**Estimation of variation in phenology and adaptability of local and exotic wheat germplasm for yield and related traits**

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**Abstract**

Characterization of the advanced lines along with elite cultivars in the target environment is one of the strategies to identify the candidate lines for future breeding. We evaluated a set of 100 diverse wheat lines comprised 67 elite local cultivars and 37 exotic germplasm for two years and adopted a series of analytical approaches to identify the potential candidate lines and phenological traits for high temperature irrigated spring wheat growing region. The analysis of variance (ANOVA) revealed significant difference in all twelve phonological traits. Number of fertile tillers showed highly significant coefficient of correlation(r=0.78) with grain yield. Similarly, other yield components were positively correlated with grain yield, however the contribution of number of spikes was greater than thousand grains weight which indicated that increasing the number of grains remained a decisive factor in increasing yield potential in target environment. The principal component analysis (PCA) was used to identify the genotype-trait relationship and most of the exotic germplasm clustered separately from the local germplasm and check cultivars. However, some of the exotic lines like HTWYT-P28 and HTWYT-P8 were clustered among the local cultivars. This approach identified the exotic germplasm showing high performance for the key phenological traits in the target environment. Finally, we identified top ten exotic lines showing high performance in the target environment and could be future candidates for deployment.

**Introduction**

Wheat (*Triticum aestivum* L.) is one of the most important cereals crop plant worldwide (De Santis et al., 2018). It ranked the third largest producing crop followed by rice and maize globally (Khan et al.,2017). Wheat was originated in the Mediterranean region and principally utilized for grain food (Abis, 2012). Pakistan is situated in arid and semi-arid region where 70% of rabbi and 37% of whole crop area is under wheat cultivation (Mahmood et al., 2020).Pakistan is one of the top 10 wheat producing countries in the world, accounting for 2% of the total wheat production (FAO, 2019). Wheat yield in Pakistan face serious challenges including biotic and abiotic stresses (Rasheed et al., 2020). There is urgent need to alleviate grain yield to fulfill the food requirement of rapidly burgeoning population.

Improving yield-related traits is one of the main aims of wheat breeding programs since inception. Improvement in such intricate quantitative traits is not easy because it is controlled by many genes as a polygenic trait and affected by environmental conditions. Wheat grain yield improvement is mainly determined through a combination of many component traits including number of grains per unit area and grain weight. Historically, wheat grain yield was successfully increased by introducing *Rht* genes that in turn increased assimilate partitioning efficiency, and then improving grain yield traits. There is clear data that many of the agronomic traits are inherited and controlled by several quantitative trait loci (QTL), such as, total number of spikelets per spike, grain number per fertile spikelet and thousand kernel weight. Accordingly, promising approaches to exploit the genetic dissimilarity and gene identification of these traits is the aim for improving yield (Cao et al., 2020)

In respect to grain production assortment and improvement can only be proficient if enough genetic variability exists in the breeding materials. Vavilov (1951) emphasized that correlation study is an important phase of breeding which was started in the last decades of 19th century and the beginning of 20th century in order to simplify breeders work and for easy handling of material. These types of investigations have to be performed in different types of crop plants. Vavilov implored pleiotropic gene effects being most important sources of genetic correlation as a number of characters are conditioned by the effect of single gene.

To improve wheat grain yield the evaluation of correlation and regression analysis amongst yield and yield components may offer helpful selection criteria (Bhutto et. al., 2016). Selection for grain yield can only be effective if desired genetic variability is present in the genetic stock.

Phenotypic and genotypic correlations are imperative in determining the degree to which many yield contributing characters are linked. Quite a lot of researchers have reported their results concerning the correlation studies. Gupta et al. (1999) reported positive correlation of grain yield with a number of grains per spike, plant height and 1000 grain weight. They found that in wheat yield components like tillers per plant, grains per spike and 1000 grain weight are major contributors to grain yield. Keeping in view the current situation, this research has been designed to meet up the objectives to estimate the correlation among yield components and seed yield in wheat.

The present study was designed to evaluate and compare the performance of a set of exotic and locally developed wheat varieties in a high temperature environment. The germplasm showing higher yield attributes will likely to have the heat tolerance traits.

