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Genetic variability, heritability and correlation analysis among morphological and yield traits in wheat advanced lines

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Abstract

The present research was carried out with the objectives to estimate genetic variability, heritability and correlation studies in bread wheat '(*Triticum aestivum* L.)' Sixty three wheat advanced lines along with a check cultivar (Pirsabak-13) were grown in simple partially balanced square lattice 8×8 design with two replication during 2015-16 at Cereal Crops Research Institute (CCRI), Pirsabak Nowshera, Pakistan. Analysis of variance revealed significant differences among genotypes for majority of traits. Mean days to 50% heading ranged from 115.0 to 130.5, days to 90% maturity ranged from 166.0 to 174.5, plant height ranged from 91.0 to 125.5 cm, spike length ranged from 9.2 to 13.1 cm, number of spikelets spike^{-1} ranged from 17.0 to 24.0, number of grains spike^{-1} ranged from 50.5 to 70.0, 1000-grain weight ranged from 32.0 to 48.3 g and grain yield ranged from 2516.5 to 5155.0 kg ha^{-1}. Genetic variances were greater than environmental variances for all the traits except spike length. Regarding genotypic (GCV) and phenotypic coefficients of variation (PCV), values ranged from 1.60 to 15.74% and 1.74 to 19.91% for tested traits. Minimum values of GCV and PCV were recorded for days to 90% maturity however; it was high for grain yield. Magnitude of broad-sense heritability was low (0.26 for spike length) to high (0.89 for days 50% heading). Rest of the traits also showed high broad-sense heritability. In case of genetic advance, the highest genetic advance was recorded in grain yield (673.96 kg ha^{-1}) followed by plant height (10.89 cm), days to 50% heading (7.43), 1000-grain weight (6.01 g), grain spike^{-1} (5.19), days to 90% maturity (3.49), number of spikelets spike^{-1} (1.74) and spike length (0.51cm). Days to heading exhibited highly significant negative inter-relationship with yield contributing traits i.e. 1000-grain weight and grain yield. This means that earliness in wheat may have effect on yield as the plant may not have sufficient time to gain proper expression. Grain yield manifested highly significant positive association with 1000-grain weight. Overall, the MPT-51 and MPT-10 advanced lines showed best performance and these lines could be used in future breeding programs to enhance the grain yield in bread wheat genotypes.

Key words: bread wheat, correlation, genetic advance, genetic variability and heritability

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1. Introduction

Bread Wheat (*Triticum aestivum* L.) belongs to the family of *Poaceae*, tribe *Triticeae* of the family *Gramineae* originated in South West Asia area known as Fertile Crescent (Mergoum *et al.*, 2009). It is the prime and important staple food of the inhabitants of Pakistan and most of the developing countries. It provides foods to 36% of the global population, and contributes 20% of food calories (Khan and Naqvi, 2011). It is the most important and widely adopted cereal crop in Pakistan. Wheat is grown under various agro-climatic conditions; from temperate to irrigated and dry to high rain-fall areas and from warm, humid to dry, cold environments (Chimdesa, 2014). In Pakistan wheat crop occupied an area of 9205 thousand hectare during 2014-15, while yield was provisionally estimated at 25086 thousand tones and per unit yield was estimated about 2725 kg ha^{-1} (Anonymous, 2015). In Khyber Pakhtunkhwa wheat crop was

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cultivated on an area of 732.6 thousand hectares during 2014-15, with the production of 1259.9 thousand tones and per unit yield was 1720 kg ha^{-1} (Anonymous, 2015).

Wheat is the 'king of cereals' due to its acreage, productivity and the prominent position in international food grain trade (Shashikala, 2006). With the progressive change in the global climate and increasing shortage of water resources and worsening eco-environment, wheat production reduced significantly (Singh and Chaudhary, 2006). Global wheat production must continue to increase 2% annually until 2030 to meet future demands of imposed population and prosperity growth (Anonymous, 2015). Genome analysis in bread wheat poses substantial challenges; in addition to the complexity associated with its hexaploid structure, the bread wheat genome is very large (~17 Gb; around 40 times the size of rice or nearly six times larger than the human genome) and consists of about 80–90% repetitive sequence (Safar *et al.*, 2010; Wanjugi *et al.*, 2009).

The success of breeding program largely depends on the choice and exploitation of potential parental genotypes for hybridization, followed by selection for favorable gene combinations. Genetic variability and heritability knowledge provide dependable tool to the breeder for improvement. Genetic variability is the measure of the tendency of individual genotypes in a population to vary from one another for certain traits of interest, which is the base of crop improvement (Chimdesa, 2014). Genetic variability among wheat genotypes can be estimated based on quantitative traits. The presence of genetic variability in a population can be divided into heritable and non-heritable variation. Heritability in general term is the ratio of genetic variance to the total variance i.e. phenotypic variance is known as heritability. The concept of heritability is associated with the relative influence of the heredity and environment. Heritability is of two types i.e. broad sense and narrow sense heritability. Broad-sense heritability estimates the ratio of total genetic variance, including additive, dominance, and epistatic variance, to the phenotypic variance, while heritability in narrow sense estimates only the additive portion of the total phenotypic variance (Raiz and Chowdhry, 2003). Knowledge about heritability helps the plant breeder in predicting the behavior of successive generation and making desirable selections, which is one of the important tools in crop improvement.

In breeding program direct selection for yield could be misleading because of the complex relationship between grain yield and its component (Ali *et al.,* 2008). Correlation analysis provides information about association of plant traits that leads to directional model for yield production. Correlation coefficient is a statistical method, which can help the plant breeder in selection for higher yield. The correlation analysis also revealed the correlated response of a particular trait with its counterpart and also provides an excellent index to predict the corresponding change which occurs in one trait at the expense of the proportionate change in the other (Ahmad *et al*., 2008). Therefore, information about the genetic potential of various genotypes, heritability and inheritance pattern of various characters and degree of association of yield with various morpho-yield traits is important for breeder to handle a problem wisely and enhance the yield to a sufficient extent (Ahmad *et al*., 2008). Keeping in view the above facts and figures, the current research was carried out in wheat to achieve the following objectives:

- Screening of advanced wheat lines on the basis of their performance.
- Estimation of genetic variability, heritability and correlation for morpho-yield traits.

Identification and selection of high yielding best lines for cultivation and future breeding programs.

2. Materials and methods

2.1. Experimental Site, Materials and Design

This experiment was carried out at Cereal Crops Research Institute, Pirsabak Nowshera located at 34^0 North Latitude, 72^0 East Longitude and 288^0 Altitude under irrigated condition during 2015-16. The experimental materials for this study consisted of 63 advanced wheat lines and 'Pirsabak-13 (Check PS-13)' as a check cultivar. Details of advanced lines are given in (Table 2.1). The experiment was designed in partially balanced square lattice 8×8 with two replications. Each plot consisted of 6 rows of 5 meter length and row spacing was 30 cm with plot area of 9 m^2. A single row between adjacent plots was kept fallow to facilitate data recording. The experiment was planted in 1st week of November 2015. The agronomic practices and inputs were applied for all the entries from sowing till the harvesting and the genotypes were grown under uniform conditions to minimize environmental variations.

