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Assessment of genotype × trait interaction of rye genotypes for some morphologic traits through GGE biplot methodology

SUMMARY

Effective interpretation of the data on breeding programs is important at all stages of plant improvement and the genotype by trait (GT) biplot was used for two-way wheat dataset as genotypes with multiple traits. For this propose, 18 rye genotypes with specific characteristics were evaluated in randomized block design with four replications. The GT biplot for rye dataset explained 61% of the total variation of the standardized data (the first two principal components explained 40 and 21% respectively). The polygon view of GT presented for 11 different traits of rye cultivars showed six vertex cultivars as G1, G3, G6, G8, G11 and G13 whose genotype G8 had the highest values for most of the measured traits. Generally based on vector view, ideal genotype and ideal tester biplots, it was demonstrated that the selection of high seed yield will be performed via seed number per spike, first internode weight, number of spike per area and harvest index. These traits should be considered simultaneously as effective selection criteria evolving high yielding rye cultivars because of their large contribution to seed yield. The genotypes G8 and G7 following to genotypes G3, G18 and G19 could be considered for the developing of desirable progenies in the selection strategy of rye improvement programs.

Keywords: genotype-by-trait, principal components, trait associations

INTRODUCTION

World production of rye (*Secale cereale* L.) is about 5% that of main winter cereals like wheat or rice but in areas with extreme climatic and poor soil conditions, it may occupy up to 30% of the cultivation (7). The main benefits of rye are its excellent tolerance to low temperatures, its high yield potential under poor environmental conditions and the lowest needs for inputs like fertilizers or pesticides, which makes it an ecologically and economically sound crop for specific poor areas. It has been estimated that world production of rye seed is about 13 million ton from an area of 4.4 million ha land with about 3,000 kg ha^{-1} mean yield performance (5). The main global part of the rye harvest is used for bread baking, especially in European countries where >11 million ton or 85% of rye is harvested in this region. The annual production of rye in Iran is near to 400 ton which was achieved from about 400 ha (5). However, the average yield of this crop in semi-arid regions like Iran is relatively low (lower than one ton per hectare). Yield performance of rye is comparable to wheat yield on good soils and superior on poor soils where wheat performs badly (6).

The insufficient knowledge of the interrelationship among various characters and the practice of unilateral selection for agronomic characters frequently results in retrograde or less than optimal results in plant breeding program. Correlations between different traits is an aspect which should be kept in mind for better planning of selection programs because they show relationships among independent characters and the degree of linear relation between these characters (12). Therefore, there is the need to examine the relationships among various traits, especially between seed yield and other agronomic traits. Bhutta (1) has concluded that the number of seeds per spike, the number of plant per area and spike length correlate with seed yield per plant and according to Koutis et al. (8) seed yield correlates with plant height, the number of plant per area and thousand seed weight.

According to Del-Blanco et al. (3) some yield components such as the number of plant per area, the number of seeds per spike and thousand seed weight have significant contribution to seed yield. It has been reported that the number of seeds per plant, plant height, thousand seed weight and spike length have significant correlation with seed yield (9). Effective interpretation of the data on breeding programs is important at all stages of plant improvement, particularly when it is only possible to select yield components. Several methods have been used in exploration for an understanding of the data structure which may differ in overall appropriateness; different methods usually lead to the similar conclusions for a given dataset. Yan et al. (14) have developed a genotype main effect (G) plus genotype by environment (GE) biplot methodology for the graphical analysis of multi-environment trial data. Yan and Rajcan (16) have used a genotype by trait (GT) biplot, which is an application of the GGE biplot to study the genotype by trait data. The present study was performed to study the interrelationship of rye yield components and their contribution to seed yield using GT biplot technique. The information so derived could be employed in reaching further breeding strategies and selection of methods to develop new high yielding rye genotypes.

