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RESEARCH PAPER

TITLE:

MORPHOLOGICAL CHARACTERIZATION OF WHEAT GERMPLASM FOR YIELD AND YIELD RELATED TRAITS

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MORPHOLOGICAL CHARACTERIZATION OF WHEAT GERMPLASM FOR YIELD AND YIELD RELATED TRAITS

ABSTRACT

Evaluation and identification of superior genotypes for general cultivation is the key objective of plant breedings programs. To investigate genotypic differences among exotic wheat germplasm and association between yield and yield associated attribute in wheat genetics, scientific research was done at Agriculture Research Station, Baffa, Mansehra in 2021. Fifty genotypes including 49 exotic wheat genotypes and one check cultivar were sown in Randomised Complete Block (RCB) design with three replications. Data were recorded on plant length (cm), spike length(cm), 1000-grains weight (gm), days to emergence, number of heads and days to maturity, biological yield (kg), tiller m^{-2}, yield plot^{-1} (kg). Significants variation were noted among all the genotypes i.e plants height (cm), 1000 grain weight (gm), days to emergence , heading and maturity days, biological yields (kg), tiller m', grains yield (kg) length of spike (cm). Maximum plants height (104 cm), spikes length (11.63 cm), 1000 grain weight (39.3 gm), emergence days(20 days), days to headings (116 days), days to maturity (180.3 days), biological yield (11.9 kg), tiller m^{-2} $^{(}$574) and grains yield (3.56 kg) were recorded for genotpye G43, G37, G37, G19, G48, G11, G40, G37 and G37, respectively. Grains yield depicted significant correlation with spike lengths, 1000 grains weight and tiller m^{-2} ; whereas, significant negative correlation with plant height and biological yield showed that these traits needs to be measured in determining selections criteria for grains yield improvement. Heritability evaluations revealed high values for all the parameters viz. plant height (0.83), 1000-grain weight (0.83), emergence days (0.61), days for heading (0.85), date to physiological maturity (0.72), biological yield (0.65), grain yield (0.77), tiller m^{-2} (0.84) and spike length (0.70). Selection response estimates revealed low values for the traits under study viz. plant height (7.9), 1000-grain weight (1.2), day to emergence (1.14), days to heading (2.892), days to maturity (2.65), biological yields (0.34), grain yield (0.59) but moderate for spike length (15.58) and high for parameter like tiller m^{-2} (25.49). Genotype G37, G3 and G38 produced maximum grain yield and thus should be suggested for breeding wheat and varietal development programme in future.

KEYWORDS: Wheat, Variances, Correlation, Genetic Advanced, Production, Yield traits.

1. INTRODUCTION

Historically, wheat is a one of the most important crop in Pakistan, is given more significance in agricultural programs and it has been utilized by a large area of promising land. The great majority of the world's population in terms of production and nutrition it is a critical cereal crop from all other cereals (Azam & Shafique, 2017). Wheat has been domesticated around 10,000 years ago from Fertile Crescent. Those previously cultivated wheat were diploid species (genome AA) (einkorn) and tetraploid (genome AABB) and those were originated from south-eastern regions of Turkey (Curtis et al., 2014). Wheat is among the biggest grain crop of the global world, which contributes 36% of solid food to the worldwide populations. It contributes 20% of foods Calories. Its production is oftenly influenced by climatically changes worldwide and increasing the shortage of water reserves and bettering the Eco-environment. (Khan et al., 2011). Food security for the world's growing population depends on our ability to increase grain production, which depends on a number of yield contributing traits (Ehrlich & Harte, 2015). Grain production can be increased by extending the wheat crop's photosynthetic cycle or grain-filling phase (Faralli & Lawson, 2020).

To cope with the world's increasing population, the primary goal is to increase food production. To enhance the agricultural productivity is somewhat critical for both present and future food securities meet ups (Stonawski et al., 2015). There is still more options for the fulfillment of increasing demands of increasing population, notably in efforts to contribute more to wheat genetic evolution. The most effective technique to enhance wheat productivity has shown to be genetic manipulation (Govindaraj et al., 2015). As in plant breeding genetic diversity is critical to take advantage of heterosis and develop viable recombinants (Ali et al., 2013; Ali et al., 2014ab; Ter Steeg et al., 2022). Wheat research has been intensively ongoing for a time long to improve grain production and grain yield per unit area (Slafer et al., 2021). It is the ruling food crop of Pakistan, and it is cultivated under the area of about 8 million hectare, taking a portion of about 38.1% of overall planted sphere, in which 66 % of orbit produce 71% grain in yield. The area under wheat cultivation of Punjab was 15896 thousand hectares, in which grains production is 17992 (000) tons with mean grains yield of 2875 kg ha^{-1} between 2006-07 (Latif et al., 2018). The total cultivated area of wheat crop in Khyber Pakhtunkhwa was 732.6 thousand hectares amid 2014-15, (Ullah et al., 2018).