2.2. Data Collection

Data were recorded on the following parameters at appropriate time, using standard procedure outlined by different authors and researchers for wheat crop.

2.2.1. Days to 50% heading (no.)

Days to heading were recorded as days from the date of sowing to the date when 50% plants completed heading.

Table 2.1. List of wheat advanced lines along with origin and parentage used in study during 2015-16 at CCRI, Pirsabak Nowshera.

S.NO	**Parentage**	**Origin 2014-15**
MPT-1	NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5/KACHU/6/KACHU	CIMMYT
MPT-2	58769//2*WBLL1*2/TUKURUCGSS05Y00134T-099B-099Y-099M-099Y-099ZTM-5WGY-0B	"
MPT-3	ATTILA/3*BCN//BAV92/3/TILHI/4/SHA7/VEE#5//ARIV92/5/BAV92//IRENA/KAUZ/3/HUITESCMSS05B01249T-099TOPY-099M-099Y-099ZTM-9WGY-0B	"
MPT-4	PIRSABAK-05 × TSH/DOVE//KAUZ/3/BCNCCSS0809S-0CC-5205CC3-0K-7216CC	CCRI
MPT-5	LIS “S”/KVZ/TRM//PTM/ANA × BLUE SILVER	"
MPT-6	BOW/VEE/5/ND/VG9144//KAL/BB/3/YACO/4/CHIL/6/CASKOR/3/CROC_1/AE.SQUARROSA (224)//OPATA/7/PASTOR//MILAN/KAUZ/3/BAV92CMSA04M01201T-050Y-040ZTP0M-040ZTY-040ZTM-040SY-6ZTM-03Y-0B	CIMMYT
MPT-7	VORB/3/T.DICOCCON PI94625/AE.SQUARROSA (372)//3*PASTORCMSA06M00667S-040ZTM-040ZTY-50ZTM-02Y-0B	"
MPT-8	CHRIS × CHAM4/CA8055	CCRI
MPT-9	WBLL1*2/TUKURU//WHEARCGSS05Y00456S-0B-099Y-099M-099NJ-099NJ-9WGY-0B	CIMMYT
MPT-10	BOW “S”/PRL//BUZ/3/STAR × WORRAKATTA/2* PASTOR	CCRI
MPT-11	BCN/WBLL1//PUB94.15.1.12/WBLL1PTSS09GHB00024S-0SHB-099Y-099B-17Y-0Y	CIMMYT
MPT-12	BOW/VEE/5/ND/VG9144//KAL/BB/3/YACO/4/CHIL/6/CASKOR/3/CROC_1/AE.SQUARROSA (224)//OPATA/7/PASTOR //MILAN /KAUZ/3/BAV92CMSA04M01201T-050Y-040ZTP0M-040ZTY-040ZTM-040SY-6ZTM-01Y-0B	CIMMYT
MPT-13	WBLL1*2/4/YACO/PBW65/3/KAUZ*2/TRAP//KAUZ*2/6/NG8201/KAUZ/4/SHA7//PRL/VEE#6/3/FASAN/5/MILAN/KAUZCMSS06Y00619T-099TOPM-099Y-099ZTM-099Y-099M-5WGY-0B	"
MPT-14	WBLL1/FRET2//PASTOR*2/3/MURGACMSS06Y00937T-099TOPM-099Y-099ZTM-099Y-099M-8WGY-0B	"
MPT-15	KACHU #1*2/WHEARCMSS06Y01282T-099TOPM-099Y-099ZTM-099Y-099M-3WGY-0B	"
MPT-16	FRNCLN//WBLL1*2/BRAMBLINGCMSS07Y00284S-0B-099Y-099M-099Y-1M-0WGY	"
MPT-17	MILAN/S87230//BAV92*2/3/AKURICMSS07Y01083T-099TOPM-099Y-099M-099Y-35M-0WGY	"
MPT-18	KISKADEE #1//KIRITATI/2*TRCHCMSS07B00254S-099M-099Y-099M-25WGY-0B	"
MPT-19	KS82W418/SPN//WBLL1/3/BERKUTCMSA02Y00636T-040M-040P0Y-040M-040SY-040M-9ZTY-04M-0Y	"
MPT-20	NG8675/CBRD//MILAN/3/SAUAL/6/CNDO/R143//ENTE/MEXI_2/3/AEGILOPS SQUARROSA (TAUS)/4/WEAVER/5/2*PASTORCMSS05B01166T-099TOPY-099M-099Y-099ZTM-11WGY-0B	"
MPT-21	BOW “S”/NN//VEE “S”/3/BIY “S” × PIRSABAK-85	CCRI
MPT-22	ESDA “S” × SERI*3//RL6010/4*YR/3/PASTOR/4/ BAV-92	"
MPT-23	F-3-71/TRM × F. SARHAD	"
MPT-24	PR-88 × WORRAKATTA/PASTOR	"
MPT-25	IAS63/ALD “S”//GLEN × PIRSABAK-05	"
MPT-26	BOW “S”*2/PRL “S” × SALEEM-2000	"
MPT-27	SW89.30.64/STAR × GEREK	"
MPT-28	SW89.30.64/STAR × GEREK	"
MPT-29	SALEEM-2000 × PR-88	"
MPT-30	SALEEM-2000 × PR-88	"
MPT-31	IBWSN-89 × EMB16/CBRED//CBRD	"
MPT-32	IBWSN-101 × PIRSABAK-05	"
MPT-33	IBWSN-101 × PIRSABAK-05	"
MPT-34	IBWSN-133 × RL6043/4*NAC//2*PASTOR	"
MPT-35	IBWSN V-133 × Tatara 96	"
MPT-36	QUAIU*2/KINDE	CIMMYT
MPT-37	SAUAL/3/ACHTAR*3//KANZ/KS85-8-4/4/SAUAL	"
MPT-38	BECARD/KACHU	"

