# WEED SUPPRESSING ABILITY OF DIFFERENT BREAD WHEAT GENOTYPES IN DRYLANDS OF WESTERN IRAN

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## ABSTRACT

A genetic option for increasing wheat production is to reduce menace of weeds through developing or screening weed tolerant wheat genotypes. To screen bread wheat genotypes tolerant to weeds in dryland conditions, twenty six genotypes and two checks were evaluated in weed-free and weed-infested plots using a strip-plot experiment in 2002-03 at Dryland Agricultural Research Institute Srarood- Kermanshah, Iran. Labeling the genotypes as G1,... ,G28, the top five genotypes for grain yield in presence of weeds were G15, G8, G26, G2 and G13. Genotypes G13, G26, G2 and G4 were found most tolerant to weed-interference. However, using the competition index, the genotypes within top 5 for yield under weed-interference were G13 and G2. The clustering of the genotypes using the tolerance and competition indices resulted into three clusters each giving a different level of tolerance and yield. Considering the tolerance, competition and high yield, genotypes G13, G26 and G8 were found most suitable for introduction in breeding program.

**Key words: Bread wheat, Competition, Drylands, Interference, Weed.**

## INTRODUCTION

Wheat covers about 6.2 million agricultural land in Iran where yield losses of up to 50% are reported owing to infestation of weeds. Importance of wheat as a main staple food, and losses in yield due to weed infestation is common in the region. An estimated 20% crop loss due to weed infestation just in Iran would be equal to crop grown in about 1.2 million ha (Rastgar, 1992). Use of herbicides to control weeds does improve crop yield but their non-target and environmental toxicities are cause of serious concern. While success achieved in breeding disease and insect resistant crop varieties and development of integrated pest management system has led to reduction in the demand for fungicides and insecticides, the use of herbicides is still increasing worldwide (Olofsdotter *et al.,* 2002). Also development of herbicide resistance in weeds, and environmental considerations increasingly encourage scientists to explore the possibilities to avoid synthetic herbicides mostly being of non-biodegradable nature and long persistence in soil. One of the promising alternatives for eco-friendly weed control is using naturally occurring phenomenon of interference which results due to cumulative effects of competition and allelopathy (Rizvi and Rizvi, 1992). Therefore, screening of wheat genotypes having strong ability to suppress weeds (interference) with acceptable yield levels could prove a better method to deal with weed menace without compromising on health and environmental issues, and can be used in the breeding program to breed weed-resistant wheat varieties.

## MATERIALS AND METHODS

The Experiment: A field experiment was conducted with 26 genotypes of bread wheat and two check cultivars, Sardari and Azar2, in strip- plots (also known as split- blocks) of a randomized complete block design (RCBD) with four replications. Experiments were performed during 2002-03 at Dryland Agricultural Research Institute (DARI), Sararood - Kermanshah, Iran. The experimental site was infected with weeds *Glycyrrhiza glabra, Cephalaria syriaca* and *Anthemis arvensis* which

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were most dominant. The weed control, studied at two levels: weed-free (WF) and weed-interfering (WI), was considered as horizontal factor and genotypes as vertical factor of the strip-plot experiment. Plot size was 10 m x1.2 m with 6 rows and 20 cm distance between rows. Grain yield from the central harvest area of each plot (6 m$^2$ area), number of seeds per spike (5 random samples), number of spikes (per 0.25 m$^2$) and plant height (5 random samples) in each genotype under both condition of with and without weeds were measured. Also number of weeds per square meter was counted. For calculation of weed dry matter, the samples of weeds were dried at 60ºC for 48 hours, and then were weighed.

