Performance evaluation of wheat (*Triticum aestivum* L.) genotypes for physiological and qualitative traits

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Abstract: Pakistan is an agricultural country and its economy mainly depends on agriculture. Wheat is an important cereal crop and is used as staple food in Pakistan. To fulfill the food supply of increasing population of the country it is basic task for plant breeders to improve the yield and quality of the crop. Present study was conducted in the Department of Plant Breeding and Genetics, PMAS- Arid Agriculture University Rawalpind to identify the potential wheat genotypes for physiological and qualitative traits. Thirty different genotypes were used as a genetic material. The analyses of variance showed highly significance variations among wheat genotypes for under consideration traits. From the results of experiment it was concluded that genotype "Bhakar-1" provided highest mean value for flour yield and protein content. Hence this genotype can be used to improve these traits. However the mean value for genotype Satluj-86 was lower for most of the studied traits such as transpiration rate, protein content and dry gluten contents, so this genotype may be avoided for cultivation in rainfed conditions and not to include in breeding programs.

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1. Introduction

Pakistan is an agricultural country consisting on a variety of climate and ecological zones. Due to variation in these natural resources country has potential to produce all types of food commodities (Ahmad *et al.,* 2012). Wheat is an important cereal crop and is cultivated throughout the world. In the world largest cropped area is devoted to wheat and quantity produced is more than that of any other crop. Bread wheat (*Triticum aestivum*) and durum wheat (*Triticum durum*) are the two principle commercial types of wheat (Raza *et al*., 2015 and Ahmad *et al.,* 2014). Mainly wheat is cultivated for its flour which is consumed directly or used for making various baking products such as bread, rusk, cakes etc. It is thought to be the first domesticated crop in the world. Due to rapid increase in world population, the requirement of the wheat has been increased. However, during last 50 years the yield remained stagnant due to various biotic and abiotic factors. Current estimates showed that 40% more wheat would be required up to 2025 to feed the rapidly growing population (Sial *et al.*, 2009). Seed quality of any crop is assumed as necessary element for successful crop cultivation (Rizwan-Ul-Haq *et al.,* 2014). Quality and quantity of protein are considered significant in the estimation of wheat end product quality (Farooq *et al.,* 2001; Farooq *et al.*, 2011ab). The protein content of the wheat varies from 6 to 22% depending on the production environment especially soil fertility, water and grain yield. Correlation has been found in types and amount of protein subunits with variation in quality among different wheat genotypes (Masood *et al.*, 2014abc; Gupta *et al.,* 1993). For improving wheat quality and manipulating end use product, gluten has been widely used in research to determine their structure and properties. The protein content of the wheat grain appears to be determined by a combination of genetic and environmental factors resulting in considerable difference in protein content within genetically determined limits. In general, a negative correlation exists between protein content and grain yield. Since yield is a major objective of the farmer and also determinant of income, there has been less attention towards developing cultivars with high protein content. Despite this negative relationship between grain yield and protein content, many plant breeders have been focusing on high quality protein content because of its importance for grain processing and end use quality. Plants adopt limited environmental conditions by modifying physiological, biochemical and molecular systems (Habibpor *et al.,* 2011) and such response depends on environmental conditions of specific area and time (Cattivelli *et al.,* 2008). Genetic makeup of plant also determines the adaptation towards these conditions. Moreover, great interspecies and intra species variations occur in plants which is quiet visible in present study data. Evaluation of genetic variation along with genetic association between genotypes is fundamental need of plant breeders (Ali and Ahsan 2015; Ali *et al*., 2012; Ashfaq *et al.,* 2014). The main objective of present study was to identify best wheat genotypes regarding quality and yield on the basis of morphological, physiological and biochemical bases.