Table 2.1. Continued

MPT-39	CHIBIA//PRLII/CM65531/3/SKAUZ/BAV92/4/MUNAL #1	"
MPT-40	FRNCLN*2/TECUE #1	"
MPT-41	MUTUS*2/AKURI	"
MPT-42	BECARD/FRNCLN	CIMMYT
MPT-43	SERI/BAV92//PUB94.15.1.12/WBLL1	"
MPT-44	SOKOLL	"
MPT-45	HPRYT (12-13) 3	"
MPT-46	HPRYT (12-13) 6	"
MPT-47	WPEPYT (13-14) 10	"
MPT-48	WPEPYT (13-14) 16	"
MPT-49	CHEN/AE.SQ//2*OPATA/3/FINSI	"
MPT-50	BAV92/SERI	"
MPT-51	W15.92/4/PASTOR//HXL7573/2*BAU/3/WBLL1	"
MPT-52	VORB*2/5/CROC_1/AE.SQUARROSA (224)//OPATA/3/RAC655/4/SLVS/PASTOR	"
MPT-53	KACHU/KINDE	"
MPT-54	QUAIU #1*2/JUCHI	"
MPT-55	WAXWING*2/4/BOW/NKT//CBRD/3/CBRDCMSS06Y00590T-099TOPM-099Y-099ZTM-099Y-099M-20WGY-0B	"
MPT-56	NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5/KACHU/6/KACHUCMSS06B00734T-099TOPY-099ZTM-099Y-099M-13WGY-0B	"
MPT-57	INQILAB-91 × TSH/DOVE//KAUZ/3/BCN	CCRI
MPT-58	SLVS/3/CROC_1/AE.SQUARROSA (224)//OPATA/5/VEE/LIRA//BOW/3/BCN/4/KAUZ/6/2*KA/NAC//TRCH	CIMMYT
MPT-59	FRET2/TUKURU//FRET2/3/MUNIA/CHTO//AMSEL/4/FRET2/TUKURU//FRET2	"
MPT-60	SUP152/BLOUK #1	"
MPT-61	BECARD/KACHU	"
MPT-62	KFA/2*KACHUCMSS06B01005T-099TOPY-099ZTM-099NJ-099NJ-28WGY-0B	"
MPT-63	D67.2/PARANA 66.270//AE.SQUARROSA (320)/3/ CUNNINGHAM /4/ WBLL1*2/TUKURUCMSA04M00492S-040ZTP0Y-040ZTM-040SY-22ZTM-02Y-0B	"
Check (PS-13)	CS/TH.SC//3*PVN/3/MIRLO/BUC/4/MILAN/5/TILHICMSS97M04005T-040Y-020Y-030M-020Y-040M-28Y-3M-0Y	CRRI

2.2.2. *Days to 90% maturity (no.)*

Days to maturity were recorded as days from the date of planting to the stage when 90% of the plants in a plot have reached physiological maturity.

2.2.3. *Plant height (cm)*

At physiological maturity, height was recorded as the length in centimeters from the soil surface to tip of the spike excluding awns.

2.2.4. *Spike length (cm)*

Eight randomly selected spikes were harvested from each plot and spike length was measured from the base of first spikelet to the tip of the spike excluding the awns.

2.2.5. *Numbers of spikelets spike^{-1}*

Number of spikelets spike^{-1} were counted on the same eight random spikes selected from each plot.

2.2.6. *Grains spike^{-1} (no.)*

Grains spike^{-1} was recorded by the given formula (Sayre *et al*., 1997)

$$Grains\ spike^{-1} = \frac{Grain\ weight\ spike^{-1}\ x\ 1000}{Weight\ of\ 1000\ grains}$$

2.2.7. *1000-grain weight (g)*

One thousand grains (g) were taken at random from the bulk grain yield of each plot in each replication and was weighed using an electronic balance.

2.2.8. Grain yield (kg ha^{-1})

After threshing, grain yield was recorded from the grain weight of each bundle and the obtained grain yield was converted into kg ha^{-1} for data analysis.

$$\text{Yield (kg ha}^{-1}\text{)} = \frac{yield\ (g) \times 10{,}000}{6 \times 0.3 \times 5}$$

2.3. Statistical analysis

All the data was subjected to analysis of variance (ANOVA) using MSTAT-C computer software (Table 2.2). After getting the significant variations among genotypes for various parameters, the means for each parameter was further separated and compared by using the least significant difference (LSD) test at 5% level of probability.

Table 2.2. Analysis of variance model used for 64 bread wheat lines, evaluated during the year 2015-16 at CCRI, Pirsabak Nowshera.

Source of Variation	DF	MS	F-Cal
Replication (r)	(r-1)	RMS	-----
Treatments (adj.)	(k^2-1)	TMS	TMS / EMS
Error			
-Effective	(k-1) (rk-k-1)	EMS	-----
-Intrablock	(k-1) (rk-k-1)	EMS	-----
Total	(r)(k^2) -1	-----	-----

2.3.1. Estimation of genetic parameters

Using the formula outlined by Singh and Chaudhary (1985) and Johnson *et al.* (1955), the GCV (Genotypic coefficients of variance) and PCV (Phenotypic coefficient of variance) were computed.

$$Genetic\ \mathrm{var}iance\ (Vg) = \frac{Genotypes\ mean\ squares(GMS) - Error\ mean\ squares(EMS)}{Number\ of\ replications(r)}$$

$$Evironmental\ \mathrm{var}iance\ (Ve) = Error\ mean\ squares(EMS)$$

$$V_P = V_g + V_e$$

Genotypic coefficient of variation (GCV) = $\frac{\sqrt{V_g}}{\bar{X}} \times 100$

Phenotypic coefficient of variation (PCV) = $\frac{\sqrt{V_P}}{\bar{X}} \times 100$

Where:
V_g= Genotypic variance
V_P= phenotypic variance
$\bar{X}$= Grand mean

The GCV and PCV values were categorized as low (0–10%), moderate (10–20%), and high (20% and above) as outlined by Singh and Chaudhary (1985) and Johnson *et al.* (1955).

2.3.2 Heritability estimate

Heritability (H^2) in broad-sense for all characters was computed using the formula adopted by Allard (1960):

$$\text{Heritability} = \left[\frac{V_g}{V_p}\right] \times 100$$

The heritability percentage was categorized as low (0–30%), moderate (30–60%), and high (≥60%) in accordance with Robinson *et al.* (1951).

2.3.3 Estimated and Expected Genetic Advance

Expected genetic advance (GA) (as % of the mean) was calculated using the method of Assefa *et al.* (1999). The expected response to selection (Re) for each trait was calculated as under:

$$GA = k\sqrt{Vp} * H^2 \qquad \text{and,}$$

$$\text{GA (as \% of the mean)} = \left[\frac{(GA)}{\bar{X}}\right] \times 100$$

Genetic advance was categorized as low (0–10%), moderate (10–20%), and high (>20%)

Where:

k = 1.40 at 20% selection intensity for a trait.
V_P = Phenotypic variance for a trait.
H^2 = Heritability in broad sense for trait.
GA= Genetic advance
$\bar{X}$= Grand mean

2.3.4. Correlation

The simple correlation of yield with other yield components was worked out according to Kwon and Torrie (1964).