Indices and the statistical analyses: Weed tolerance ability of a genotype was measured using the following three indices. Denoting the genotypes by G1, G2,..., G28, weed interference tolerance index (WITI) for the genotype G$i$ ($i$ = 1, 2... 28) was derived as stress tolerance index (STI) due to (Fernandez, 1992)

$$WITI_i = \frac{YWF_i \times YWI_i}{\overline{YWF}^2}$$

where $YWI_i$ and $YWF_i$ are grain yields of genotype G$i$ under weed interfering (WI) and weed free (WF) conditions respectively, and $\overline{YWF}$ is mean grain yield over all the genotypes under no interference of weeds. A higher value of WITI shows relatively more tolerant genotype. Another simpler measure of tolerance which does not depend on the other genotypes can be defined as change in the yield from WF to WI conditions relative to its performance under WF as relative loss (RL) in yield:

$$RL_i = \frac{YWF_i - YWI_i}{YWF_i}$$

for the genotype G$i$. Normally with interfering weeds, RL would be positive; however, in case weed presence appears to be beneficial, RL would be negative which may also indicate lack of tolerance, or, may arise due to sampling and experimental errors associated with the plots. Therefore, an absolute value of RL should be considered as a measure of tolerance. Lower the absolute value of RL, more tolerant is the genotype for yield, in its perfect tolerance case RL is zero.

A third index, competition index (CI) due to Baghestani and Zand (2004) was used for the genotype G$i$ as:

$$CI_i = (Y_i / \overline{Y}) / (WDM_i / \overline{WDM})$$

where $Y_i$ = grain yield of genotype G$i$ ($i$ = 1,...,28) under weed interfering condition, $\overline{Y}$ = mean grain yield in interfering condition, $WDM_i$ = weed(s) dry matter for genotype G$i$, and $\overline{WDM}$ = mean weed dry matter. Higher the value of CI implies better competing ability of wheat genotype to weeds.

Statistical analysis of data was carried out to evaluate variation due to genotype, weed interfering condition, and their interaction using analysis of variance (ANOVA) for each of the traits measured. The association between the traits was assessed using simple correlation coefficient. Whether the association between the traits is affected by the weed condition was tested by comparing the two correlations under the two situations by using inverse tanh transformation (Fisher's test). The tolerance and competition indices were modeled in terms of the yield components under both the conditions or WF condition alone using all possible subsets formed for the regression analysis and the subset of traits leading to the highest percent variance accounted for was selected.

Further, the relationship among genotypes was studied for similarity of a) the tolerance indices (WITI and RL), and b) competition index (CI). For the purpose of grouping the genotypes, the hierarchical cluster analysis based on Euclidian distance and un-weighted paired-group method using arithmetic averages (UPGMA) clustering method was used for each of the above three sets of traits. The computations on ANOVA, correlations and regressions and clustering, were carried out using Genstat software (Payne, 2009).

## RESULTS AND DISCUSSION

Genotypic variation: Genotype main effect was significant (P < 0.01) for grain yield, plant height, number of spikes per meter square and number of seeds per spikes. The main effects of the weed interfering treatment and its interaction with genotypes were not significant (P > 0.05) for all the above variables, except that the interaction was

significant (P < 0.05) for number of seeds per spike. The genotypic differences were not significance for weed dry weight and number of weeds.

The means of genotypes for various traits and under the two weed treatments are presented in Tables 1 and 2. Genotypes G1 and G13 had significantly (P < 0.05) higher mean yield compared to the average of the two checks (G2: Azar-2 and G3: Sardari) under no weed interfering (WF) condition. The top five genotypes for grain yield were G13, G1, G6, G26 and G8 under WF condition and G15, G8, G26, G2 and G13 under WI condition.

Although there were no statistically significant differences due to genotypes for weed dry-matter, five lowest weed dry matter values corresponded to the genotypes G9, G13, G27, G7 and G10 respectively. These genotypes, in comparison to the remaining genotypes, were found to suppress weeds growth, and thus have stronger interference (allelopathic and competitive) effect on weeds. Similar trends have been observed in wheat cultivars with ability to inhibit *Avena ludoviciana* in greenhouse condition (Rizvi *et al.*, 2000), rye (Rahimian *et al.*, 2004) and other weeds (Rizvi *et al.*, 2005; Farhodnia *et al.* 2009).This indicates that wheat varieties with weed suppressing capability can be bred to keep the weed population below the threshold level to avoid the necessity of chemical weed control.