2. Materials and methods

The present study was conducted in the Department of Plant Breeding and Genetics, PMAS-Arid Agriculture University Rawalpindi during the years 2012-2013.The research material was comprised of thirty potential wheat genotypes grown under uniform agronomic practices to achieve the research aims. Ten plants were selected randomly from each genotype to evaluate the physiological traits i.e. measurements of photosynthetic rate, stomata conductance, transpiration rate and stomata resistance (*r*s) were made on fully expanded flag leaf of each wheat plant using open system LCA-4 ADC PIGA (portable infrared gas analyzer). These measurements were taken from 11:00 to 13:00 hrs with the following condition: temperature of chamber which carried leaf varied from 34.5 to 39.6 °C, pressure was kept 991 mBar, CO_2 concentration was absolute 373 µmol/mol, sub-stomata CO_2 concentration 110-313 µmol/mol, water vapor pressure was kept in chamber 34.7 mBar. Flow of air per unit leaf area was kept 206.6 mol/ms and PAR at the leaf surface was maximum up to 1200 µmol/ms. The biochemical analysis for protein contents, wet gluten, flour quality and dry gluten was determined by the methods given by AACC (2000) and AOAC (2005). For statistical analysis of morphological traits as well as biochemical/quality traits, analysis of variance (ANOVA) was carried out according to (Steel *et al.,* 1997) and means was compared at 5%LSD.

3. Results and discussion

Thirty wheat genotypes were evaluated by physiological and biochemical analyses to find out the desired genotype. Analyses of variance showed highly significant results for studied physiological and quantitative traits as represented in table 1.

3.1 Physiological characterization

Physiological processes are foundation for improvement of yield and yield stability in stress conditions (Harris, 1989). Productivity genes have specific effect on yield which is indirectly affected by physiological processes (Evans, 1981). The analysis of variance provided the information on the relative contribution of various components of physiological and biochemical to yield and its quality. In present study thirty genotypes of wheat were subjected to physiological analysis for photosynthesis rate (A), stomata conductance (gs), transpiration rate (E), and stomata resistance (rs). Results demonstrated significant differences among genotypes for physiological analysis at $p \leq 0.05$. Brief descriptions of the physiological results are given below.

Table 1. Analysis of variance for biochemical and physiological traits in wheat genotypes

SOV	**DF**	**PSR**	**SC**	**TR**	**SR**	**P %age**	**WG**	**DG**	**FY**
Replication	**2**	162.337	0.11165	17.2484	0.15028	17.3361	257.211	0.05069	196.924
Genotype	**29**	33.240*	0.02469*	0.6645*	0.53968*	7.9407*	105.171*	0.11767*	9.940*
Error	**58**	0.101	0.00007	0.0020	0.00163	0.0083	0.246	0.07492	0.006
Total	**89**								

Where * = Significant at 5% probability level, PSR= photosynthetic rate, SC= Stomata conductance, TR= Transpiration rate, SR= Stomata resistance, P %age= protein percentage, WG= Wet gluten, DG= Dry gluten, FY= Flour yield

Figure 1. Mean values of wheat genotypesfor photosynthetic rate (A)

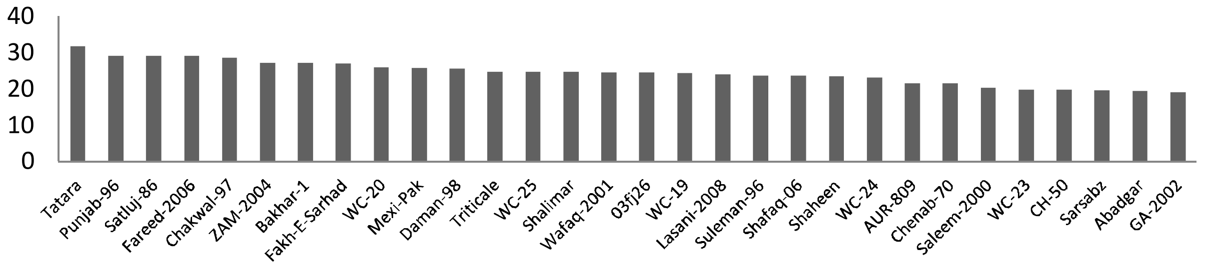


Figure 2. Mean values of wheat genotyes for stomata conductance (gs)