3. Results

3.1. Days to 50% heading (no.)

Analysis of variance (ANOVA) showed highly significant ($P \leq 0.01$) differences for days to 50% heading among the tested 64 wheat advanced lines (Table 3.1). Days to heading in all wheat genotypes ranged between 115.0-131.5. Among all the genotypes, maximum number of days to 50% heading were observed for MPT-24 (131.5) followed by MPT-33 and MPT-34 each of 130.5 days (Table 3.2). While minimum number of days to 50% heading were recorded each for MPT-38 and MPT-61 (115.0). There was huge diversity within the tested genotypes for days to 50% heading, which showed that the pedigree, source and origin of the parental population of these lines were of high diversity. Genetic variance (31.48) was greater than the independent effect of environmental variance (3.73), though it was slightly less than that of the overall phenotypic variance for days to 50% heading (Table 3.4). Similarly, for genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) there was not a huge gap as the estimated values were 4.60 and 4.86% respectively indicating narrow range of variability. However, the estimates of broad-sense heritability recorded for days to 50% heading was higher (0.89%) which shows that selection is possible and easy in early generation. Moreover, the genetic advance was computed as 7.43 units suggested that genetic variance could play an important role in the inheritance and improvement of earliness. Furthermore, the low values of standard error and coefficient of variability states that the experiment has been conducted very well and all the parameters were handled judiciously. Days to 50% heading exhibited highly significant ($P \leq 0.01$) positive correlation with days to 90% maturity (r= 0.64**), whereas non-significant but positive casual linkage with plant height, spike length, spikelet spike^{-1} and grain spike^{-1} was noted. However, highly significant negative correlation with 1000-grain weight (r=-0.38**) and grain yield (r=-0.31**) for days to 50% heading indicating earliness in wheat that might have negative effect on grain yield and grain size (Table 3.4). Early heading is desirable and plant breeders are interested in development of new wheat genotypes with early maturity. As a result of delayed heading, little time is left for grain filling, which ultimately reflects in reduced grain weight. Genotypes earlier in heading can have longer grain filling period and thus complete a greater fraction of the grain filling earlier in the season when air temperature is lower and generally more favorable in wheat (Tewolde *et al*., 2006). Early heading is an important escape mechanism in terminal stress condition during grain-filling period (Jaradat, 1991). Khan (2013) observed highly significant differences for days to 50% heading along minimum values for GCV and PCV. High heritability in conjugation with low genetic advance were observed for days to 50% heading indicated the non-additive gene action for the expression of said attribute and the selection for such trait may be effective in the early generations. Present findings are in harmony with the work of Kumar *et al*. (2010) and Baranwal *et al*. (2012) who have reported low GCV and PCV for the said attribute. However, these results are in contrast with the findings of Mollasadeghi *et al.* (2011) as they reported high PCV and GCV for days to 50% headings that could be due to the testing sites of the experiment and variation in the sample size which may affect the entire population. This may also be due to the variation of the genotypes used in the study. Present results revealed that days to 50% heading showed highly significant negative association with 1000-grain weight and grain yield already reported by Munir *et al*. (2007).

3.2. Days to 90% maturity (no.)

ANOVA revealed highly significant variation ($P \leq 0.01$) for days to 90% maturity among all the evaluated genotypes (Table 3.1). As stated in Table 3.2, average days to 90% maturity ranged between 166.0-174.5. Among all the genotypes, late maturing genotypes were MPT-24, MPT-32 and MPT-34 (174.5) while early maturing lines were MPT-6 (166.0), MPT-3, MPT-4 and MPT-17 each matured in 167.0 days (Table 3.2). Although phenotypic variance for days to 90% maturity was higher (8.84) however, the contribution due to genetic component / variance was more than 80% (7.41). While the variance due to environment (1.43) was absolutely less (Table 3.4). Magnitude of GCV was comparatively less (1.60) than the PCV (1.74). Similarly, broad-sense heritability was higher (0.84) for days to 90% maturity with a genetic advance of 3.49 units and 2.05 percent mean. Low values of standard error (0.25) and coefficient of variation (0.7) were observed. Days to 90% maturity manifested highly significant ($P \leq 0.01$) positive correlation with days to 50% heading (r= 0.64**) only, while plant height (r=0.15), spike length (r=0.01), spikelet spike^{-1} (r=0.06) and grains spike^{-1} (r=0.06) exhibited non-significant positive correlation with days to 90% maturity. However, 1000-grain weight (r=-0.25**) had a highly significant negative correlation with days to 90% maturity and grain yield exhibited non-significant but negative correlation with days to 90% maturity (Table 3.5). In grain crops, physiological maturity refers to the achievement of maximum seed dry weight. Knowledge of the time of physiological maturity is very important under some circumstances because the crop is subjected to different sources like lodging, pre-harvest sprouting, hail and biological stresses due to which reductions in yield will take place (Calderini *et al*., 2000). Reduction in yield occurs up to 10% due to stress during the process of maturation (Bauder, 2001). Significant differences have been reported among wheat genotypes for days to 90% maturity (Khan *et al*., 2013; Singh and Upadhyay, 2013). Days to maturity displayed high heritability with low genetic advance. However, GCV and PCV for the said trait were low, indicated low variability for such traits among genotypes. In contrast, high estimates for GCV and PCV and moderate genetic advance were observed in bread wheat for days to 90% maturity for different set of genotypes (Mohsin *et al*., 2009). Contradiction among past findings might be due to diverse breeding materials and the environment in which the study was conducted. These results are also in agreement with the findings of Tripathi *et al*. (2015). Present results depicted that maturity was non-significant and negatively correlated with grain yield, which have also been confirmed (Khan, 2013). Moreover, Wahidy *et al*. (2016) reported positive inter-relationship between days to 90% maturity and grain yield.

3.3. Plant height (cm)

Highly significant differences ($P \leq 0.01$) were observed for plant height among all the tested genotypes as explained by the ANOVA (Table 3.1). Mean value for plant height ranged between 91.0-122.5 cm (Table 3.2). Among the population, tallest lines were MPT-50 (122.5 cm) followed by MPT-60 (121.5 cm) while short stature genotypes were MPT-24 (91.0 cm) followed by MPT-7 (95.0 cm). All the tested lines had huge diversity for plant height and breeders could have the opportunity to breed for the plant of choice. For plant height though the overall phenotypic variance (93.53) was comparatively greater in magnitude than the genotypic variance (75.26) however, the percent contribution of genotypic variance was much higher than the environmental variation (18.27). Similarly, genotypic and phenotypic coefficients of variation for the said attribute were 7.93 and 8.84%, and broad-sense heritability was 0.80% respectively, while the genetic advance 10.89 (Table 3.4). High estimates of heritability and appreciable genetic advance coupled with low values of error and CV suggested that there are great chances of improvement for plant height in these lines. Plant height revealed non-significant positive correlation (Table 3.5) with days to maturity (r=0.15), days to heading (r=0.09), spike length (r=0.04), and 1000-grain weight (r=0.07), whereas non-significant negative correlation was also found with the spikelet spike^{-1} (r=-0.08) and grains spike^{-1} (r=-0.09). Plant height is a key parameter in wheat breeding programs. Plant breeders select short stature genotypes for the region where there are chances of lodging and tall varieties for regions of drought nature (Khan *et al*., 2010). Short plant height is required in wheat because taller plants are likely to lodge and need more energy to transport photosynthates to the grains in wheat (Inamullah *et al*., 2006; Çifci, 2012). A semi-dwarf stature of wheat has been depicted to induce increased yield through more efficient utilization of available assimilates correlated with crop lodging (Dalrymple, 1986). Results of our investigation are in accordance with the findings of Singh and Upadhyay (2013), Amin *et al*. (2015) and Khiabani *et al*. (2015) for the significant variation in plant height. The high heritability accompanied with moderate genetic advance for plant height has been reported in wheat genotypes (Degewione *et al*., 2013). Most likely the heritability of the plant height would be due to dominant gene effects and selection may be effective in early generations for such trait (Ali *et al*., 2007). High estimates of heritability suggested that the genetic variance could play an important role in the inheritance and improvement of the said trait. However, plant height displayed low genotypic and phenotypic coefficients of variability in present investigation. With minimum GCV and PCV scope of selection might also be less as the lines may be under the influence of environment (Degewione *et al*., 2013). In wheat lines, Bhutto *et al*. (2016) reported non-significant negative linkage between plant height and grain yield.