The knowledge on genetic diversity of wheat landraces should be the initiating point of their utilization and conservation management. To every breeding project the selection of parents is critical. Therefore, understanding germplasm's genetic diversity and relatedness is critical for agricultural improvement efforts. When genetic diversity decreases, crop sensitivity to disease and negative environmental changes increases (Varshney et al., 2021). Thus, to improve the genetics of wheat crop, diverse genotypes from accessible germplasm should be chosen and employed in subsequent breeding programs. Plant breeder’s focused on producing high-yielding wheat cultivars by combining excellent general combiner lines and selecting transgressive segregents for grain yield and other traits from the resulting hybrids (Mason & Batley, 2015). Therefore, some researchers suggested that general combining ability significantly influences grain production and other traits in parent selection for grain yield (Liu et al., 2020). Likewise, yield is an important and prime breeding objective of any crop because the population is increasing day by day, and the production area is decreasing daily. The breeders focus on the characters that are positively associated with the grain yield. This study was conducted to get subsequent goals; To estimates the heritability, genetic advance and variability in studied genotypes and to identify and select the potential lines for future wheat breeding program.

2. MATERIALS AND METHODS

This experiment was typically conducted at the Agriculture Research Station (ARS) Baffa Mansehra while during the growing year of 2020-2021 in December, during rabbi season. Fifty (50) wheat genotypes of exotic wheat germplasm were received from CIMMYT corded as to conduct this research work respectively. These genotypes were planted in randomized completely block design with three replications at Agriculture Research Station, Baffa Mansehra, Pakistan during 2020-2021. The field was deeply ploughed three to four multiplication followed by rotavator operations. Standard doses of fertilizers were applied to the field. Experiment was sown in Randomized Complete Block Design. The row to row distance was kept 30 cm apart.

3. DATA COLLECTION

Data were recorded on five plants in each entry, which were chosen randomly and tagged for following parameters Viz, Days to emergence, Days to heading, Days to maturity, Tillers m^{-2} Plant Height (cm), Spike Length (cm), 1000 grains weight (g), Biological yield (kg), Yield $plot^{-1}$. The recorded data of every trait were analyzed for estimation of variance by statistical model of Singh and Chaudhary (1985).

Estimation of Genetic Parameters

Genotypic and phenotypic variances, genotypic coefficients of variances (GCV) and phenotypic coefficients of variances (PCV), heritability (bs) and genetic gain will be calculated as outlined by Singh and Chaudhary (1985).

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

Environmental variance (Ve) = Error mean square (EMS)

Phenotypic variance (Vp) = Vg + Ve

Heritability (bs) h^2 calculated as = h^2 = vg/vp

The expected genetic advance (Re) for each parameter will be calculated as under:

$Re = i \times \sqrt{vp} \times h^2$

Where:
i = at 20% is 1.40 selection intensity for a parameter.
Vp = phenotypic variance for a parameter.
h^2 = heritability (bs) for a parameter.
Phenotypic coefficient of variation PCV%= $\sqrt{vp}$ /G.M × 100
Genotypic coefficient of variation GCV% = $\sqrt{vg}$ /G.M × 100

Where:
Vp = phenotypic variance
Vg = genotypic variance
G.M = grand mean of the trait

Correlation Analysis

The analysis of correlation coefficient for yield and its associated traits will be carried out for each environment separately as outlined by Kwon and Torrie (1964).

$$\gamma = \frac{\sum xy - \frac{\sum x . \sum y}{n}}{\sqrt{\left[\sum x^2 - \frac{(\sum x)^2}{n}\right]\left[\sum y^2 - \frac{(\sum y)^2}{n}\right]}}$$

4. RESULTS AND DISCUSSION

4.1. Days to emergence

Extremely significant difference was noted between all genotype for the day to emergence (Table 1). Maximum emergence days (20 days) were recorded in **ARS-1019** and minimum (15 days) were recorded in

ARS-1042 (Table 4.2) and the grand mean value was (17.49 days) (Table 1). These results were in consistent to the Alam et al (2013). The significant difference was also recorded by them between all the germplasm for days to emergence. Same results were noted byYağdı *et al* 2009 besides Sukram *et al* 2006. The values of genetic and environmental variances were recorded as 1.09 and 0.70 for the days to emergence. Selection response and heritability values were observed as 1.14 and 0.61 respectively. Genetic coefficient of variation was found to be less than that of phenotypic coefficient of variation at current location. The values of genetic and the phenotypic coefficient of variations for days to emergence were calculated to be 5.9693 & 7.6510 respectively (Table 4.3). High heritability estimates were observed for days to emergence. Same results were revealed by Bhuri Singh (2013). High heritability estimates were also observed for days to emergence by Teich et al 1984 Wahidy et al (2016) which are in consistant with our findings. Days to emergence showed greatly positive significant correlation alongside tiller m^{-2} whereas they disclosed extremely negative significant correlation along with biological yield and days to heading. Khan et al (2015) also found the same outcomes in his work. Similar results were also reported by following authors Khiabani et (2015); Mondal et all (1997).