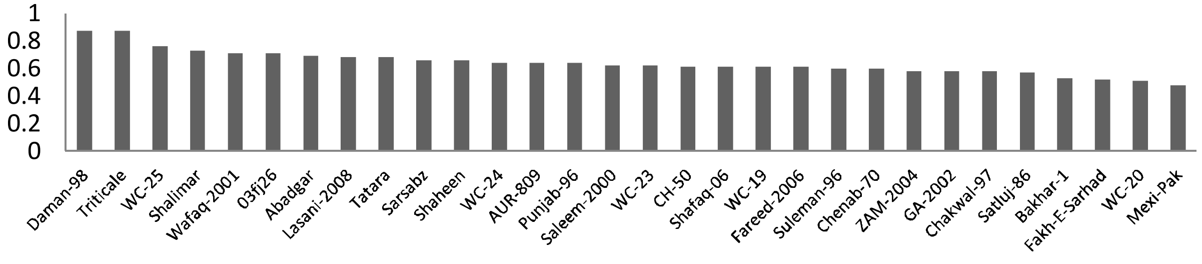


Figure 3. Mean values of wheat genotypes for transpiration rate (E)

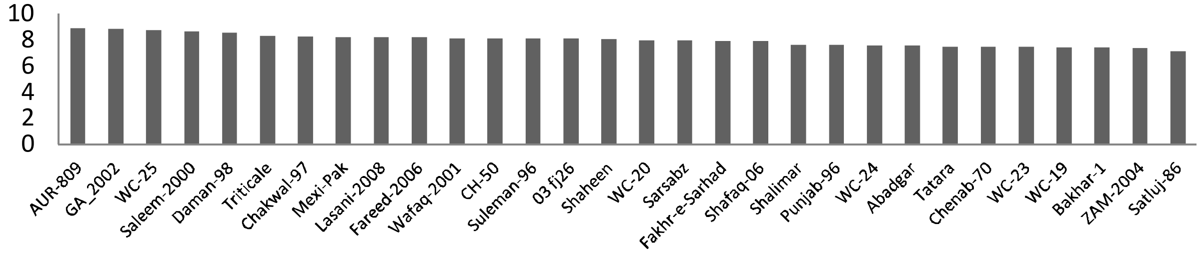


Figure 4. Mean values of wheat genotypes for stomata resistance (rs)

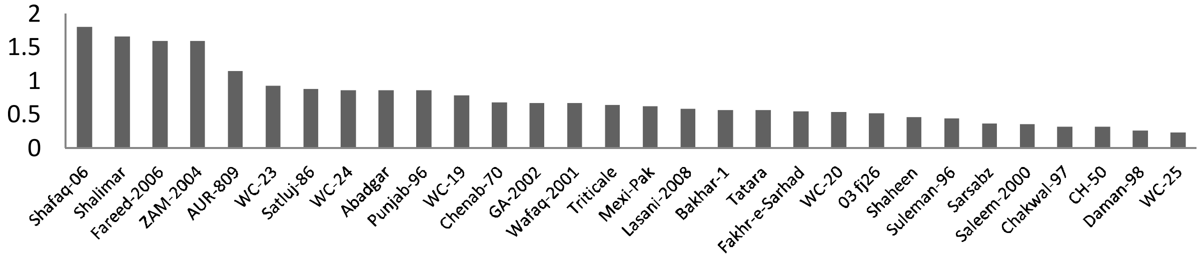


Figure 5. Mean values of wheat genotypes for for protein (%age)

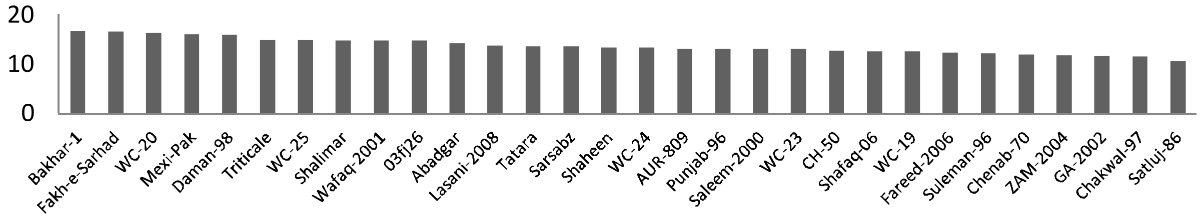


Figure 6. Mean values of wheat genotypes for wet gluten (%age)

