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RESEARCH PAPER

# Pursuit of stripe rust resistance and association of yield contributing traits in elite bread wheat yield trial

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## Abstract

Among the foliar diseases stripe rust caused by *Puccinia striiformis* f. sp. *tritici*, is a severe threat to wheat crop. In the history its epidemics have caused severe wheat yield losses in Pakistan. This study was thus anticipated to evaluate genetic diversity for stripe rust resistance and association of yield contributing traits in wheat germplasm to mitigate the yield damages. Data on morphological traits was recorded on five randomly selected plants. Disease severity %age and the host reactions notes were taken three times in the field. Highest variance 61.256 found for coefficient of infection described different levels of host reaction against pathogen. Factor 1 with eigen value 2.015 highlighted the trend of variability in days to physiological maturity, spike length and thousand grain weight. Factor 2 (eigen value 1.478) depicted the extent of change in spikes per plant, grain yield and coefficient of infection for stripe rust and these two factors showed 58% of total variability. Cluster analysis described that cluster one exhibited medium mean value (11.66) of CI for yellow rust and high value (1.45) for grain yield. Results revealed high variability in traits of genotypes under study. Genotypes from cluster I and III can be selected and exploited for durable yellow rust resistance, higher grain yield and for early maturity respectively.

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## Introduction

Wheat (*Triticum aestivum* L.) is an essential part of daily food that provides about 20% of calories and 55% carbohydrates for millions of people around the globe. Approximately 600 million tons wheat is produced annually from about 220 million hectares of land worldwide. Pakistani wheat producers have a bigger challenge to feed 178 million people with high per capita wheat consumption in country around a huge yield output gap. Among the biotic barriers to wheat production wheat rusts diseases are serious threats to grain high yields. Yellow or stripe rust caused by *Puccinia striiformis* f. sp. *tritici*, can cause about 30 to 100% yield losses (Chen, 2005; Ali *et al.,* 2009). The foremost objective of plant breeding programs is to develop new genotypes that are genetically diverse to those currently available for a specific target mega-environment or a target population of environments (TPE). To attain this objective, plant breeders employ a range of selection methods.

International Maize and Wheat Improvement Center (CIMMYT), Mexico wheat breeding programme is currently distributing advanced lines to more than 60 countries. Joshi *et al.* (2007) reported that increasing land area under wheat production is challenging, the main task will be to breakdown the yield gaps by rational genetics and progressive methodologies. Main barriers to wheat yields in South Asia are biotic/abiotic stresses plus rusts that are most threatening pathogens for the region. The total spring bread wheat (*Triticum aestivum* L.) area in developing countries, excluding China, is around 63 million ha, of which 36 million ha or 58% are planted to cultivars derived from CIMMYT germplasm. The impact of CIMMYT's Wheat Breeding Program has been significant (Rajaram, 1999).

Several inter-related parameters results in grain yield and plant breeders continuously looking for genomic diversity amongst the characteristics to pick the desired types. Various traits of these are greatly linked to each other and with yield. Like other cultivated crops plants, the foremost cultivation objective of wheat is for high quality and high grain yield.

As genetic and environmental dynamics are the key gears for defining quality and yield in crop plants, a main goal must be to resolve effects of genetic aspects for selection. Since the influence of environment on quality and yield in crop plants is not exclusively genetic, it is essential that those facets be examined. The present study was thus intended to analyse genetic diversity and association of yield contributing traits under yellow rust pressure in 7th Elite Bread Wheat Yield Trial (EBWYT) donated by CIMMYT. It is important to ascertain the set of morphological traits and genetic resistance to wheat rusts to exploit in our national ongoing breeding program that has yield maximization as the major objective.

## Material and methods

*Plant material and experimental design*

A study was designed to analyze the genetic diversity, trait association and response against yellow rust in twenty four genotypes of Elite Bread Wheat Yield Trial (7th EBWYT) contributed by CIMMYT (Table-1) with NARC-2009 as commercial check. The experiment was conducted in a randomized complete block design with three replications in our Programme at NARC, Islamabad, during the winter 2013-2014. Each plot consisted of four rows of 4.0 m length with 30 cm row-row distance and the trial was subjected to standard recommended cultural practices. The entire trial was bordered by a rust susceptible spreader (Morocco) and in addition, a row of susceptible check was also planted after every 20th row.