Association between traits: Correlations with various traits and indices are presented in Table 3. Grain yields under WF and WI conditions were significantly correlated (r = 0.74; P< .001), which implies that the direct selection of genotypes for grain yield can be carried out in either of the two weed condition. Genotype selection based on significant correlation in the two conditions has also been reported already (Fernandez, 1992).

Grain yield was significantly correlated (P < 0.05) with plant height and spikes/m² under both the conditions, except for seeds/spike. Importance of plant height for selection of better genotypes has also been reported earlier (Rahimian *et al.*, 2004). The grain yield is significantly negatively correlated with weed dry weight (r = -0.451; P< 0.05) but not with number of weeds. The three indices WITI, CI and RL are significantly correlated with grain yield;

therefore, the yield components can also be used for selecting the genotypes for tolerance to weed interfering activity.

Using Fisher's transformation on the correlation coefficient, none of the correlations between grain yield, plant height, spikes/me and seeds/spikes (Table 3) statistically varied with the weed condition (P > 0.05). This implies that the level of weed interfering did not distort the trait relationships, as may be expected.

Weed interference indices: Weed interference tolerance index (WITI) had positive significant correlation with grain yield in both the conditions. Therefore, genotypes for high WITI can be selected using high yield in any of the conditions. WITI index has been reported for drought tolerance and the tolerant genotypes selected based on it (Fernandez, 1992). For the weed interference tolerance and competition, the top five genotypes found were: G13, G26, G2, G8 and G6 using WITI; G2, G12, G14, G3 and G8 using RL; G9, G13, G2, G10 and G27 using CI. Thus, the common genotypes within top five lines for grain yield under WI, and WITI were G8, G26 and G2. Of these G8 and G2 stood selected in also for RL. For competition (CI) and yield under WI, the genotypes selected were G2 and G13. This indicated that the genes for tolerance and competitiveness shared one common genotype, G2. Thus, using 20% marginal selection intensity, the combined set of genotypes G8, G26, G13 and G2 can be selected for yield and weed-interference or competitiveness.

The regression equations to predict the tolerance (WITI) and CI in terms of yield components are given in Table 4. When the variables used were from only WF conditions the predictability power in terms of percent variance accounted for; $\overline{R}^2$ ,was 31.5% while incorporating the information from WI (weed interference) condition enhanced the to 46.9%. The CI did not show significant explanation in terms of yield components under WF condition alone. However, a significant improvement (P < 0.05) was found by incorporating traits observed under WI condition. For instance, the plant height in the WF condition and number of spikes in the WI condition gave $\overline{R}^2$ = 21%. This implies that a satisfactory prediction model requires information from the components under both the conditions.

**TABLE 1: Wheat genotypes means for grain yield (GY), plant height and number of spikes under weed free (WF) and weed interfering (WI) conditions.**