3.4. Spike length (cm)

Sources of variations among the tested genotypes were recorded non-significant for spike length as described by the ANOVA (Table 3.1). The mean value for spike length ranged between 9.2-13.1 cm. Among the tested genotypes, lengthy spike length was observed for the accession MPT-10 (13.1 cm) followed by MPT-14 (12.7 cm). On the other hand short spike length was recorded for MPT-28 (9.2 cm) and MPT-8 (9.8 cm). Rest of the lines also showed diversity for spike length though the variations among the lines were non-significant (Table 3.2). Phenotypic variance (1.92) and variance due to environment (1.42) was greater in magnitude than the estimated variance due to genetic variation (0.50). Similarly, GCV (6.38) was less in magnitude than the PCV (12.50). Since the magnitude of variability is less and the influence of the environment is greater on spike length hence, the magnitude of broad-sense heritability (0.26) and genetic advance is also low (0.51). Low magnitude of heritability suggests that breeder must have to wait for later generation for the improvement of spike length (Table 3.4). CV for spike length is high compared to other traits under study suggested that the effect of environment / external factors is greater although the standard error is appreciable. Highly significant ($P \leq 0.01$) and positive correlation for spike length were observed with spikelets spike^{-1} (r=0.61**) and number of grains spike^{-1} (r=0.61**) while non-significant positive correlation were observed with the days to 90% maturity (r=0.01), days to 50% heading (r=0.04), plant height (r=0.04) 1000-grain weight (0.06) and grain yield r=0.02 as given in Table 3.5. Spike length is one of the key yield components, which contributes towards the grain yield. On average, spike length could contribute 20-30% of the dry matter accumulated in the kernels in wheat (Thorne, 1965). There is direct relationship between spike length, grain weight spike^{-1} and grain yield unit^{-1} area as well. Our results are in line with the findings of Singh and Upadhyay (2013) for the said trait. In present investigation low heritability and low genetic advance were observed which indicates the limited scope of improvement for said attribute through selection (Teich, 1984; Chaturvedi and Gupta, 1995; Monopara, 2009). The PCV value was higher than the GCV value for said trait, which reflects the influence of environment on the expression of traits in wheat (Abinasa *et al*., 2011; Gashaw *et al*., 2013). For correlation studies, our present findings are in harmony with the work of Nawaz *et al*. (2013) for non-significant positive correlation between spike length and grain yield.

3.5. *Number of spikelets spike^{-1} (no.)*

ANOVA explained significant differences ($P \leq 0.05$) were observed for number of spikelets spike^{-1} among all the studied genotypes (Table 3.1). Average number of spikelets spike^{-1} ranged between 17.0-24.0. Among all the genotypes, more number spikelets spike^{-1} were observed for MPT-23 (24.0) followed by MPT-10 and MPT-51 each with 23.5 number of spikelets. While less numbers of spikelets spike^{-1} were recorded for MPT-8 and MPT-46 each with 17.0 and 17.5 number of spikelets respectively (Table 3.3). Table 3.4 stated that genetic variance (3.01) was slightly greater than environmental variance (2.85) for spikelets spike^{-1} however; the overall phenotypic variance (5.86) was higher. Similarly, the GCV and PCV for the said attribute were respectively 8.43 and 11.77 with broad-sense heritability of 0.51. While the genetic advance was 1.74 with standard error of 0.18 and CV of 8.2. Spikelet spike^{-1} revealed highly significant ($P \leq 0.01$) positive correlation with grain spike (r=1.00**) and spike length (r=0.61**) while days to 50% heading (r=0.05) and days to 90% maturity (r=0.06) manifested non-significant positive correlation with spikelet spike^{-1}. However, spikelet spike^{-1} had a non-significant negative correlation with plant height, 1000-grain weight and grain yield (Table 3.5). Longer spikes produce more spikelets and resulted in increased production in wheat (Akram *et al*., 2008). Selection of genotypes with more spikelets spike^{-1} leads to increased grain yield in wheat (Mohammadi *et al.,* 2011). Significant differences were observed in all 64 wheat genotypes for spikelets spike^{-1} are in line with the findings of Salman *et al*. (2014) and Nawaz *et al*. (2013). Spikelets spike^{-1} manifested moderate heritability and low genetic advance. Result may indicate possibility due to influence of the environment on the polygenic nature of said trait (Degewione *et al.,* 2013). Regarding GCV and PCV our results exhibited that spikelets spike^{-1} had non-significant negatively correlation with grain yield. In harmony to this investigation, Khokhar *et al*. (2010) also reported non-significant negative linkage between spikelets spike^{-1} and grain yield.