*Data recording on disease and morphological traits*

Percent severity of rust infection was taken according to Modified Cobb's Scale (Peterson *et al.,* 1948) and the reaction referred to the infection type on each genotype was estimated following (Roelf *et al.,* 1992; Mcintosh *et al.,* 1995). Rust notes for severity and infection type were taken together with severity first. Stripe rust was scored at the heading stage when the susceptible spreader exhibited maximum disease severity. Coefficient of infection (CI) was calculated by multiplying disease severity (DS) with constant values of infection type (IT). Constant values for infection types were used based on; R=0.1, MR=0.25, M=0.5, MS=0.75, S=1 (Pathan and Park, 2006).

Data was recorded on plant height (cm), number of spikes/plant, spike length (cm), number of days to maturity, 1000 grain weight (g) and grain yield (kg/m²).

*Statistical analysis*

Data on yield components was then statistically analyzed i.e., mean, standard deviation, standard error and Pearson's correlation were estimated. Traits were analyzed by cluster and principal component analysis by using XLSTAT 3.06 software program. Principal component analysis was carried out to streamline the data by transforming number of correlated variables into a smaller number of variables.

Cluster analysis classifies variables which are further grouped into core groups and subgroups. Basic statistics were also computed for accessions in each cluster.

**Results and discussion**

*Descriptive statistics*

Variation in quantitative traits can be seen through descriptive statistics in Table 2. Thousand grain weight with mean value 42.178, ranged from 37 to 47.12 having (6.291) value for variance. Narrow range with high variance indicated greater variability among the genotypes. Mean value for coefficient of infection for stripe rust remained 6.063 with high variability within the genotypes and is pretty low.

**Table 1.** Genotypes in 7th elite bread wheat yield trial.

| Sr. No. | Entry | Pedigree 7th EBWYT |
|---------|-------|--------------------|
| 1 | 503 | FRET2/TUKURU//FRET2/3/MUNAL #1 |
| 2 | 504 | KACHU//WBLL1*2/BRAMBLING |
| 3 | 505 | KACHU/KIRITATI |
| 4 | 507 | THELIN#2/TUKURU//KIRITATI |
| 5 | 510 | WBLL4/KUKUNA//WBLL1/3/WBLL1*2/BRAMBLING |
| 6 | 511 | FRET2*2/BRAMBLING/3/FRET2/WBLL1//TACUPETO F2001/4/WBLL1*2/BRAMBLING |
| 7 | 512 | ALTAR 84/AE.SQUARROSA (221)//3*BORL95/3/URES/JUN//KAUZ/4/WBLL1/5/ KACHU/6/KIRITATI//PBW65/2*SERI.1B |
| 8 | 513 | FRNCLN*2/TECUE #1 |
| 9 | 514 | MILAN/S87230//BAV92*2/3/AKURI |
| 10 | 515 | KACHU/KINDE |
| 11 | 516 | MUU/FRNCLN |
| 12 | 517 | MUU/KBIRD |
| 13 | 518 | BECARD #1/4/KIRITATI/3/2*SERI.1B*2//KAUZ*3/BOW |
| 14 | 519 | BECARD/FRNCLN |
| 15 | 520 | WBLL1/KUKUNA//TACUPETO F2001/4/WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1 |
| 16 | 521 | WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1/4/QUAIU |
| 17 | 522 | WBLL1*2/BRAMBLING//CHYAK |
| 18 | 523 | BECARD//ND643/2*WBLL1 |
| 19 | 524 | ATTILA/3*BCN*2//BAV92/3/KIRITATI/WBLL1/4/DANPHE |
| 20 | 525 | ATTILA/3*BCN//BAV92/3/PASTOR/4/TACUPETO F2001*2/BRAMBLING/5/PAURAQ |
| 21 | 526 | ATTILA/3*BCN//BAV92/3/PASTOR/4/TACUPETO F2001*2/BRAMBLING/5/PAURAQ |
| 22 | 527 | KACHU/BECARD//WBLL1*2/BRAMBLING |
| 23 | 528 | PFAU/SERI.1B//AMAD/3/WAXWING*2/4/TECUE #1 |
| 24 | 530 | ND643//2*ATTILA*2/PASTOR/3/WBLL1*2/KURUKU/4/WBLL1*2/BRAMBLING |
| 25 | 501 | NARC-2009 (commercial check) |

This highlighted that most of the genotypes were stripe rust resistant or possessed a high level of partial resistance. Ali *et al.* (2009) also reported different levels of stripe rust resistance in the evaluated wheat germplasm. Days to physiological maturity also showed high level of variance (17.641) indicating the presence of early maturing genotypes that ranged was 156.333 to 169 with a mean of 164.586 days.