4.2. Days to heading

Extremely significant differences were estimated among all biological group for days to heading (Table 4.1). Maximum days to heading (116 days) were recorded in **ARS-1048** and minimum (106 days) were noted in **ARS-1042** (Table 4.2) and the grand mean value was calculated to 111.20 days (Table 4.2). The results matched with the findings of Tsegaye et al 2012. Similar findings were also presented by Afridi et al 2018. Dessalegn et al 2012 observations were also similar to these results. Genetical and environment variance were found to be 5.14 and 0.93, respectively. Heritability was 0.85 along with selection response was at 2.92. Genetic coefficient of variations was less than phenotypic coefficient of variation and their values are 2.0364 and 2.2130 respectively (Table 4.3). High heritability and genetic components of variance recommended that there would be prominent role of inheritance in the improvement of said traits through selection. These findings were in agreement with the work of Kumar et al. (2010) and Baranwal et al. (2012) who have reported low GCV and PCV for the said attribute. The broad sense heritability estimation noted for days to heading were higher which displays that the selection is achievable and easy in early generations (Ullah et al 2018). Significant level of heritability was also discovered for the number of days to heading by Kalim et al 2011 which were similar to our findings. Similar results were also presented by Atta et al. (2008) Days to emergence indicated negative significant cor-relations with days to heading while biological yield, plant tallness and thousand grains weight displays highly non-significant correlational statistics with the day to headings along with days to maturity, grain yield .Tiller m^{-2} showed negative non significance correlation with day to heading. Our outcomes matched with the findings of Tsegaye *et al* 2012 who found non-significant correlation of day to heading, 1000-grains weight, biological yield and the grains yield. The same was also found before by Hisham *et al*. (2007).

4.3. Days to maturity

Highly significant differences were calculated among all the genotypes for the days to maturity (Table 4.2). Maximum days to heading (180.3 days) were noted in **ARS-1011** and minimum (173 days) were recorded in **ARS-1027** and **ARS-1034** (Table 4.2.1) and the grand mean value was noted to be 176.01 days (Table 4.2). The same results were also observed by Khan *et al* 2008 for the maturity. These results were in harmony with the findings of Hidayat *et al* 2018. Significant differences were also reported amongst wheat for the days to maturity by Zaman et al (2013), Upadvay and Singh, 2014. Genetic variance, environmental variance, phenotypic variance, heritability and selection response were recorded as 5.02, 1.99, 7.01, 0.72 and 2.65 respectively (Table 4.3). High heritability estimates for maturity days were also noted by Khans *et al* 2011. The day to maturity displayed high heritability with low genetic advance as reported by Hidayat et al 2018. The values of genetic coefficients of variance were found slightly less than the PCV. The values recorded for genotypic coefficient of variation and phenotypic coefficient of variation were calculated to be 1.2706 and 1.5015 (Table 4.3). Our results were also in compatibility with Tripathi *et al*. (2015). The Day to maturity showed highly significant cor-relation to Spikes length where as highly significant correlation was recorded with the plant length and negative significant correlation was found with biological yield. Same results for days to maturity have also been found by Khan *et al* (2007). These finding were strengthened by the results reported by Wahidy et al. (2016). Present results described that maturity was non-significant correlated to grain yield, The data were similar with the findings of Khan, 2013.

4.4. Tillers m^{-2}

The highly significant differences were determined amongst all the genotypes for tiller m-^{2} (Table 4.1). Maximum tillers m-2 (574) were noted in **ARS-1037** and minimum (512) were noted in **ARS-1036** (Table 4.2) and the grand mean value was calculated to be 546.78 (Table 4.2). The results were in consistent to the Baranwal et al (2012) for tiller m-2. Same were the findings of of Ali et al. (2008) and Tsegaye et al (2012). For tiller m^{-2} genetic, environmental and phenotypic variances were 395.09, 75.85 and 470.95 respectively. Whereas heritability, selection response, genetic coefficient of variation and phenotypic coefficient of variation were recorded to be 0.84, 25.49, 3.6351 and 3.9688 respectively (Table 4.3). High heritability with high selection response were observed. Similarly, genetic coefficient of variation was also found to be less than phenotypic coefficient of variation. The phenotypic coefficient of variation (PCV) values were higher than genetic coefficient of variation (GCV) values for all the traits;same was reported by Ali et al 2008. High heritability for number of productive tillers were noted by Yousaf et al (2008),Sharma and Garg (2002) and Dwivedi et al., (2002) which matched our results. Grain yield, spike length, 1000 grains weight and days to emergence presented highly positive significant correlation with tiller m^{-2} while plant height and biological yield presented negative significant correlation with tiller m^{-2}. Similar results for tiller m^{-2} have also been presented by Baranwal et al 2012. Productive tillers were found to had highly significant and negative genotypic correlation with plant height (Ali et al., 2008). The significant positive correlation of tiller m^{-2} with the grains yield had also been shown by by khan *et al*., (2010). These findings also displayed the agreement to results of Kiara and Aikman (2006) and Tsegaye et al (2012).