| Genotype | Genotype pedigree | Grain yield (kg/ha) (WF) | Rank (GY, WF) | Grain yield (kg/ha) (WI) | Rank (GY, WI) | Plant height (cm)(WF) | Plant height (cm) (WI) | Spikes/m² (WF) | Spikes/m² (WI) |
|---|---|---|---|---|---|---|---|---|---|
| G1 | CA8646/GRK//85.24 | 2397 | 2 | 1792 | 8 | 83.3 | 77.2 | 522 | 525 |
| G2 | Azar_2 | 1914 | 12 | 1900 | 4 | 90.6 | 86.5 | 540 | 581 |
| G3 | SARDARI | 1901 | 13 | 1808 | 6 | 85.7 | 83.8 | 583 | 585 |
| G4 | Trakia//Maga"s"74/Mon"s"/3/Sha | 1927 | 11 | 1743 | 11 | 86.6 | 83.4 | 515 | 596 |
| G5 | HENG-SXL-7004/BOW//KS794681/SX | 2068 | 6 | 1804 | 7 | 86.4 | 79.9 | 506 | 568 |
| G6 | Turkey 13//F9.1O/Maya s 1RW92 | 2282 | 3 | 1668 | 14 | 83.4 | 84.0 | 565 | 513 |
| G7 | 4848 Mashad/Tui "s" IRW92 1 D 6 | 1685 | 24 | 1433 | 22 | 94.3 | 87.5 | 604 | 613 |
| G8 | UN KNOWN  3 | 2102 | 5 | 1944 | 2 | 92.2 | 86.2 | 635 | 536 |
| G9 | 914 Gene Bank Material | 1979 | 9 | 1785 | 9 | 85.0 | 81.4 | 575 | 542 |
| G10 | Sabalan/6/Shahi/KVz/5/Shahl/4/ | 1998 | 7 | 1679 | 13 | 90.3 | 85.3 | 411 | 552 |
| G11 | 5294karage 98-99 | 1357 | 27 | 927 | 27 | 74.3 | 70.2 | 460 | 381 |
| G12 | Roshan/3/F12.71/Coc//Gn079 | 1696 | 22 | 1777 | 10 | 89.0 | 85.7 | 575 | 620 |
| G13 | 777TWWON87/3/F12.71/SKA//CA805 | 2466 | 1 | 1825 | 5 | 83.5 | 80.8 | 634 | 650 |
| G14 | UN KNOWN 1 | 1799 | 20 | 1713 | 12 | 89.3 | 85.5 | 500 | 451 |
| G15 | 1002 Gene Bank Material | 1618 | 26 | 1990 | 1 | 65.2 | 67.1 | 372 | 494 |
| G16 | 87ZHONG291 | 1817 | 19 | 1449 | 19 | 78.3 | 76.3 | 474 | 525 |
| G17 | WA467/3/391//NUM/5/W22/5/ANA/6 | 681 | 28 | 502 | 28 | 71.0 | 68.5 | 372 | 309 |
| G18 | F9.1O/May1 s //Sabalan 1RW92 1 | 1890 | 15 | 1385 | 23 | 91.3 | 89.8 | 593 | 470 |
| G19 | 98 YRRGP | 1717 | 21 | 1215 | 25 | 79.7 | 79.4 | 485 | 570 |
| G20 | 72YRRGP | 1941 | 10 | 1197 | 26 | 77.8 | 72.4 | 588 | 672 |
| G21 | NEMURA/HD2329//AGRI/NAC | 1865 | 17 | 1439 | 20 | 85.5 | 79.3 | 523 | 569 |
| G22 | UN KNOWN 2 | 1989 | 8 | 1631 | 15 | 87.4 | 86.0 | 606 | 553 |
| G23 | Turkey 13//F9.1O/Maya s  1RW93 | 1895 | 14 | 1548 | 17 | 94.8 | 89.6 | 596 | 649 |
| G24 | OGOSTA/SEFID | 1661 | 25 | 1468 | 18 | 85.7 | 79.9 | 426 | 481 |
| G25 | V*0555/6/PAJO/KAL/3/74/3B/CNO | 1687 | 23 | 1438 | 21 | 84.8 | 81.5 | 465 | 581 |
| G26 | 14 Gene Bank Material | 2239 | 4 | 1934 | 3 | 82.2 | 87.3 | 638 | 709 |
| G27 | TX71A1039-V1*AMIRLCTK/VEE | 1870 | 16 | 1618 | 16 | 96.7 | 87.5 | 512 | 473 |
| G28 | 4851 Mashad/Sabalan IRW92 -1- D | 1821 | 18 | 1301 | 24 | 84.3 | 79.6 | 506 | 604 |
| | S.E. | 195 | | 195 | | 7.7 | 7.7 | 62 | 62 |
| | Mean | 1867 | | 1568 | | 84.9 | 81.5 | 528 | 549 |
| | LSD (5%) | 477 | | 477 | | 18.7 | 18.7 | 151 | 151 |

S. E.: standard error of mean. LSD: Least significant difference to compare mean of the checks vs. mean of a genotype (other than the checks).