Selection can be made for heat tolerant and early maturing lines from this genotypes set. Masood *et al.* (2005) and Ajmal *et al.* (2013) also suggested the selection of early maturing genotypes to use in breeding programs to develop early maturing cultivars. Spikes per plant, spike length and grain yield with low values for variance (0.533, 0.889 and 0.032) described the constant expression of the germplasm.

These findings proposed that high yielding genotypes can be selected based on these characteristics as advocated by (Ramzan *et al.,* 1994). Such a substantial range of variation has brought a solid footing for high yielding cultivar development.

Zarkti *et al.,* (2012) stated that agronomic characteristics have been effectively employed for assessment of genetic variability and crop improvement because they offer an easy approach of assessing diversity.

**Table 2.** Descriptive statistics for six quantitative traits of 24 wheat genotypes.

| Traits | Mean | Standard Error | Median | Mode | Standard Deviation | Sample Variance | Range | Minimum | Maximum |
|---|---|---|---|---|---|---|---|---|---|
| Yr (CI) | 6.063 | 1.565 | 1.250 | 0 | 7.827 | 61.256 | 23.333 | 0 | 23.333 |
| DM | 164.586 | 0.840 | 165.333 | 168 | 4.200 | 17.641 | 12.667 | 156.333 | 169.000 |
| SPP | 9.093 | 0.146 | 9.000 | 9 | 0.730 | 0.533 | 3.000 | 8.000 | 11.000 |
| SPL (cm) | 10.186 | 0.190 | 10.000 | 10 | 0.948 | 0.899 | 3.333 | 8.333 | 11.667 |
| TGW (g) | 42.178 | 0.502 | 42.333 | 44 | 2.508 | 6.291 | 10.120 | 37.000 | 47.120 |
| GY/plot | 1.392 | 0.036 | 1.367 | 1.233 | 0.178 | 0.032 | 0.633 | 1.100 | 1.733 |

**Table 3.** Principal component and factor analysis.

| | F1 | F2 | F3 | F4 | F5 | F6 |
|---|---|---|---|---|---|---|
| Eigen value | 2.015 | 1.478 | 1.055 | 0.854 | 0.366 | 0.233 |
| Variability (%) | 33.577 | 24.630 | 17.576 | 14.234 | 6.104 | 3.879 |
| Cumulative % | 33.577 | 58.207 | 75.783 | 90.017 | 96.121 | 100.000 |

*Correlation analysis*

Days to maturity have shown significantly positive correlation with spike length and negative correlation with coefficient of infection (CI) for stripe rust (Table 4). Numbers of spikes per plant and spike length were positively correlated with grain yield. Mollasadeghi *et al.* (2011) and Degewione *et al.* (2013) also stated that

grains per spike and number of spikes per plant showed positive and direct association with grain yield. Number of spikes per plant, spike length, 1000 grain weight and grain yield showed positive but non-significant correlation with coefficient of rust infection, this might be due to rust resistance or high level of partial resistance against yellow rust.

**Table 4.** Correlation coefficient (Pearson's Correlation) matrix shown for estimated traits.

| Variables | Yr (CI) | DM | SPP | SPL (cm) | TGW (g) |
|---|---|---|---|---|---|
| DM | -0.366 | | | | |
| SPP | 0.084 | 0.024 | | | |
| SPL (cm) | 0.056 | 0.432 | 0.168 | | |
| TGW (g) | 0.281 | -0.569 | 0.160 | -0.042 | |
| GY | 0.262 | 0.318 | 0.273 | 0.072 | -0.313 |

Values in bold are different from 0 with a significance level alpha=0.05.