4.5. Plants Height

Analysis of variance demonstrated the significant differences between all the genotypes for the plants height (Table.4.1). Maximum plants height (104) was recorded in **ARS-1043** and minimum (90cm) was observed in **ARS-1037** (Table 4.2) and the grand mean value was recorded to be 96.71 (Table 4.2). These results were according to the Baloch *et al* (2012) whose findings were also same for plants height. Same conclusions were also presented by (Baranwal *et al.,* 2012). Related results were also presented by Arain *et al* 2006. Genetic variance and environmental variances values were found to be 38.61 and 7.99 respectively whereas heritability was 0.83 along with selection response at 7.92. Genetic coefficients of variation (GCV) were less than that of phenotypic coefficient of variation. Values of GCV, PCV for plant height were calculated to be 6.4213cm and 7.0593cm respectively (Table 2). Heritability and genetic component of the variance calculations are high so, here is a high chance of improvement via selection. High h^2 with low selection response was observed for the plants height demonstrate that the attribute is less inspired by the environmental effect and selection will be efficient. Afridi *et al* (2018) reported that the proportion contribution of genotypic variance was much higher than environmental modification with high heritability. The high heritability with moderate genetic advance for plant height was reported by Degewione *et al.,* (2013) in wheat genotypes. High heritability estimates were also recorded for plant height by Kalim *et al.,* 2011. Higher heritability was also reported for the plants tallness by Sachan & Singh (2003). Broad judgment of heritability recommended that genetic variance might show an essential role in inheritance and improvement of that trait. The same work was also reported by Naimat *et al* (2018). Correlation analysis was conducted at genotypic level to understand the relationship between the attributes studied in plant height. Biological yield showed highly significant correlation with the plants height while grains yield, Spikes length, days to maturity, and tiller m^{-2} exhibited highly negative significant correlation with plant height. Baranwal *et al* ((2012) found the same result in his research work. He also found negative correlation of plant height with yield. Bhatto *et al*. (2016) recorded significant correlatin among the plant height and grains yield. Same data were also presented by Ali *et al.,* 2009.

4.6. Spikes length

ANOVA disclosed the higher significant difference amongst all the genotypes for the spike's length (Table.4.1). Maximum spikes length (11.63cm) was recorded in **ARS-1037** and minimum (8.8cm) was noted in **ARS-1043** (Table 4.2.1) and the grand mean value was claculated to be 10.872cm (Table 2). Naimat et al 2018 found the same result in his research. These collections are in compatible with work of Nawaz *et* al., (2013). This is in consistant with the findings of Gupta and Khan (2009). Genetical and environmental variances for the spike's length were 0.56, 0.24. Heritability and selection response were 0.70 and 15.58 respectively and the values of GCV & PCV for spike length located at 6.9213 and 8.3240 (Table 4.3). These results revealed that high heritability was recorded for spike length .Same were the findings of Kalim *et al* (2018). High heritability and moderate genetic advance were also detected which shows the high scope of improvement for said attribute through selection.Same were the observations of Baranwal *et al,* (2012. The PCV value was higher than the GCV value for said trait, which shows the influence of environment on the expression of traits in wheat. Similar results were presented by Abinasa *et al* (2011) and Gashaw *et al* (2013). Grain yield, thousands grains weight, maturity date and tiller m^{-2} presented highly positive significant correlation to spikes length while biological yield and plants height showed highly negative significant correlation with spike length. Naimat et al. (2018) findings were also same to this result. Mohsin *et al* (2009) results were also in accordance to these results. Ali et al. (2009) also found a higher significant correlation between spike length and grain yield.

4.7. 1000-grains weight

High significant differences were recorded among all genotypes for thousand grains weight (Table. 4.1). Maximum 1000 grains weight (39.3gm) was noted in **ARS-1037** and minimum (36.1gm) was reported in **ARS-1043** (Table 4.2.1) and the grand mean value was recorded to be 37.48gm (Table.4.2.1). The outcomes were in accordance to Ali *et al* 2012. Significant difference between genotypes of 1000-grain weight were also observed by Korkut *et al.*, (2001) and Ali et al (2008). Genetic and environmental variances were 0.88, 0.18 respectively. The heritability was 0.83 and selection response were calculated to be 1.20. The values of GCV and PCV for 1000 grains weight were estimated to be 2.5024 & 2.7593. (Table.4.3). Genetic coefficients of variations were found to be less than phenotypic coefficient of variation. High heritability values were discovered for 1000-grains weight. Tsegaye *et al* (2012) reported high heritability values for 1000 grain weight. High heritability associated to grains weight were observed in the study conducted by Safir UL-Hassan *et al.*, (2005) and Tanzeen *et al.*, (2009). Grain yield, spike length and tiller m^{-2} displayed highly positive significant correlation with 1000 - grains weight while the plants height and biological yield exhibited highly negative significant correlation with 1000 grains weight. Ali et al. (2012) found the same result in his research work. Arain et al. (2018) findings were also same to these results. Likewise, highly significant correlation was found between the 1000 grains weight and grains yield. Our result matched to the findings of Mohammadi et al. (2012) and Desheva et al. (2015). Correspondent effects were also presented by Khan et al. (2010) and Khokhar *et al.*, (2011).