3.6. *Grains spike^{-1} (no.)*

ANOVA revealed significant variations ($P \leq 0.05$) for number of grains spike^{-1} in all the tested wheat genotypes (Table 3.1). Average number of grains spike^{-1} ranged between (50.5-70.0). Among all the tested genotypes, maximum number of grains spike^{-1} were recorded for MPT-23 (70.0) followed by MPT-10 (68.5) while minimum number of grains spike^{-1} were recorded for MPT-46 (50.5) followed by MPT-1 and MPT-57 each with 51.3 number of grains (Table 3.3). Variance due to genetic expression (26.56) was greater than the corresponding variance due to environment (24.58) for number of grains spike^{-1}. However, the overall phenotypic variance recorded was 51.24. Estimates of GCV and PCV for number of grains spike^{-1} were 8.69 and 12.07%, respectively while broad-sense heritability was 0.52 with a genetic advance of 5.19. Standard error and coefficient of variability for the said trait was 0.55 and 8.37 respectively, stated that the layout plan and model of the experiment was appropriate (Table 3.4). Number of grains spike^{-1} exhibited highly significant ($P \leq 0.01$) positive association with spike length (r=0.61**) and spikelet spike^{-1} (r=1.00**) whereas days to heading (r=0.06) and days to maturity (r=0.06) showed non-significant positive association with number of grains spike^{-1}. However, negative and non-significant association was found between number of grains spike^{-1} and plant height (r=-0.09), 1000-grain weight (r=-0.16) and grain yield (r=-0.04) respectively (Table 3.5). Number of grains spike^{-1} is one of very important components of yield in wheat which directly affect yield potential of the genotype, and thus plant breeders are interested in development of new wheat genotypes with increased number of grains spike^{-1}. Grains spike^{-1} could be used as selection criteria for development of new wheat varieties. Significant differences were observed in all tested wheat genotypes for number of grains spike^{-1} and are in accordance with the findings of Çifci (2012) and Baranwal *et al*. (2012). Moderate heritability and low genetic advance was observed for number of grains spike^{-1} and the same has also been reported (Mohsin *et al*., 2009; Cheema *et al*., 2006). Present investigation displayed low genotypic coefficient of variation and high phenotypic coefficient of variation for the said attribute. Laghari *et al*., (2010) also observed tlow GCV and PCV for number of grains spike^{-1}. The GCV value was comparatively greater than PCV value for number of grains spike^{-1}, which reflects the low influence of environment on the expression of trait and positive association with inheritance. In accordance to these results, Hama *et al*. (2016) also observed non-significant negative association between grains spike^{-1} and grain yield.

3.7. 1000-grain weight (g)

The analysis of variance manifested highly significant ($P \leq 0.01$) variation among all the studied genotypes for 1000-grain weight (Table 3.1). Average 1000-grain weight ranged between 32.0-48.3 g. Amongst all the genotypes, maximum 1000-grain weight were observed for MPT-2 (48.3 g) and MPT-61 (48.1 g) while minimum 1000-grain weight of 32.0 g was recorded for MPT-33 (Table 3.3). Estimates of genetic variance (28.00) were greater than the corresponding environmental variance (14.58) for 1000-grain weight. However, the GCV (13.05) was slightly less than the PCV (16.09) for the said attribute. Estimates of broad-sense heritability (0.66) and genetic advance of 6.01 units was recorded for 1000-grain weight (Table 3.4). Thousand grain weight manifested highly significant ($P \leq 0.01$) positive correlation with grain yield (r= 0.24**) while plant height (r=0.07) and spike length (r=0.06) exhibited non-significant positive association with thousand grain weight. However, highly significant but negative correlation for thousand grain weight were observed with days to 50% heading (r=-0.38**) and days to 90% maturity (r=-0.25**) whereas spikelet spike^{-1} (r=-0.16) and number of grains spike^{-1} (r=-0.16) had a non-significant negative association with thousand grain weight (Table 3.5). Thousand-grain weight is an important yield-contributing trait and could be used as selection criteria for high production in wheat. Highly significant differences and wide range of variation for 1000-grain weight were stated which revealed sufficient genetic variability among the wheat genotypes (Alam *et al*., 2013; Desheva and Cholakov, 2014; Badran and Moustafa *et al*., 2014). Thousand-grain weight showed high heritability with low genetic advance indicated effectiveness of selection among the current pool of genotypes (Degewione *et al*., 2013). Moderate genotypic and phenotypic coefficients of variation were recorded for 1000-grain weight (Degewione *et al*., 2013). High PCV and GCV indicated that selection may be effective based on these traits and their phenotypic expression would be a good indication of the genotypic potential (Singh *et al*., 1994). Similarly, highly significant positive interrelationship existed between 1000-grain weight and grain yield, so it could be considered as indirect selection criteria for better yield in breeding programs (Mohammadi *et al*., 2011; Desheva, 2016).

3.8. Grain yield (kg ha^{-1})

Variations amongst the studied genotypes were highly significant ($P \leq 0.01$) for grain yield as explained by ANOVA (Table 3.1). The average grain yield ranged between 2993.5-5155.0 kg ha^{-1}. Among all the genotypes maximum grain yield were recorded for MPT-36 (5155.0 kg ha^{-1}) followed by MPT-17 (4730.0 kg ha^{-1}) while minimum grain yield of 2993.5 Kg ha^{-1} was observed for MPT-6 (Table 3.3). Estimates of genetic variance (370550.56) was greater than the environmental variance (221938.27) for grain yield showed that the contribution of due to genetic architecture of the genotypes is higher. Similarly, GCV was slightly less than the PCV for the said attribute stated that the overall influence of phenotypic expression dominate over the genotypic expression. Estimates of broad-sense heritability (0.63) and genetic advance (673.96) were appreciable and could be effective for the breeders to improve the said trait. Meanwhile, the error variance and coefficient of variability was controllable (Table 3.4). Highly significant ($P \leq 0.01$) and positive correlation for grain yield was found with 1000-grain weight (r=0.24**) only, while plant height (r=0.14) and spike length (r=0.02) had a non-significant but positive correlation with grain yield. Similarly, highly significant negative association with days to 50% heading (r=-0.31**) while days to 90% maturity (r=-0.13), spikelet spike^{-1} (r=-0.04) and grain spike^{-1} (r==0.04) showed non-significant negative correlation with grain yield (Table 3.5). Grain yield is a complex trait and plant breeders are mostly interested in development of high yielding genotypes to cope with food demand of the country by improving either directly or indirectly this particular trait. Differences among genotypes for grain yield and yield related traits in wheat is the most important concern in wheat plant breeding programs (Talebi *et al*., 2009). High heritability in conjugation with high genetic advance was observed for grain yield. It indicated predominance of additive gene action. Therefore, direct selection for traits such as grain yield would not be effective due to their quantitative nature (Yadav *et al*., 2014; Ibrahim *et al*., 2012). Grain yield manifested moderate genotypic and phenotypic coefficients of variation (Tripathi *et al*., 2015). Non-significant negative association were observed between grain yield and grains spike^{-1} and are in conformity with Fellahi *et al*. (2013). Moreover, Desheva, (2016) indicated highly significant positive association between grain yield and grain spike^{-1}.

4. Conclusions and discussion

Highly significant ($P \leq 0.01$) differences were observed among genotypes for majority of the attributes except number of spikelets spike^{-1} and number of grain spike^{-1}, which exhibited significant ($P \leq 0.05$) variation. Wide range of variability expressed and observed in different traits suggested that the genotypes has great chances of improvement and might have the potential to be released as cultivars for site specific cultivation. Therefore, there is higher chance of selecting genotypes for different quantitative traits. Of the total 64 genotypes, MPT-51 and MPT-10 outclassed check cultivar for maximum number of spikelets spike^{-1}, number of grains spike^{-1}, 1000-grain weight and eventually increased grain yield. On the other hand wheat genotypes MPT-38 and MPT-61 were found as early heading genotypes however, MPT-6 was declared as early maturing genotype. Similarly, MPT-24, MPT-32 and MPT-34 were identified as late maturing genotypes. Genotypes have some site or location specific features such as plant height; in this regard wheat genotype MPT-50 was the tallest whereas MPT-24 was identified as dwarf cultivar. Keeping in view the importance of other yield contributing traits it was concluded that the tested genotypes had maximum diversity and hence these genotypes might be even a potential source to improve the existing cultivars or population by transferring some of the traits of interest.