*Principal component and factor analysis*

In the present study principal component and factor analysis (Fig. 1) revealed that factor F1 with eigen value 2.015 (Table 3) highlighted the trend of variability in days to physiological maturity, spike length and thousand grain weight. Factor 2 (eigen value 1.478) depicted the extent of change in spikes

per plant, grain yield and coefficient of yellow rust infection and these two factors showed 58% of total variability. Soleymanfard *et al.* (2012) revealed that plant height, 1000-grain weight and spikes/m² played significant role in diversity for grain yield and also stated that 75% variation contribution by these factors.

**Table 5.** Three cluster grouping of genotypes based on six quantitative traits.

| Cluster | Frequency | Entries ID | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 4 | 503 | 520 | 526 | 527 | | | | | |
| 2 | 17 | 504 | 505 | 507 | 511 | 512 | 513 | 514 | 515 | 516 |
| | | 517 | 518 | 519 | 521 | 524 | 529 | 530 | 501 | |
| 3 | 4 | 510 | 522 | 523 | 525 | | | | | |

**Table 6.** Arithmetic means with standard deviation of each cluster for studied trait.

| Cluster | Yr (CI) | DM | SPP | SPL (cm) | TGW (g) | GY (Kg/m²) |
|---|---|---|---|---|---|---|
| 1 | 11.66 | 164.25 | 9.5 | 10.58 | 43.83 | 1.45 |
| | ±1.36 | ±2.98 | ±0.79 | ±1.1 | ±1.75 | ±0.12 |
| 2 | 1.27 | 165.95 | 9.02 | 10.08 | 41.16 | 1.37 |
| | ±2.11 | ±3.56 | ±0.81 | ±0.91 | ±2.32 | ±0.16 |
| 3 | 20.83 | 161.33 | 9 | 10 | 43.33 | 1.45 |
| | ±1.66 | ±5.01 | ±0.27 | ±1.12 | ±1.05 | ±0.23 |

*Cluster analysis*

The main aim of cluster analysis was to describe the extent of similarity in yielding capacity under yellow rust pressure and optimal agro-climatic conditions in 7th EBWYT genotypes. Evaluation, characterization, conservation and exploitation of germplasm effectively need precise assessment of extent of variability available in germplasm.
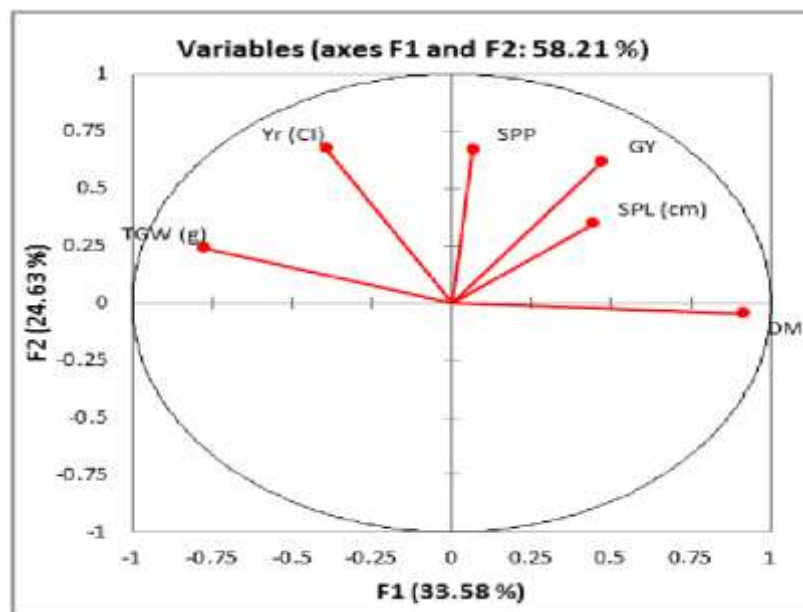


**Fig. 1.** Principal component and factor analysis.

The cluster analysis divided 25 genotypes into three clusters (Fig. 2) which showed high similarity within a cluster and high heterogeneity between clusters. Cluster one composed of 4 genotypes 503, 520, 526 and 527 (Table 5) with medium mean value (11.66) for yellow rust CI and high number of spikes per plant and spike length. Mean value 1.45 for grain yield was also higher for these genotypes of cluster one (Table 6).