4.8. Grains Yield

Highly significant differences were recorded amongst all genotypes of grains yield (Table 4.1). Maximum days to heading (3.56 kg) was recorded in **ARS-37** and minimum (1.40kg) was noted in **ARS-43** (Table 4.2.1) and the grand mean value was recorded to be 2.60kg (Table 3). Hidayat et *al.*, 2018 also recorded significant difference amongst all the genotypes for the grains yield. Khan *et al* (2014) findings were also similar to these results. Same results were issued by Mishra *et al*. (2008). For grain yield, the genetically and the environmental variances were 0.23 , 0.068 severally. The heritability and selection response values were recorded as 0.77 and 0.59 correspondingly. The genetic coefficients of variations (GCV) were lower than that of phenotypic coefficient of variations (PCV) the magnitude of (GCV) and (PCV) for grains yield was noted to be 18.4362 and 21.0557 (Table 4.3). Ali *et al* (2008) findings for heritability were similar to these results. Sachan and Singh (2003) recorded high heritability estimation for grain yield. Spike length, 1000-grains weight and tiller per meter square displayed highly positive significant correlations with grains yield whereas plants height and biological yield showed negative highly significant correlation with the grains yield. Gerema *et al* (2020) recorded the similar result in his research work. Same results have also been prsented by Baranwal *et al* (2012). The results are in consistant with the conclusions of Budak, (2003) and Yağdı and Sözen (2009). Similar results were observed in the findings of Tsegaye et al. (2012). These results match to the findings of of Mishra et al. (2009).

4.9. Biological Yield

Higher significant difference was calculated among most of genotypes for biological yield (Table 4.1). Highest biological yield (13 kg) was noted in **ARS-43** while lowest (11.9 kg) was recorded in **ARS-40** (Table 4.2.1) and the grand mean value were recorded to be 12.36 kg (Table. 4.2.1). Baloach et al., (2016) as well noted the significant variations midst all the genotypes on behalf of biological yields which were accordant to this result. Related findings were also prsented by Baloch et *al.*, (2014a) and Balaoch et_al. (2014b). The genetic, environmental and phenotypic variances for said parameters were 0.09, 0.048 and 0.14 severally. Heritability, selection responses were calculated to be 0.65 and 0.34, respectively. As genetic coefficients of variation (GCV) were less that phenotypic coefficient of variation so, values recorded on behalf of genetic coefficient of variation and phenotypic coefficient of variation were 2.4267 & 3.0267 respectively (Table. 4.3). High heritability was noted for biological yield. These findings were in consistence with report of Khodaidadi *et al*. (.2011), Kaleem Ullah *et al*. (.2015) and Rahman *et al*. (2015). Plant height demonstrated highly significant correlation to the biological yields while grain yield, spikes length, 1000 grains weight, and days to emergence displayed negative significant correlations. Maturity days showed negative significant correlation to the biological yield. Related findings were also recorded by Baloch *et al.,* 2016. The results match to the findings of Gibson and Paulsen, (1999).

4.10. Correlation analysis

Correlation aids the scientist to know a mutual relationship between various variables alongside direction and size. Environmental factor play an important role correlation. Environmental factors and genetic causes of correlation give phenotypic correlation.

Correlation analysis (Table.4.4) revealed that days to heading exhibited significant negative relationship to days to emergence (r= -0.02) only, whereas plant tallness had significant positive association with biological yield (r=0.12) only but had significant negative assiciation with spike lemgth, 1000 grains weight, days to maturity, tiller m-^{2} and grains-yield. The spike length showed significant correlation to 1000 grains weight (r= 0.29), days to maturity (r= 0.01), tiller m-^{2}(r= 0.13), and grains yield (r= 0.22), but significant negative relationship for bilogical yield (r = -0.22). 1000 grains weight exhibitted significant positive correlation with spike length (r= 0.28), tiller m-2 (r= 0.32) and the grains yield (r=0.27) and significant negative correlation with plant length (r= -0.12) and biological yield (r= -0.34). Days to emergence showed significant positive correlation with tiller m-^{2} (r= 0.07) only but revealed significant negative assosiation with days to heading (r= -0.02) and biological yield (r= -0.11). Days to maturity indicated significant negative correlation with biological yield (r= -0.09) only but revealed non-significant positive correlation with all other traits. Biological yield showed significant posivive correlation with plant height (r= 0.12) only but showed significant negative correlation with the spikes length (r= -0.22), 1000 grains weight (r= -0.34, days to emergence (r= -0.11), days to maturity (r= -0.09), and grain yield (r =-0.12). Tiller m-2 exhibitted significant correlation to length of spike (r= 0.13), 1000 grains weight (r,= 0.32), days to emergence (r= 0.08), grains yield (r= 0.47). Grains Yield showed significant positive correlation with spike length (r= 0.22), 1000 grains weight (r=0.27) and tiller m-^{2} (r= 0.17).