High genotypic variance as compared to environmental variance for majority of the traits suggested that the variation is under the control of genetic expression of the genotypes and will be sustainable. Similarly, high estimates of broad-sense heritability were observed for days to 50% heading, days to 90% maturity, plant height, 1000-grain weight and grain yield suggested that selection will be effective in early generation. Medium heritability estimates were also noted for number of spikelets spike^{-1} and number of grains spike^{-1} indicated that selection should be delayed till later generations for these particular traits. Genetic advance as a percent of mean of the top 20% of the base population could result in an advance of 2.05% to 17.43% over the their respective population mean.

Majority of the traits including grain yield exhibited highly significant positive correlation with 1000-grain weight, suggested that enhancing one trait may have direct relation with other traits. Overall, the wheat advanced line MPT-51 was declared as superior genotype, followed by MPT-10 and could be relased as potential cultivar after conducting yield trials at multi location or may be used as source accession for the improvement of existing cultivars. Based on the present investigation, the following specific conclusions were drawn for use of these wheat lines in future breeding programs for the breeders.

- Wheat advanced lines showed highly significant differences for majority of the traits, and revealed greater genetic variability and hence can be used for improvement of existing cultivars or releasing as new variety.
- Almost all the traits were found highly heritable by having high heritability range of 0.63 to 0.89 suggested that improvement for most of the yielding traits is possible in early generation of selection.
- Some of the traits had positive association with other yield or morphological traits suggested that on low budget, improvement is possible simultaneously for two or more traits such as grain yield and1000-grain weight.

Of the total tested genotypes, MPT-51 and MPT-10 were identified as superior lines for future wheat breeding programs and could be released as new variety after conducting yield and multi-location trials..

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Table 3.1. ANOVA for days to 50% heading of 64 wheat advanced lines including check cultivar evaluated during the year 2015-16 at CCRI

Source	DF	Days to 50% heading	Days to 90% maturity	Plant height	Spike length	Spikelets spike^{-1}	Grains spike^{-1}	1000-grain weight
Replication	1	20.32	0.63	406.12	0.05	0.03	0.19	45.84
Treatment (adj)	63	33.35**	8.12**	84.39**	1.21^{NS}	4.43*	38.89*	35.29**
Error								
-Effective	49	3.73	1.43	18.27	1.41	2.85	24.67	14.58
-Intrablock	49	3.39	1.21	16.11	1.35	2.56	22.08	15.15
Total	127	------	------	------	-----	-----	------	-----

** (Probability at 1%), * (Probability at 5%), NS (Non-significant)

Table 3.4. Estimates of variances (genotypic, environmental, phenotypic), coefficient of variation (genotypic, phenotypic), broad-sense heri
mean of genetic advance, standard error and cooeficient of variability computed for 8 important yield traits for 64 wheat advanc
during the year 2015-16 at CCRI, Pirsabak Nowshera

Traits	GV	VE	VP	GCV	PCV	H^2	GA	G
Days to 50% heading	31.48	3.73	35.21	4.60	4.86	0.89	7.43	6.
Days to 90% maturity	7.41	1.43	8.84	1.60	1.74	0.84	3.49	2.
Plant height	75.26	18.27	93.53	7.93	8.84	0.80	10.89	9.
Spike length	0.50	1.42	1.92	6.38	12.50	0.26	0.51	4.
Spikelets spike^{-1}	3.01	2.85	5.86	8.43	11.77	0.51	1.74	8.
Grains spike^{-1}	26.56	24.68	51.24	8.69	12.07	0.52	5.19	8.
1000 grain weight	28.00	14.58	42.58	13.05	16.09	0.66	6.01	14
Grain yield	370550.56	221938.27	592488.83	15.74	19.91	0.63	673.96	17

GV= Genotypic variance, VE= Environmental variance, VP= Phenotypic variance, GCV= Genotypic coefficient of variance, PCV= Pheno
Broad-sense heritability, GA= Genetic advance and GAM (%) = Genetic advance as percent of mean, SE= Standard error, CV= Coefficien

Table 3.5. Simple correlation among eight important traits of 64 bread wheat advanced lines including check cultivar evaluated during the y
Nowshera

Traits	**Days to 50% heading**	**Days to 90% maturity**	**Plant height**	**Spike length**	**Spikelet spike^{-1}**	**Grain spike**
Days to 90% maturity	0.64**					
Plant height	0.09^{NS}	0.15^{NS}				
Spike length	0.04^{NS}	0.01^{NS}	0.04^{NS}			
Spikelet spike^{-1}	0.05^{NS}	0.06^{NS}	-0.08^{NS}	0.61**		
Grains spike^{-1}	0.06^{NS}	0.06^{NS}	-0.09^{NS}	0.61**	1.00**	
1000-grain weight	-0.38**	-0.25**	0.07^{NS}	0.06^{NS}	-0.16^{NS}	-0.16
Grain yield	-0.31**	-0.13^{NS}	0.14^{NS}	0.02^{NS}	-0.04^{NS}	-0.04

* and **, significant at 5 % and 1 % level of probability, respectively, and NS means Non-Significant

Table 3.2.Mean performance of 64 wheat advanced lines evaluated for days to 50% heading, days to 90% maturity, plant height and spike length in MPT (N) at CCRI Pirsabak Nowshera during 2015-16