17 genotypes of cluster 2 showed lowest mean values 1.27 and 1.37 for yellow rust CI and grain yield respectively. This cluster of genotypes showed the highest mean value (165.95) for days to physiological maturity. Cluster 3 is comprised of 4 genotypes (510,522,523 and 525) having the highest mean value (20.83) for CI of yellow rust and higher mean value (1.45) for grain yield (Table 6).

This genotype group showed lowest mean values (161.33) for days to physiological maturity and can be selected and utilized for development of early maturing wheat varieties. These genotypes have been selected in CIMMYT on their slow rusting behavior and high level of adult plant resistance so in present study they showed lower variance of

CI for yellow rust. Genotypes from cluster 2 can be selected and utilized for development of yellow rust resistant cultivars. Jaynes *et al.* (2003) also found that cluster analysis assists to categorize germplasm into clusters which illustrate high similarity and heterogeneity within and between groups respectively.
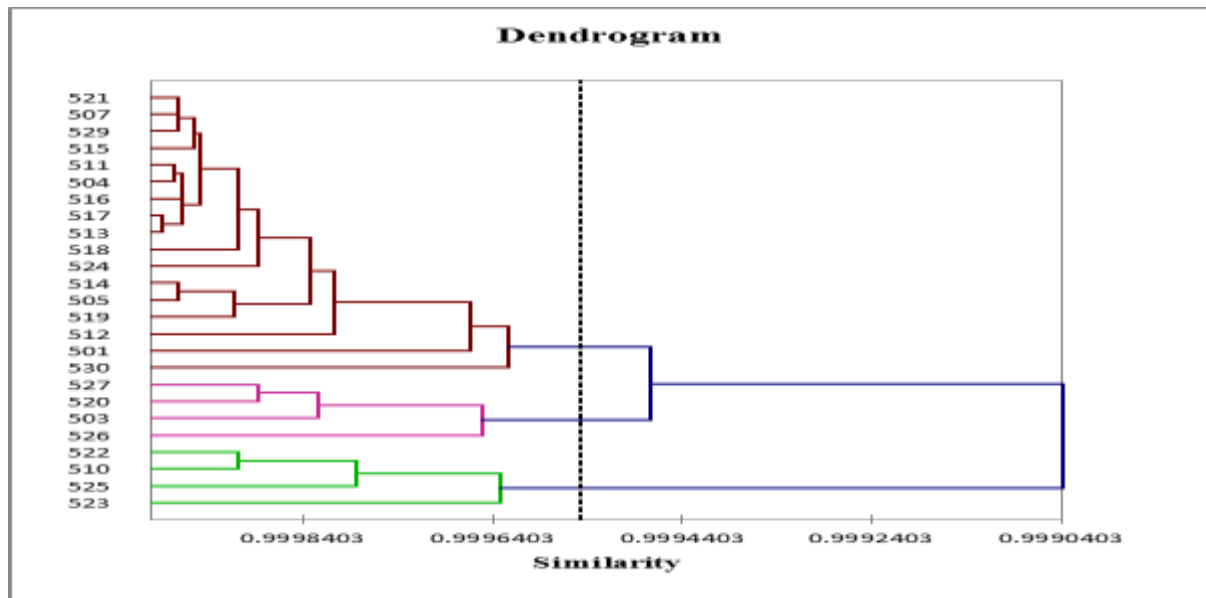


**Fig. 2.** Dendrogram showing cluster in sub-group of 24 wheat genotypes.

In the present study cluster analysis indicated tremendous variation among genotypes of three different clusters produced. It possibly seems that future selections from the evaluated germplasm can be made by keeping these three clusters in view. As there is high diversity between the clusters and not within the clusters so, recommendations for further breeding strategies could be made for wheat improvement from these three different clusters. Genotypes from cluster I, II and III can be further selected and exploited for higher grain yield, yellow rust resistance and for early maturity respectively.

**Conclusion**

Genotypes 517, 525, 526 and 530 are promising genotypes in this set of germplasm and these have been selected by and are being exploited for further breeding goals. Improvement in yield potential and in genes conferring resistance to major biotic and abiotic stresses resides in these advanced lines and harnessing has been selected from the specific clusters for breeding our program.

This will be important to identify, select and combine diversified genetic material to improve existing cultivars with broad genetic base for disease resistance and high grain yield.

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