Table 4.1. Mean square for quality and quantity related traits of exotic wheat germplasm.

Traits	GMS	EMS	F. Ratio	P-Value	CV (%)
Days to emergence (%)	3.96204	0.70449	5.62	0.0000	4.80
Days to heading (%)	16.3468	0.9382	17.42	0.0000	0.87
Days to maturity	17.0476	1.9917	8.56	0.0000	0.80
Tiller M^{-2}	1261.13	75.85	16.63	0.0000	1.59
Plant height (cm)	123.835	7.996	15.49	0.0000	2.92
Spike length (cm)	1.93248	0.24241	7.97	0.0000	4.55
1000 grains weight (gm)	2.84230	0.18764	15.15	0.0000	1.16
Grain yield (kg)	0.75414	0.06864	10.99	0.0000	10.07
Biological Yield (kg)	0.31455	0.04807	6.54	0.0000	1.77

Table 4.2. Mean values comparison of exotic wheat germplasm for Plants Height (PH), Days for Emergence (DE), Days to Heading (DH), Days to Maturity (DM), Tiller^{-2}.

Labels	DE	DH	DM	TM^{-2}	PH (cm)	Labels	DE	DH	DM	TM^{-2}	PH (cm)
ARS-1	17.6 b-g	110.6 c-j	179 a-c	535 f-m	98 ag	**ARS-26**	18 a-f	112.3 a-g	175 c-i	562 a-h	98.2 ag
ARS-2	16 g	111 b-i	177.6 a-f	543.6 a-l	100.4 ae	**ARS-27**	19.3 ab	109 e-j	173 h-i	563.6 a-g	98.6 af
ARS-3	17.3 c-g	110.6 c-j	177.6 a-f	571.3 a-b	91.6 gj	**ARS-28**	17.6 b-g	115 ab	175.3 b-i	545.3 a-l	96 bh
ARS-4	18.6 a-d	110 c-j	179.3 a-b	558.3 a-i	97 ah	**ARS-29**	16 g	112 a-h	173 h-i	551.3 a-j	98.3 ag
ARS-5	16.3 fg	111.3 a-i	174.3 e-i	539.6 c-m	96 bh	**ARS-30**	18.3 a-e	109.3 d-j	174.3 e-i	563 a-g	98.3 ag
ARS-6	17.6 b-g	110 c-j	177 a-h	542.3 b-m	94 ej	**ARS-31**	18.3 a-e	110.3 c-j	174 e-i	557 a-j	96 bh
ARS-7	18 a-f	113.3a-d	178.6 a-d	543.3 a-m	97.6 ag	**ARS-32**	16 g	108.6 f-j	175.3 b-i	518.3 l-m	101ad
ARS-8	18.3 a-e	111 b-i	179.3 a-b	536 e-m	98.6 af	**ARS-33**	17 d-g	111 b-i	174.3 e-i	564.3 a-f	96.6 bh
ARS-9	17.6 b-g	106 j	173.3 g-i	544 a-l	98 ag	**ARS-34**	17 d-g	112 a-h	173 h-i	539.6 c-m	97.6 ag
ARS-10	17.6 b-g	110.3 c-j	179.3 a-b	533.3 g-m	97.3 ah	**ARS-35**	18 a-f	110 d-j	174.33 e-i	520 k-m	100.6 ae
ARS-11	16.6 e-g	112 a-h	180.3 a	569 a-d	95 ch	**ARS-36**	16.6 e-g	115 a-b	175 c-i	512m	103.67 a
ARS-12	19.6 a	111 b-i	177.6 a-f	545.6 a-l	99.6 ae	**ARS-37**	18.6 a-d	110.6 c-j	179.3 a-b	5734 a	90 hj
ARS-13	17.6 b-g	112 a-h	174.3 e-i	531.3 h-m	88 ij	**ARS-38**	17.6 b-g	111 b-i	179. a-c	571 a-b	95 ch
ARS-14	16.3 f-g	112.6a-f	175 c-i	529.6 i-m	101ad	**ARS-39**	17 d-g	111.3 a-i	177 a-h	531 i-m	101.6 ac
ARS-15	19 a-c	108.3g-j	176.6 a-i	566.6 a-e	99.3 a-e	**ARS-40**	18 a-f	113.6 a-c	174.3 e-i	538.3 d-m	100.3 ae
ARS-16	19 a-c	112 a-h	177.3 a-g	544.3 a-l	92.3 fj	**ARS-41**	17.6 b-g	114 a-c	177.3 a-g	540.6 b-m	100.3 ae
ARS-17	16.3 f-g	113 a-e	173.6 f-i	549 a-l	97.3 ah	**ARS-42**	15 g	108 h-j	175 c-i	552.3 a-j	95 ch
ARS-18	16.6 e-g	110.6 c-j	177.3 a-g	552.6 a-j	98 ag	**ARS-43**	18.3 a-e	114 a-c	173.6 f-i	527.6 i-m	104 ae
ARS-19	20 a-c	111 b-i	177.3 a-g	549.3 a-k	101ad	**ARS-44**	18 a-f	112 a-h	173 h-i	548.3 a-l	99 af
ARS-20	17.3 c-g	114 a-c	179.3 a-b	551.6 a-j	87.3 j	**ARS-45**	18.3 a-e	110.3 c-j	173.6 f-i	530 i-m	101.6 ac
ARS-21	16.6 e-g	112 a-h	177.3 a-g	536 e-m	96 bh	**ARS-46**	18 a-f	112 a-h	176.6 a-i	569.3 a-c	98.9 af
ARS-22	17 d-g	111 b-i	178 a-e	553.3 a-j	102 ab	**ARS-47**	17.3 c-g	110.3 c-j	173.6 f-i	533.3 g-m	97 ah
ARS-23	17.6 b-g	110.3 c-j	179. a-c	527 j-m	97ah	**ARS-48**	17.3 c-g	116 a	177 a-h	566.6 a-e	96 bh
ARS-24	17.3 c-g	108.3g-j	174.6 d-i	570.3 a-c	95.3 c-h	**ARS-49**	18 a-f	110.3 c-j	173 h-i	554.3 a-j	98.6 af
ARS-25	16.6 e-g	107.6 ij	175 c-i	540.6b-m	94.6 di	**Khaista-17**	16 g	111.6 a-i	172.6 i	541.6 b-m	95.3 ch