Entry Name	Days to 50% heading (days)	Days to 90% maturity (days)	Plant height (cm)	Spike length (cm)
MPT-1	126.0	169.5	115.0	11.5
MPT-2	116.0	170.0	110.5	12.0
MPT-3	117.5	167.0	112.5	11.7
MPT-4	123.0	167.0	103.0	10.0
MPT-5	127.0	173.5	119.0	9.9
MPT-6	117.5	166.0	118.5	10.6
MPT-7	120.0	172.0	95.0	11.4
MPT-8	118.5	172.5	109.0	9.8
MPT-9	119.0	168.5	114.0	11.5
MPT-10	122.0	170.0	107.5	13.1
MPT-11	122.0	170.5	110.0	11.5
MPT-12	119.5	169.0	115.0	11.0
MPT-13	122.5	171.0	106.5	11.7
MPT-14	122.0	169.0	110.0	12.7
MPT-15	121.5	168.0	104.0	11.0
MPT-16	121.0	171.5	105.5	11.6
MPT-17	116.5	167.0	102.5	11.5
MPT-18	120.0	170.5	111.5	11.5
MPT-19	120.0	170.5	105.0	11.8
MPT-20	124.5	170.5	96.0	10.9
MPT-21	129.5	174.0	112.5	11.8
MPT-22	117.5	170.0	109.5	11.1
MPT-23	119.0	168.0	97.5	11.3
MPT-24	131.5	174.5	91.0	10.2
MPT-25	121.0	168.5	111.5	10.3
MPT-26	120.5	169.5	104.0	10.4
MPT-27	119.0	171.0	118.5	10.6
MPT-28	119.0	170.0	95.0	9.2
MPT-29	122.0	172.0	115.0	11.2
MPT-30	125.5	172.0	111.0	11.2
MPT-31	126.5	172.0	109.0	10.4
MPT-32	130.5	174.5	105.0	11.8
MPT-33	130.5	174.0	113.5	10.6
MPT-34	130.5	174.5	105.5	11.8
MPT-35	116.5	168.0	102.5	11.2
MPT-36	122.0	171.0	112.0	11.1
MPT-37	125.0	172.0	112.5	9.9
MPT-38	115.0	167.5	102.5	11.4
MPT-39	120.0	169.5	105.5	10.7
MPT-40	126.0	171.0	105.0	11.8
MPT-41	117.0	168.5	107.5	10.5
MPT-42	116.0	169.0	105.0	12.0
MPT-43	126.0	171.5	114.0	11.3
MPT-44	124.5	171.5	105.0	11.6
MPT-45	124.0	169.5	112.5	12.0
MPT-46	126.5	171.5	112.5	10.0
MPT-47	120.0	169.0	107.5	10.6
MPT-48	123.0	172.0	108.0	10.0
MPT-49	121.5	173.0	110.0	10.7
MPT-50	127.0	173.5	122.5	11.6
MPT-51	127.5	171.5	115.0	11.5
MPT-52	125.5	173.0	115.0	11.0
MPT-53	118.0	170.5	100.0	10.9
MPT-54	123.0	170.5	113.5	10.5
MPT-55	126.5	171.5	115.0	12.0
MPT-56	121.5	170.5	112.5	11.9
MPT-57	124.0	173.0	115.0	9.9
MPT-58	121.5	170.0	115.0	11.8
MPT-59	121.0	169.5	115.0	10.5
MPT-60	117.5	170.0	121.5	9.9
MPT-61	115.0	167.5	107.5	11.2
MPT-62	120.0	170.5	111.5	10.4
MPT-63	120.0	170.0	116.0	11.1
Check (PS-13)	122.0	171.5	114.5	12.3
LSD$_{(0.05)}$	3.88	2.40	8.59	2.39

Table 3.3.Mean performance of 64 wheat advanced lines evaluated for spikelet spike^{-1}, grains spike^{-1}, 1000-grain weight and grain yield in MPT (N) at CCRI Pirsabak Nowshera during 2015-16

Entry Name	Spikelets spike^{-1} (no.)	Grains spike^{-1} (no.)	1000-grain weight (g)	Grain yield (kg ha^{-1})
MPT-1	17.8	51.3	38.3	3900.0
MPT-2	20.8	60.3	48.3	4157.0
MPT-3	19.0	55.0	40.3	4082.0
MPT-4	19.5	56.5	35.9	3710.0
MPT-5	19.0	55.0	40.5	3586.5
MPT-6	18.3	52.8	41.7	3955.0
MPT-7	19.5	56.5	47.0	3721.5
MPT-8	17.0	49.0	46.0	2993.5
MPT-9	19.8	57.3	46.4	3877.0
MPT-10	23.5	68.5	39.0	3802.0
MPT-11	20.5	59.5	41.6	3586.5
MPT-12	21.0	61.0	41.4	4348.0
MPT-13	20.8	60.3	38.6	4383.5
MPT-14	21.5	62.5	46.3	3920.0
MPT-15	18.3	52.8	43.0	4166.5
MPT-16	22.0	64.0	44.6	3950.0
MPT-17	19.9	57.6	47.8	4730.0
MPT-18	20.3	58.8	40.3	4355.0
MPT-19	21.3	61.8	35.7	3311.5
MPT-20	20.5	59.5	46.5	4040.0
MPT-21	22.8	66.3	33.8	3328.5
MPT-22	20.3	58.8	40.7	4275.0
MPT-23	24.0	70.0	33.9	3480.0
MPT-24	20.3	58.8	34.1	3035.0
MPT-25	20.3	58.8	35.0	3401.5
MPT-26	20.0	58.0	36.3	4153.0
MPT-27	20.5	59.5	45.4	3033.0
MPT-28	21.5	62.5	33.6	3291.5
MPT-29	21.5	62.5	40.3	3593.5
MPT-30	20.5	59.5	34.5	3018.5
MPT-31	19.0	55.0	34.0	2516.5
MPT-32	21.5	62.5	36.6	3906.5
MPT-33	20.5	59.5	32.0	4220.0
MPT-34	21.3	61.8	37.3	3496.5
MPT-35	21.8	63.3	43.4	4168.5
MPT-36	20.0	58.0	37.1	5155.0
MPT-37	18.8	54.3	41.6	3603.5
MPT-38	20.3	58.8	43.9	4301.5
MPT-39	20.8	60.3	36.6	3778.5
MPT-40	20.0	58.0	42.1	3558.5
MPT-41	19.0	55.0	39.6	4363.0
MPT-42	21.5	62.5	41.5	4388.5
MPT-43	20.5	59.5	41.6	4403.0
MPT-44	20.9	60.6	41.7	3465.0
MPT-45	21.3	61.8	39.3	3420.0
MPT-46	17.5	50.5	39.7	3940.0
MPT-47	19.0	55.0	45.8	3747.0
MPT-48	20.0	58.0	44.7	3876.5
MPT-49	18.0	52.0	48.0	4913.5
MPT-50	20.5	59.5	38.1	3305.0
MPT-51	23.5	68.5	42.3	3965.0
MPT-52	19.8	57.3	42.6	3438.0
MPT-53	20.5	59.5	37.1	3745.0
MPT-54	18.8	54.3	44.3	4390.0
MPT-55	21.3	61.8	41.3	3563.0
MPT-56	21.5	62.5	43.0	4032.5
MPT-57	17.8	51.3	37.1	4345.0
MPT-58	22.5	65.5	36.7	4328.5
MPT-59	20.9	60.6	37.2	4385.0
MPT-60	19.0	55.0	43.7	4453.0
MPT-61	19.5	56.5	48.1	4125.0
MPT-62	21.5	62.5	42.0	3898.5
MPT-63	20.5	59.5	41.0	3505.0
Check (PS-13)	22.8	66.3	39.0	3600.0
LSD$_{(0.05)}$	3.39	9.98	7.63	946.71