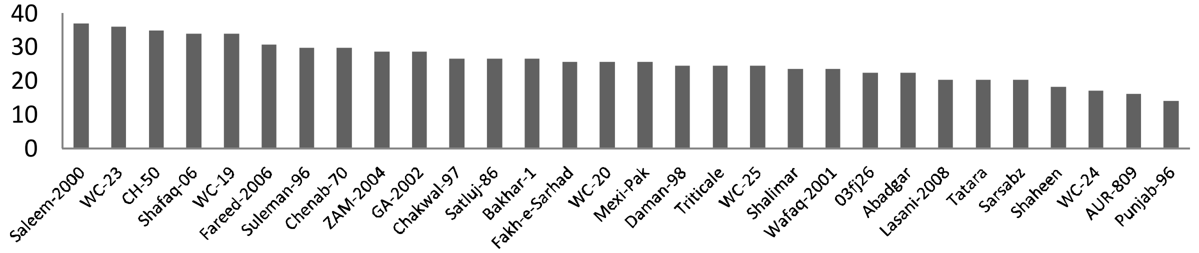


Figure 7. Mean values of wheat genotypes for dry gluten (%age)

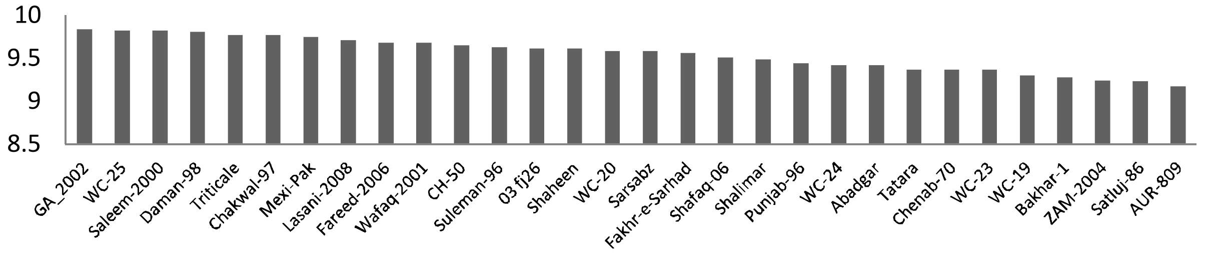
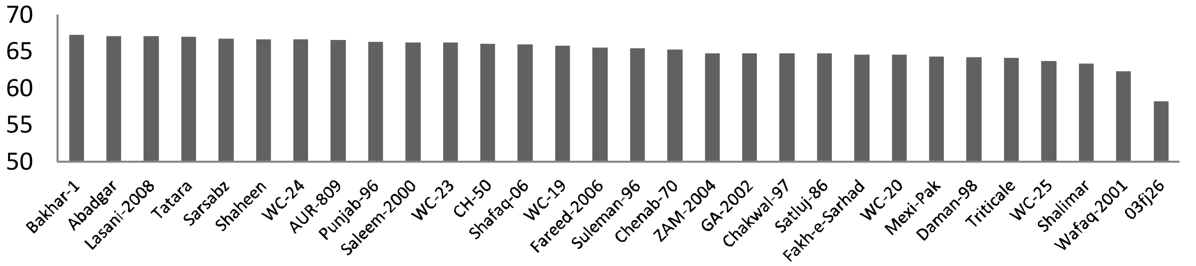


Figure 8. Mean values of wheat genotypes for flour yield (%age)



Photosynthesis rate (µmol $m^{-2}s^{-1}$)

Statistical analysis of data regarding photosynthesis rate (P_N) showed significant variation among genotypes as shown in Table 4.2.1. Results demonstrated that highest photosynthesis rate (P_N) 31.75 (µmol $m^{-2}s^{-1}$) was observed in genotype Tatara followed by Punjab-96 and Satluj-86 where it was recorded 29.11 and 29.07 respectively. However, lowest photosynthesis rate (P_N) 19.09 (µmol $m^{-2}s^{-1}$) was found in genotype GA-2002 followed by Abadgar and Sarsabz where it was 19.48 and 19.63 respectively as shown in figure 1. Drought induced reduction in photosynthesis has been reported in various crops by Malik and Ashraf (2012). Similar results were reported by Hafid *et al*. (1998) in wheat, Kreig and Hutmacher (1993) in sorghum and Ali et al., 2014bc; Ali and Ashraf (2011) in maize.