**Materials and Methods**

**Plant Material and Field Trials**

A set of 100 wheat lines comprised of local wheat cultivars (n=5), locally adapted advanced lines (n=58) and exotic wheat germplasm from CIMMYT (n=37) were used in this study (Table 1). The material was planted for two consecutive years (2018-2019 and 2019-2020) at the experimental station of Cotton Research Institute (CRI), Multan. The planting in the field was done by following randomize complete block design in two replicates.

**Phenotypic data**

The data for twelve different phenological parameters including tillers per plant (TPP), plant height (cm) (PH), number of spikelet per spike (SPS), number of seeds per spike (SP), yield per plant (YPP) were recorded at different growth stage. The data for flag leaf length, width and area were recorded at Z96 stage at the onset of physiological maturity. Plant height (PH) (measured from the surface of soil (base of the plant) to the spike tip excluding awns), tillers per plant (TPP) (from randomly selected plants for each genotype) were recorded. After harvesting, the number of seeds per spike (SPS) (grains on 10 random spikes from each line were counted) and thousand grain weight (TGW) were recorded.

**Statistical analysis**

Descriptive statistic tools were applied on the phenotypic data for obtaining the standard deviation, coefficient of variance and mean on the diversity panel. SAS version 9.4 (SAS Institute, Cary, NC, USA) was used for the analysis of variance (ANOVA), and correlation analysis. Biplot analysis was conducted using GGEbiplot software version 4.1. The ggplot2 function in the R version 10.2 was used to generate the histogram and PCA biplot.

**Results and Discussion**

Basic statistics and the analysis of variance (ANOVA) of the traits estimated in the diversity panel for two years is illustrated in Table I. Mean squares (Table I) due to genotypes from analysis of variance of across two years were significant (P ≤ 0.01), indicating considerable diversity among wheat genotypes (exotic and local) for all studied traits. Coefficient of variation (CV%) ranged from lowest 9.78% for SPS and highest 179.6% for ST. Genotype by year interaction was significant for all the traits under study except FLA.

The analysis of variance discovered highly considerable differences among the genotypes.

Highest YPP was observed for E-68 (20.7 g) and lowest detected in E-161(2.7 g) with an average of 8.6g in 2019. Similarly, in 2020, highest in E-157 (12.54 g) and lowest in HTWYT-P-30 (5.8 g) with an average of 42.04 g. TGW ranged between 14.9 g (E-163) to 44 g (E-154) with an average of 29.8g in 2019, while 77.68g for E-147 and least 32.5g in E-158 in 2020. The phenological values were significant in 2020 compared to 2019 mainly due to the favorable environmental conditions, high rainfall and low ambient temperature.

**Coefficient of correlation**

In the current study, simple correlation coefficients were computed amongst 12 characters.

According to coefficient of correlation the YPP exhibited highly significant and positive correlation with spikes per plant (0.58), SPS (0.34), ST (0.20), PH (0.21) and TGW (0.28). YPP have shown maximum value of correlation with TPP (0.78) and FT (0.78) as shown in Figure 1.

The highest correlation was observed between TPP and FT (r=1.00) and the lowest correlation was observed between SF and FLA (r=0.00036). Noteworthy negative correlation was observed between FT and TGW & FLL (r=-0.17).

Thus, the high yielding wheat genotypes are likely to possess higher YPP, SP, SPS, ST, PH, TPP, FT and TGW. The strong positive relationship of grain yield with the traits stated above have also been described previously in wheat (Kumar et al., 2014; Phougat et al., 2017 and Nukasani et al., 2019). Yield per plant had shown negative association with spikelet fertility (r=-0.057), flag leaf length (r=-0.076), flag leaf width (r=-0.075) and flag leaf area (r=-0.071). Tillers per plant have shown maximum and positive correlation with fertile tillers (r=1.0) and significant correlation with sterile tillers (r=0.38)

**Table I. Basic statistics and the analysis of variance (ANOVA) of the traits estimated in the diversity panel for two years**