**TABLE 2:** Wheat genotypes means for seeds per spike under weed free (WF) and weed interfering (WI) conditions, number of weeds and weed dry weight under weed interfering condition, and the weed tolerance and competition indices.

| Genotype | Genotype pedigree | Seeds/spike (WF) | Seeds/spike (WI) | No of weeds | Weed dry matter | WITI[@] | CI[$] | RL[#] |
|---|---|---|---|---|---|---|---|---|
| G1 | CA8646/GRK//85.24 | 27.9 | 32.0 | 20.0 | 56.7 | 1.23 | 1.25 | 0.25 |
| G2 | Azar_2 | 23.0 | 25.1 | 22.5 | 49.5 | 1.04 | 1.52 | 0.01 |
| G3 | SARDARI | 24.8 | 20.7 | 26.0 | 57.6 | 0.99 | 1.24 | 0.05 |
| G4 | Trakia//Maga's'74/Mon's'//3/Sha | 22.4 | 22.2 | 24.0 | 66.5 | 0.96 | 1.08 | 0.10 |
| G5 | HENG-SXL-7004/BOW//KS794681/SX | 23.6 | 23.6 | 27.3 | 67.2 | 1.07 | 1.06 | 0.13 |
| G6 | Turkey 13//F9.10/Maya s 1RW92 | 26.7 | 28.3 | 19.5 | 60.8 | 1.09 | 1.08 | 0.27 |
| G7 | 4848 Mashad/Tui 's' IRW92 1 D 6 | 18.7 | 22.9 | 17.5 | 46.6 | 0.69 | 1.22 | 0.15 |
| G8 | UN KNOWN 3 | 25.0 | 23.5 | 12.1 | 79.5 | 1.17 | 0.97 | 0.08 |
| G9 | 914 Gene Bank Material | 22.7 | 18.9 | 21.0 | 36.1 | 1.01 | 1.95 | 0.10 |
| G10 | Sabalan/6/Shahi/KVz/5/Shahl/4/ | 27.7 | 23.4 | 32.0 | 47.7 | 0.96 | 1.39 | 0.16 |
| G11 | 5294karage 98-99 | 27.9 | 22.8 | 17.0 | 78.5 | 0.36 | 0.47 | 0.32 |
| G12 | Roshan/3/F12.71/Coc//Gn079 | 24.0 | 22.4 | 17.8 | 72.4 | 0.87 | 0.97 | -0.05 |
| G13 | 777TWWON87/3/F12.71/SKA//CA805 | 21.2 | 18.4 | 24.3 | 45.5 | 1.29 | 1.58 | 0.26 |
| G14 | UN KNOWN 1 | 27.6 | 23.2 | 20.5 | 59.9 | 0.88 | 1.13 | 0.05 |
| G15 | 1002 Gene Bank Material | 26.9 | 27.2 | 21.0 | 66.8 | 0.92 | 1.18 | -0.23 |
| G16 | 87ZHONG291 | 23.8 | 26.4 | 37.0 | 55.8 | 0.76 | 1.08 | 0.20 |
| G17 | WA467/3/391//NUM5/W22/5/ANA/6 | 22.8 | 22.6 | 31.5 | 93.3 | 0.10 | 0.21 | 0.26 |
| G18 | F9.10/May1 s//Sabalan 1RW92 1 | 22.6 | 21.2 | 24.8 | 82.3 | 0.75 | 0.66 | 0.27 |
| G19 | 98 YRRGP | 19.5 | 15.2 | 20.3 | 71.2 | 0.60 | 0.67 | 0.29 |
| G20 | 72YRRGP | 19.7 | 13.1 | 25.8 | 54.4 | 0.67 | 0.87 | 0.38 |
| G21 | NEMURA/HD2329//AGRINAC | 27.3 | 17.3 | 23.0 | 59.6 | 0.77 | 0.95 | 0.23 |
| G22 | UN KNOWN 2 | 26.8 | 24.8 | 20.5 | 65.7 | 0.93 | 0.98 | 0.18 |
| G23 | Turkey 13//F9.10/Maya s 1RW93 | 22.8 | 22.4 | 21.0 | 56.3 | 0.84 | 1.09 | 0.18 |
| G24 | OGOSTA/SEED | 23.8 | 18.8 | 22.8 | 70.4 | 0.70 | 0.82 | 0.12 |
| G25 | V* 0555/6/PAJO/KAL/3/74/3B/CNO | 26.7 | 27.1 | 24.5 | 74.0 | 0.70 | 0.77 | 0.15 |
| G26 | 14 Gene Bank Material | 18.2 | 16.8 | 22.0 | 59.1 | 1.24 | 1.29 | 0.14 |
| G27 | TX71A1039-V1*AMIRLCTK/VEE | 20.3 | 19.9 | 25.0 | 46.4 | 0.87 | 1.38 | 0.13 |
| G28 | 4851 Mashad/Sabalan IRW92 -1- D | 19.0 | 22.1 | 20.5 | 53.7 | 0.68 | 0.96 | 0.29 |
| | S.E. | 2.5 | 2.5 | 5.3 | 11.6 | 11.6 | 5.3 | |
| | Mean | 23.7 | 22.2 | 22.9 | 61.9 | 61.9 | 22.9 | |
| | LSD (5%) | 6.1 | 6.1 | 12.9 | 28.3 | 28.3 | 12.9 | |