Table 4.2.1 Mean values comparison of exotic wheat germplasm for Spike Length (SL), 1000-grains weight (1000 GW), biological yield (BY) and Grain yield(kg) (GY).

Labels	SL (cm)	1000GW (g)	GY (kg/plot)	BY (kg/plot)	Labels	SL (cm)	1000GW (g)	GY (kg/plot)	BY (kg/plot)
ARS-1	11.2 a-d	37.2 b-I	2.43 I-o	12.3 c-j	**ARS-26**	10.6 b-d	36.9 d-I	2.20 l-r	12.2 d-j
ARS-2	10.6 b-d	37.5 a-h	2.23 k-r	12.2 e-j	**ARS-27**	11.2 a-c	38.2 a-f	3.23a-e	12.1 f-j
ARS-3	11.5 ab	38.8 a-b	3.53 ab	12.7 a-e	**ARS-28**	11.2 a-d	38.2 a-e	3.23 a-e	12.5 a-I
ARS-4	10.6 b-d	36.9 d-I	2.93 c-I	12.5 a-I	**ARS-29**	10.6 b-d	38 a-g	2.83 c-j	12.1 e-j
ARS-5	10.6 b-d	37.5 a-h	2.20 l-r	12.4 b-j	**ARS-30**	11.2 a-d	38.0 a-g	2.70 e-l	12.2 e-j
ARS-6	10.9 a-d	37.3 b-h	2.23 k-r	12.4 a-j	**ARS-31**	10.9 a-d	36.9 d-I	3.16 a-f	12.4 b-j
ARS-7	10.9 a-d	36.9 d-I	2.23 k-r	12 g j	**ARS-32**	10.3 d	36.2 g-I	1.70 rs	12.5 a-h
ARS-8	11 a-d	38 a-g	2.46 h-o	12.4 b-j	**ARS-33**	10.9 a-d	37.2 b-I	2.50 h-o	12.3 c-j
ARS-9	11.2 a-d	37 c-I	2.76 d-k	12.2 e-j	**ARS-34**	10.9 a-d	38 a-g	3.06 a-g	12.4 b-j
ARS-10	10.9 a-d	37.3 b-h	2.63 f-n	12.4 b-j	**ARS-35**	10.6 b-d	36.5 e-I	2.30 j-p	12.8 a-d
ARS-11	11.2 a-d	38.2 a-e	3.23 a-e	12.5 a-I	**ARS-36**	10.5 c-d	36.4 f-I	1.83 p-s	12.6 a-f

