated for all traits studied presented in table 4. In present investigation heritability for different traits were found as days to 50% heading (84%), days to 50% maturity (61%), plant height (84 %), number of grains per spike (65%), straw yield plot^{-1}(99%), yieldper ha^{-1} (99%), and harvest index (99%). High heritability indicated that phenotype is mostly due to genotype, variations are heritable to next generation and section on the bases of phenotypic variation would be effective for crop improvement in future. Similar finding were also reported by Tabbal and Fraihat, (2012); Kaddem *et al.,* (2014) and Navin *et al.,* (2014).

Genetic advance

Genetic advance was estimated present in table 4.

High genetic advance as percent of mean was calculated for traits viz. yield per plot (32.32%), yield ha^{-1} (32.33%), straw yield plot^{-1}(26.78%) and harvest index (21.83%) indicated that these traits are controlled by additive genes. High heritability to gather with high genetic advance for these traits indicated wide scope for simple phenotypic selection to improve these traits. Moderate genetic advance as percent of mean was computed for plant height (14.34%), 100 grain weight (13.84%) and number of grains spike^{-1} (12.77%) revealed additive gene action. Simple selection would be not effective for improvement and modified selection would be play important role in improvement of these characters. Whereas, low genetic advance as percent of means was estimated for days to 50% heading (3.85%) and days to 50% maturity (2.54%) indicated that these traits are controlled by non additive genes and selection is not effective for improvement and hybridization should done for improvement of these traits. Our findings were supported by findings of Kaddem *et al.,* (2014); Haq *et al.,* (2016) and Navin *et al.* (2014).

Table 3. Value of genotypic and phenotypic variance, genotypic and phenotypic coefficient of variation, heritability, genetic advance and genetic advance as percent of mean for different traits.

Characters	Vg	Vp	GCV %	PCV %	h^2 %	GAM %
Days 50 % heading	8.36	9.84	2.37	2.57	84	3.85
Days 50 % maturity	8.9	14.39	1.83	2.33	61	2.54
Plant height	40.58	47.89	8.85	9.61	84	14.34
Number of grain spike^{-1}	13.95	62.28	8.94	11	65	12.77
Straw yield plot^{-1}	273072.6	273419.7	15.23	15.24	99	26.78
100 Grain weight	0.08	0.08	8.06	8.27	95	13.84
Grain yield plot^{-1}	161709.6	163765.2	18.48	18.59	98	32.32
Yield hectare^{-1}	199641.3	202179.1	18.48	18.6	99	32.33
Harvest index	23.52	23.84	12.49	12.58	99	21.83

Vg = Genotypic variance, Vp= Phenotypic variance, GCV= Genotypic coefficient of variation, PCV= Phenotypic coefficient of variation, h^2=broad sense heritability, GAM= Genetic advance as percent of mean.

Correlation studies

The information about association among different characters is an important aspect to start a breeding program as it offers various opportunities for the selection of superior genotypes having attractive qualities Ali *et al*., (2015). Correlation coefficient for different trait present table 4. Days to 50 % heading showed positive and highly significant correlation with plant height (r = 0.426**) indicated simultaneous improvement of these traits is possible. However this trait showed not significant correlation with rest of the traits. Significant association between plant height and days to 50 % heading was also reported by Ali *et al.* (2007). Whereas Degewione *et al.* (2013) reported non-significant association of days to 50 % heading with different traits.

Days 50 % maturity displayed positive and significant correlation with 100 grain weight (r= 0.337*) and harvest index (r = 0.381*) and negative and significant association with straw yield plot^{-1} (r= -0.355*). Days to 50% maturity showed positive and non significant correlation with plant height and total grain yield per plot. While negative and non-significant association was found with number of grains per spike. Our findings are in agreement with early reports of Degewione *et al.* (2013) and Tabbal *et al.* (2012). Positive and significant association of plant height was notice with number of grains per spike (r = 0.233*) and negative and significant correlation with 100 grain weight (r = -0.322*). It showed non-significant correlation with rest of the traits Majumder *et al.* (2008), Zafar *et al.* (215) also similar findings earlier.

Number of grains per spike have positive and highly significant association with straw yield per plot (r = 0.460**), positive and significant correlation with yield ha^{-1} (r = 0.326*) and negative and significant with 100 grain weight (r = -0.324*).while non significant correlation was observed among grain yield plot^{-1} and harvest index.

Table 4. Phenotypic Correlation coefficient for different traits.

	DH	DM	PH	NG	SYP	GW	GYP	YH	HI
DH	1	0.115	0.426**	0.259	0.041	0.229	-0.188	-0.188	-0.183
DM		1	0.284	-0.280	-0.355*	0.337*	0.160	0.160	0.381*
PH			1	0.233*	0.020	-0.322*	0.027	0.027	-0.004
NG				1	0.460**	-0.324*	0.226	0.326*	-0.161
SYP					1	-0.445**	0.259	0.259	-0.562**
GW						1	0.435**	0.489**	0.468**
GYP							1	0.989**	0.648**
YH								1	0.648**
HI									1

DH = Bays to 50 % heading, DM = days to 50 % maturity, PH = Plant height (cm), NG = Number of grains spike^{-1}, GYP = Grain yield plot^{-1}, SYP = Straw yield plot^{-1}, GW = 100 grain weight (g), YH = yield hectare^{-1} and HI = Harvest index. * = significant at (0.05) and ** = significant at (0.01) level.

Similar results were also reported by Gautam *et al.* (2002), Degewione *et al.* (2013) and Chimdesa. (2014). Straw yield per plot showed negative and highly significant correlation with 100 grain weight (r = -0.445**) and harvest index (r = -0.562**). This character showed non-significant correlation with grain yield per plot and yield per ha^{-1}. 100 grain weight showed highly significant and positive association with grain yield per plot (r = 0.435**), yield ha^{-1} (r = 0.489**) and harvest index (r = 0.468**) indicated that improvement in any one of these traits have positive effects on other traits. These findings are in accordance with results of Hussain *et al.*, (2014) and Majumder *et al.* (2008). Yield per plot showed highly significant and positive correlation with yield per hectare (r = 0.989**) and harvest index (r = 0.648**). Yield per hectare showed positive and highly significant correlation with harvest index (r = 0.648**), yield per plot (r = 0.989**) and 100 grain weight (0.489**) reveled that an increase in yield per plot, harvest index and 100 grain weight altimetry results increase in yield. Similar results were also reported by Hussain *et al.*, (2014) and Chimdesa, (2014).

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