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  |  |  |  |  |  | Mean square |  |
| Traits | Year | Average | Min | Max | St. Dev | CV | Reps | Genotypes | Year | G x Y |
| FT | 2019 | 6.44 | 2.67 | 13.00 | 2.10 | 32.60 | NS | \*\*\* | \* | \*\* |
| 2020 | 14.17 | 1.67 | 32.33 | 6.71 | 47.34 |  |  |  |  |
| ST | 2019 | 0.32 | 0.00 | 1.56 | 0.34 | 107.81 | NS | \*\*\* | \*\*\* | \*\*\* |
| 2020 | 0.39 | 0.00 | 4.00 | 0.71 | 179.62 |  |  |  |  |
| TPP | 2019 | 6.72 | 3.22 | 13.11 | 2.12 | 31.49 | NS | \*\*\* | \*\*\* | \*\*\* |
| 2020 | 14.56 | 2.33 | 33.67 | 6.95 | 47.73 |  |  |  |  |
| SPS | 2019 | 49.71 | 29.11 | 83.84 | 10.10 | 20.32 | NS | \*\*\* | \*\*\* | \*\*\* |
| 2020 | 18.02 | 14.33 | 22.33 | 1.76 | 9.78 |  |  |  |  |
| SP | 2019 | 38.63 | 15.00 | 58.77 | 7.74 | 20.04 | NS | \*\*\* | \*\*\* | \*\*\* |
| 2020 | 53.01 | 30.67 | 84.00 | 11.89 | 22.43 |  |  |  |  |
| SF | 2019 | 78.29 | 51.85 | 117.22 | 11.13 | 14.21 | NS | \*\*\* | \*\*\* | \*\*\* |
| 2020 | 78.42 | 51.85 | 117.22 | 11.23 | 14.32 |  |  |  |  |
| YPP | 2019 | 8.68 | 2.77 | 20.71 | 4.16 | 47.86 | NS | \*\*\* | \*\*\* | \*\*\* |
| 2020 | 42.04 | 5.82 | 121.54 | 24.00 | 57.08 |  |  |  |  |
| PH | 2019 | 75.03 | 59.15 | 96.89 | 7.63 | 10.17 | NS | \*\*\* | \*\*\* | \*\*\* |
| 2020 | 86.70 | 71.00 | 105.00 | 7.02 | 8.09 |  |  |  |  |
| TGW | 2019 | 29.81 | 14.90 | 44.00 | 5.34 | 17.90 | NS | \*\*\* | \*\*\* | \*\*\* |
| 2020 | 55.22 | 32.55 | 77.68 | 9.62 | 17.43 |  |  |  |  |
| FLL | 2019 | 21.59 | 13.43 | 32.82 | 3.68 | 17.06 | \* | \*\*\* | \*\*\* | \*\*\* |
| 2020 | 21.18 | 13.54 | 28.74 | 3.34 | 15.77 |  |  |  |  |
| FLW | 2019 | 1.45 | 0.74 | 6.35 | 0.89 | 61.23 | NS | \*\*\* | \*\*\* | \*\*\* |
| 2020 | 1.30 | 0.73 | 3.09 | 0.36 | 27.92 |  |  |  |  |
| FLA | 2019 | 27.89 | 9.64 | 77.29 | 11.26 | 40.37 | \* | \*\*\* | NS | NS |
| 2020 | 28.19 | 10.33 | 76.31 | 11.03 | 39.12 |  |  |  |  |

Similarly TGW recorded highly considerable and positive correlation with SP (r=0.45) and SPS (r=0.31). But it has shown negative correlation with SF (r=-0.032), tillers per plant (r=-0.18), ST (r=-0.15), FT (r=-0.17) and FLL (r=-0.086). SP has shown considerable positive and linear correlation with SPS (r=0.59). The work of Mecha et al. (2017) also supports these results. Flag leaf length, width and area have shown a positive and noteworthy association with one another but negative with yield per plant.

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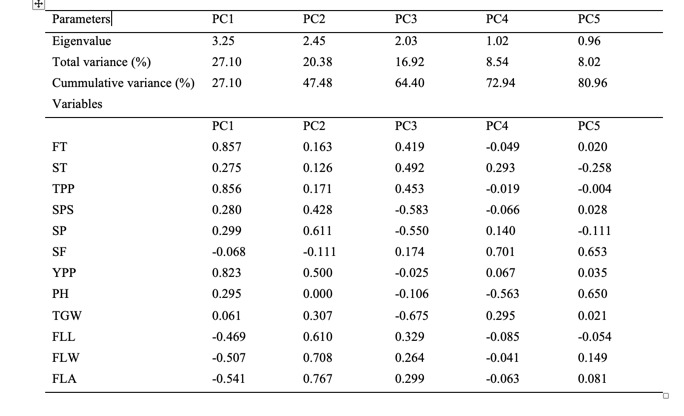
**Figure I: The coefficient of correlation, histograms and relationship plots between phenological traits in diversity panel. The upper diagonal shows coefficient of correlation between two traits, the midline shows the histogram for each traits and the lower diagonal shows biplot between two traits fitted with the regression curve (red line).**