Stomata Conductance (mol $m^{-2}s^{-1}$)

From the experimental results it was concluded that maximum stomatal conductance (*gs*) 0.873 (mol $m^{-2}s^{-1}$) was observed in genotype Daman-98 and Triticale followed by WC-25 (0.762 mol $m^{-2}s^{-1}$) and Shalimar (0.732). However, minimum stomatal conductance 0.481 was found in genotype Mexi-Pak followed by WC-20 (0.512) and Fakhr-e-Sarhad (0.521) as shown in figure 2. Stomatal conductance of plants is well reduced because of the drought phenomena (Shah and Paulsen, 2003; Flexas *et al*., 2004; Ali and Ashraf, 2011).

Transpiration rate (mmol $m^{-2}s^{-1}$**)**

Rate of transpiration and conductance of stomata also regulate stress (Ashraf, 2009). Significant differences have been found among genotypes regarding transpiration rate (E_N) as shown in table 1.

Analysis of data showed that maximum transpiration rate (E_N) 8.887 (mmol $m^{-2}s^{-1}$) was observed in genotype AUR-809 followed by GA-2002 (8.817 mmol $m^{-2}s^{-1}$) and WC-25 (8.716). However, minimum transpiration rate (E_N) 7.098 was found in genotype Satluj-86 followed by ZAM-2004 (7.389 mmol $m^{-2}s^{-1}$) and Bakhar-1 (7.395 mmol $m^{-2}s^{-1}$) as shown in figure 3.

Stomata resistance (mol $m^{-2}s^{-1}$**)**

Results demonstrated that highest stomatal resistance (*r*s) 1.801 (mol $m^{-2}s^{-1}$) was observed in genotype Shafaq-06 followed by Shalimar and Freed-2006 where it was recorded 1.657 and 1.589 respectively. However, lowest stomata resistance (*r*s) 0.237 (mol $m^{-2}s^{-1}$) was found in genotype WC-25 followed by Daman-98 and CH-50 where it was 0.257 and 0.315 respectively as given in figure 4.

Biochemical characterization

In present study thirty genotypes of wheat were subjected to biochemical analysis for protein contents, wet gluten, flour quality and dry gluten determined by the methods given by AACC (2000) and AOAC (2005). Results demonstrated significant differences among genotypes for biochemical analysis at $p \leq 0.05$. Brief description of the biochemical results are given below.

Protein contents (%age)

Variation in protein contents among genotypes of wheat is due to genetic makeup as well as differences in environmental and production conditions prevailed during growth stages (Ali *et al*., 2014abc). The data presented in figure 5 clearly showed that protein contents of genotype Bakhar-1 was ranked at top where it was 16.7% followed by Fakhr-e-Sarhad and WC-20 with 16.6% and 16.3% respectively. However, lowest protein contents were recorded in genotype Satluj-86 where it was 10.6% followed by Chakwal-97 and GA-2002 with 11.5% and 11.6% respectively.

Wet gluten (%age)

The composition of gluten in durum wheat determines the quality for end products. Cultivars with high gluten contents make pasta with greater firmness after cooking and tolerance is also increased for over cooking (Pogna *et al*., 1990). The wet gluten %age in present study showed that genotype Saleem-2000 have highest (37.1%) wet gluten followed by WC-23 (36.1%) and CH-50 (35.0%). However, lowest wet gluten 14% was found in Punjab-96 followed by AUR-809 and SWC-24where it was 16.1% and 17.2% respectively as presented in figure 6.

Dry gluten (%age)

Data presented in figure 7 showed significance differences among selected genotypes for dry gluten. Results demonstrated that maximum dry gluten 9.84% was found in GA-2002followed by WC-25 (9.82%) and Saleem-2000 (9.82%) whereas minimum 9.17% was observed in AUR-809.

Flour yield (%age)

Flour quality is very important for bread quality (Robert *et al*., 2001). Data revealed that higher flour yield 67.2% was obtain in genotype Bakhar-1 followed by Abadgar and Lasani-2008 where it was 67.1%. However, lowest flour yield 58.2% observed with genotype 03fj26 followed by Wafaq-2001 and Shalimar where it was 62.3% and 63.3% respectively as shown in figure 8.

Conclusion

From the results of experiment it was concluded that genotype “Bhakar-1” provided highest mean value for flour yield and protein content. Hence this genotype can be used to improve these traits. However the mean value for genotype Satluj-86 was lower for most of the studied traits such as transpiration rate, protein content and dry gluten contents, so this genotype may be avoided for cultivation in rainfed conditions and not to include in breeding programs.

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