[@]WITI: Weed interference tolerance index. [$]CI: Competition index. [#]RL: Relative loss due to weed interference. S. E.: standard error of mean. LSD: Least significant difference to compare mean of the checks vs. mean of a genotype (other than the checks).

Interrelationships among the genotypes could be explored in various ways depending on the nature of similarity one is looking for in these genotypes; for example, similarity for yield and yield components, tolerance or competitiveness. Hierarchical clusters have been generated (Table 5) for similarity for the tolerance indices (WITI and RL) and for CI alone.

**Similarity of genotypes:** The two clustering approaches grouped the genotypes into three clusters each when considered at 90% similarity level. The clusters and mean values of the indices and grain yield in those clusters are given in Table 5. The cluster A2 (7 genotypes) obtained using similarities for WITI and RL had maximum values of tolerance indices, and the average grain yields under the two conditions (WF, WI) were closest. Thus A2 is the set of similar and most tolerant lines. The group contained 4 (G2, G12, G3, G14) of the top tolerant lines based on RL index and thus represented a cluster with minimum yield loss due to the condition. The least tolerant group A3 (2 genotypes) had lowest yield levels in the two conditions. The cluster A1 (with 19 genotypes) was on average the relatively less tolerant

**TABLE 3: Matrix of correlation coefficients between the traits observed under the two weed interference conditions$**

| Traits | Grain yield | Plant height | Spikes/m² | Seeds/ spike | No of weeds | Weed dry matter | WITI | CI | RL |
|---|---|---|---|---|---|---|---|---|---|
| **Grain yield** | - | 0.470* | 0.494 ** | 0.220 | -0.252 | -0.451 | 0.925 ** | 0.758 ** | -0.636 ** |
| **Plant height** | 0.393 * | - | 0.413 ** | -0.040 | -0.226 | -0.285 | 0.472 * | 0.39 * | -0.120 |
| **Spikes/m²** | 0.623 ** | 0.524 ** | - | -0.310 | -0.127 | -0.507 | 0.539 * | 0.463 * | -0.031 |
| **Seeds/spike** | -0.010 | -0.140 | -0.350 | - | -0.032 | 0.118 | 0.183 | 0.022 | -0.280 |
| **No of weeds** | -0.184 | -0.209 | -0.419 | -0.033 | - | -0.082 | -0.210 | -0.046 | 0.164 |
| **Weed dry matter** | -0.553 | -0.336 | -0.307 | 0.237 | NA | - | -0.490 | -0.869 | 0.048 |
| **WITI** | 0.907 ** | 0.356 | 0.537 ** | 0.070 | NA | NA | - | 0.756 ** | -0.329 |
| **CI** | 0.657 ** | 0.362 | 0.374 * | -0.095 | NA | NA | 0.756 ** | - | -0.370 |
| **RL** | 0.037 | -0.039 | 0.146 | -0.222 | NA | NA | -0.329 | -0.370 | - |

$For yield and yield components. Lower diagonal is for weed-free. Upper diagonal is for weed-interference.
WITI: Weed interference tolerance index. CI: Competition index. RL: Relative loss due to weed interference.
*: P< 0.05. **: P< 0.01. DF= 26