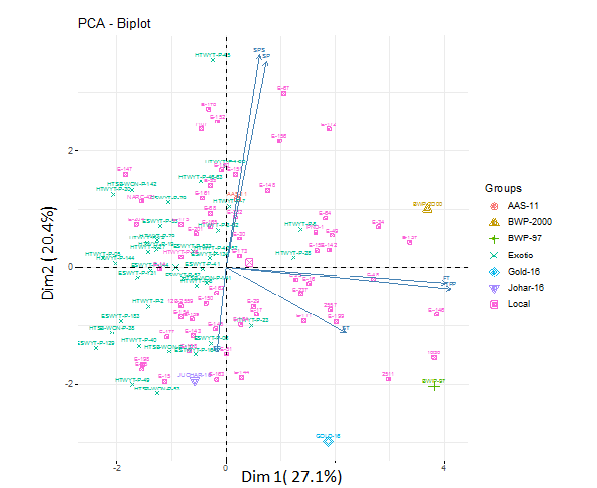
**Principal component analysis**

To display the genetic variability among wheat genotypes, a principal component analysis of standardized data was applied to display wheat trait relationships, and its application in genotype characterization and comparison (Table II). Because different traits use different units, the data standardization was necessary to remove the units. Among principal components, PC1 and PC2 were scaled so that values are symmetrically distributed between the genotype scores and trait scores. A genotype by trait biplot is generated by plotting the PC1 scores adjacent to the PC2 scores for every genotype (100) and each trait (12). The genotype-trait biplot effectively revealed the interrelationships between wheat traits (Figure II). It also provided a tool for visual association between genotypes based on multiple traits. The results of the genotype-trait biplot revealed that first five PCs explained 80.96% of the total variation

The PC1-4 had an eigenvalue greater than 1 explaining 72.9% of the total variation (Table II). The first principle component (PC-1) accounted for 27.10% of the total variability with an eigenvalue 3.25 followed by PC-2 explaining 20.4% of the total variation with eigenvalue 2.45, PC-3 (16.92%) with eigenvalue 2.03, PC-4 (8.54%) had an eigenvalue 1.02 and PC-5 (8.02%) had an eigenvalue 0.96. It is evident graphically that first principal component extracted maximum amount of variation among yield characteristics in the data (Figure II). The highest loading was observed in case of FT, TPP followed by YPP with respect to PCA I, which suggests that these three characters are mainly responsible for highest amount of variation in the wheat data, with FT contributing maximum to the first principal component whereas SF contributed minimum to the first principal component (Table II).

**Table II: Principle component analysis of yield traits and other morphological traits of 100 wheat genotypes**





**Figure II: Principal component analysis (PCA) biplot showing the genotypes and traits scattered over the first two principal components. The local and exotic germplasm are differentiated with different shapes along with local cultivars used as checks.**



**Figure III: Comparison of the exotic and local wheat germplasm for 12 phenological traits evaluated for two consecutive years**

**Conclusion:**

In the set of 100 genotypes, 63 lines were local wheat cultivars and 37 exotic wheat germplasm from CIMMYT. A phenotypic distinction was observed among these lines where local germplasm have shown significant variation for fertile tillers, yield per plant, tillers per plant and thousand grains weight whereas spikes per plant, plant height, spikelet fertility and sterile tillers have shown almost same mean values for both locally adapted and exotic germplasm. In case of flag leaf length, flag leaf width and flag leaf area exotic lines have shown more variation as compared to local germplasm.

The identification of genotypic variability for agronomical and physiological traits is of huge interest for breeders because selected genotypes with favorable traits can be used as parents in cross breeding. The exotic germplasm showed promising features for FT, TGW and flag leaf traits, and some high-yielding varieties were also identified. The PCA clearly separated exotic lines from the local germplasm indicating the unique phenological architecture in exotic germplasm could be used not only to get better yield related traits but also to expand diversity of breeding gene pool.

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