ARS-12	11.2 a-d	38.2 a-f	2.76 d-k	12 g-j	**ARS-37**	11.63 a	39.3 a	3.56 a	12.1 f-j
ARS-13	10.9 a-d	37.2 b-I	2.93 c-i	12 I-j	**ARS-38**	11.3 a-c	38.8 a-c	3.50 ab	12.1 f-j
ARS-14	10.6 b-d	36.6 d-I	2.63 f-n	12.5 a-I	**ARS-39**	11 a-d	36.5 e-I	2.60 g-o	12.8 a-c
ARS-15	11.0 a-d	38.2 a-e	3.0 b-h	12.4 b-j	**ARS-40**	10.3 d	35.4 I	1.73 q-s	11.9 j
ARS-16	11.2 a-d	38 a-g	3.06 a-g	12.1 e-j	**ARS-41**	10.6 b-d	36.6 d-I	2.13 m-r	12 II
ARS-17	11 a-d	37.2 b-I	2.33 j-p	12.9 ab	**ARS-42**	11 a-d	36.8 d-I	2.36 j-p	12.4 b-j
ARS-18	10.9 a-d	37 c-I	2.43 i-o	12.4 b-j	**ARS-43**	8.8 e	36.1 hi	1.40 s	13. a
ARS-19	10.6 b-d	36.8 d-I	2.33 j-p	12.4 a-j	**ARS-44**	10.8 a-d	36.9 d-I	2.60 g-o	12.6 a-f
ARS-20	10.6 b-d	37.20 b-I	2.13 m-r	12.3 c-j	**ARS-45**	10.5 c-d	36.4 e-I	2.10 n-r	12.8 a-d
ARS-21	10.8 a-d	36.9 d-I	2.26 k-q	12.4 b-j	**ARS-46**	11.2 a-c	38.2 a-e	3.30 a-d	12.5 a-j
ARS-22	10.5 c-d	36.3 g-I	2.06 o-r	12.2 e-j	**ARS-47**	11.2 b-d	37.2 b-I	2.73 e-l	12.4 b-j
ARS-23	10.5 c-d	36.4 f-I	2.06 o-r	12 h-j	**ARS-48**	10.9 a-d	37.9 a-h	2.40 i-o	12.2 d-j
ARS-24	11.2 a-c	38.4 a-d	3.36 a-c	12.06 g-j	**ARS-49**	11.2 a-d	37.6 a-h	2.73 e-l	12.6 a-g
ARS-25	10.9 a-d	37.2 b-h	2.66 f-m	12.2 e-j	**Khaista-17**	11 a-d	37.3 b-h	2.53 g-o	12.4 b-j

Table 4.3. Genetic, environmental and phenotypic variances along with heritability and selection response for morphological and yield traits of exotic wheat germplasm.

TRAITS	***Vg***	***Ve***	***Vp***	***GCV***	***PCV***	***H^2***	***Re (20%)***
Days to emergence	*1.09*	*0.70*	*1.79*	*5.9703*	*7.6508*	*0.61*	*1.14*
Days to heading	*5.14*	*0.93*	*6.07*	*2.0364*	*2.2130*	*0.85*	*2.92*
Days to maturity	*5.02*	*1.99*	*7.01*	*1.2706*	*1.5015*	*0.72*	*2.65*
Tiller/M^2	*395.09*	*75.85*	*470.95*	*3.6351*	*3.9688*	*0.84*	*25.49*
Plant height	*38.61*	*7.99*	*46.61*	*6.4250*	*7.0593*	*0.83*	*7.92*
Spike length	*0.56*	*0.24*	*0.81*	*6.9213*	*8.3240*	*0.70*	*15.58*
1000 grains weight	*0.88*	*0.18*	*1.07*	*2.5024*	*2.7593*	*0.83*	*1.20*
Grain yield	*0.23*	*0.068*	*0.30*	*18.4362*	*21.0557*	*0.77*	*0.59*
Biological yield	*0.09*	*0.048*	*0.14*	*2.4267*	*3.0267*	*0.65*	*0.34*

Table 4.4. Correlation between yield and yield related attributes of exotic wheat germplasm.

Traits	**BY**	**DE**	**DH**	**DM**	**GY**	**PH**	**SL**	**THGW**
DE	-0.11**							
DH	0.09	-0.02*						
DM	-0.09*	0.05	0.02					
GY	-0.12**	0.08	0.16	0.07				
PH	0.12**	-0.02	0.03	-0.13**	-0.27**			
SL	-0.22**	0.14	0.01	0.01**	0.22**	-0.30**		
THGW	-0.34**	0.10	0.05	0.04	0.27**	-0.12**	0.28**	
TM^{-2}	-0.13	0.07**	-0.04	0.17*	0.47**	-0.28**	0.13**	0.32**

Days for emergence (DE), Days to heading (DH), Maturity Days (DM), Tiller/m^2(TM), Plants Height (PH), Spike Length (SL), 1000-grains Weight (GW), Grain Yield (GY), Biological Yield (g).

5. CONCLUSIONS AND RECOMMENDATIONS

On the basis of present study, the analysis of variance revealed completely significant differences between all the genotypes for every trait.

Heritability evaluations revealed high rates for all the parameters viz. days to emergence, day to headings, day of physiological maturity, tiller m-^{2}, plants height, thousands grains weight, grains yield, biological yield and spike length.

Selection response evaluation revealed low values for the traits under study like. days to emergence, days to heading, days for physiological maturity, plant height, 1000-grains weight, grains yield and biological yield, but moderate for parameter like spike length and high for tiller m-^{2}.And grains yield depicted significant positive association with days for maturity, tiller m-^{2}, spike lengths and thousand grains weight.

Genotypes viz. **ARS-37**, **ARS-38** and **ARS3** produced maximum grain yield and thus might be included in wheat breeding's programs.

- **Author's Contributions:**

Khalil Ur Rehman: Conducted the research work, sampling and field activities.

Izhar Hussain: Contributed in conceptualization and validation of the study.

Hassan Mujtaba: Participated in writing and edited the methodology section.

- **Conflict of interest:**

All the authors mentioned in the manuscript have no conflict in the research work and compilation.

Nadia Jabeen: Critically reviewed along with manuscript writing.

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