**TABLE 4: Best models selected from the all possible subsets of variables under the weed free and weed interference conditions.**

| **Best models using all possible variable subset selection@** | | $\overline{R}^2$ (%) | P-value |
|---|---|---|---|
| **Variables (only weed free condition)** | WITI = -0.900 + 0.0253 Seeds/spike + 0.002207 Spikes/m2 | 31.5 | 0.003 |
| | CI = -0.500 + 0.0112 Height + 0.001158 Spikes/m2 | 11.2 | 0.087 |
| **Variables under weed free and weed interference conditions** | WITI = -1.606 + 0.0222 Seed/spike (WF) + 0.0179 Seeds/spike (WI) + 0.001341 Spike (WF) + 0.001525 Spikes (WI) | 46.9 | < 0.001 |
| | CI = -0.801 + 0.01175 Height (WF) + 0.001573 Spikes (WI) | 20.8 | 0.021 |

@WITI: Weed interference tolerance index. CI: Competition index. WF: Weed free condition. WI: Weed interference condition.
$\overline{R}^2$ = percent variance accounted for. P-value: Probability level for significance of the fitted model.

**TABLE 5: Clusters of genotypes for similarity of weed interference tolerance and competitiveness$**

| Cluster | Genotypes | No. of genotypes | Mean | | | |
|---|---|---|---|---|---|---|
| **Based on WITI and RL** | | | WITI | RL | Grain yield under WF (kg/ha) | Grain yield under WI (kg/ha) |
| A1 | G1, G13, G6, G5, G8, G26, G7, G25, G24, G16, G21, G10, G22, G23, G27, G18, G28, G19, G20 | 19 | 0.896 | 0.203 | 1968 | 1567 |
| A2 | G2, G3, G4, G9, G14, G12, G15 | 7 | 0.955 | 0.082 | 1833 | 1817 |
| A3 | G11, G17 | 2 | 0.230 | 0.290 | 1019 | 714 |
| **Based on CI** | | | CI | | | |
| B1 | G1, G3, G7, G26, G14, G15, G4, G16, G5, G6, G23, G8, G12, G22, G21, G28, G2, G13, G10, G27 | 20 | 1.164 | | 1967 | 1700 |
| B2 | G11, G17, G18, G19, G20, G24, G25 | 7 | 0.639 | | 1562 | 1162 |
| ungrouped | G9 | 1 | 1.951 | | 1979 | 1785 |

$ Cluster analysis based on Euclidean distance and UPGMA (un-weighted pair-group method using arithmetic averages).
WITI: Weed interference tolerance index. CI: Competition index. WF: Weed free condition. WI: Weed interference condition

than A2 but had higher average yield levels. This group contained 4 (G13, G26, G8 and G6) out of top 5 genotypes for WITI, top 5 genotype for yield under WF and 3 (G8, G26, G13) of top 5 under WI.

The clusters formed on the similarity based on CI, B1 (20 genotypes) had maximum CI on average and higher average yield levels compared to the second cluster B2 (7 genotypes) with much lower yield levels. The group B1 contained top 5 genotypes for weed tolerance using indices (WITI and RI) as well as 5 high yielding genotypes under WF and WI conditions. The genotype clusters A2 and B1, therefore, showed the potential for screening for tolerant and competitive genotypes for weed interference.

Finally, using the above selection and grouping approaches for weed tolerance and yield (from cluster A2 and yield), the genotypes G13, G26 and G8 may be selected as the best tolerance and competitor with weeds and producing high grain yield.

Twenty six promising genotypes along with two checks were evaluated in weed-free and weed-infested conditions in a strip-plot experiment conducted in dryland environment at Srarood-Kermanshah, Iran. Grain yield, yield components (plant height, spikes/me and seeds/spkies) and number of weeds and weed dry weight were analyzed. Indices for tolerance to weed interference were obtained. Differences among genotypes for various traits and similarity for the tolerance and competition were studied. The approaches presented here were used to obtain high yielding, highly tolerance and competitive genotypes. Three genotypes, G13, G26 and G8, were found highly tolerant, competitive and grain yielding.

## ACKNOWLEDGMENTS

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