MATERIALS AND METHODS

Field experiment was conducted at the experimental field of the Faculty of Agriculture of the University of Maragheh (latitude 37° 23′ N, longitude 46° 16′ E, altitude 1,478 m). The region occurs in a semiarid climate zone characterized by relatively long winters with 375 mm average annual precipitation which consists of 73% of rain and 27% of snow. Soil texture was sandy loam and the experiment was sown in usual autumn planting dates in 2017. The experimental field design was a randomized complete block design (RCBD) arrangement with four replications. The experiment included 18 rye genotypes, which represent a range of phenotypic variation in maturity, adaptation zone, yield potential and date of release. The small samples of experimental seed materials were obtained from Genebank Department of Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) in Gatersleben, Germany. These samples were propagated in growing season 2014 and their name and origin are given. Tillage of all plots was performed prior to sowing date and fertility was constrained by low organic matter and phosphorus contents.

The fertilizer application was performed before sowing, 50 kg ha^{-1}of N, 25 kg ha^{-1} of P and 15 kg ha^{-1} of K were spread on the surface and tilled into the soil and the weeds were controlled chemically by MCPA (2-methyl-4-chlorophenoxyacetic acid). Plant density was 250–300 plants/m^{-2}. Plant height (PH), spike length (SL), awn length (AL), seed number per spike (SNS), first internode weight (FIW), spike weight (SW), flag leaf length (FLL), and the number of spike per area (NSA) were measured based on ten guarded plants, which were randomly selected from each plot. Also, thousand seed weight (TSW) and seed yield (SY) of each plot were measured and harvest index (HI) were computed based on ratio of SY to biological yield. The genotype × trait (GT) biplot was used to show the two-way pattern of rye genotypes' traits in a biplot based on the following formula:

$$\frac{\alpha_{ij}-\beta_j}{\sigma_j}=\sum_{n=1}^{2}\lambda_n\xi_{in}\eta_{jn}+\varepsilon_j=\sum_{n=1}^{2}\xi_{in}^{*}\eta_{jn}^{*}+\varepsilon_j$$

where α_{ij} is the mean value of genotype i for trait j, β_j is the mean value of all genotypes in trait j, σ_{ij} is the standard deviation of trait j among the genotype means, λ_n is the singular value for principal component n (PCn), ξ_{in} and η_{jn} are scores for genotype i and trait j on PCn, respectively, and ε_{ij} is the residual associated with landrace i in trait j. To achieve symmetric scaling between the genotype scores and the trait scores, the singular value λ_n has to be absorbed by the singular vector for genotypes ξ_{in} and that for traits η_{jn}. That is, $\xi_{in}^{*}=\xi_{in}\lambda_n^{0.5}$and $\eta_{jn}^{*}=\eta_{jn}\lambda_n^{0.5}$. Because of n=2, only PC1 and PC2 are retained in the model and such a model tends to be the best for extracting pattern and rejecting noise from the data. Because the traits were measured in different units, the biplots were generated using the standardized values of the trait means with the use of GGE biplot software (13).

RESULTS AND DISCUSSION

The GT biplot for rye dataset explained 61% of the total variation (40 and 21% for PC1 and PC2 respectively) of the standardized data and this relatively moderate percentage reflects the complexity of the relationships among the measured traits. The polygon view of the GT biplot helps identify genotypes with the highest values for one or more traits and provides the best way for visualizing the interaction patterns between genotypes and traits and to effectively interpret a biplot. Figure 1, as polygon view, presents data of 18 rye genotypes in eleven traits and the following information can be understood: the vertex genotypes in this investigation are G1, G3, G6, G8, G11 and G13. These genotypes are the best or the poorest genotypes in some or all of the traits since they had the longest distance from the origin of biplot. Therefore, genotype G8 had the highest values for seed number per spike (SNS), first internode weight (FIW), plant height (PH), spike weight (SW) and thousand seed weight (TSW) traits while genotype G3 had the highest values for spike length (SL) and awn length (AL). Genotype G11 had the highest values for the number of spike per area (NSA), seed yield (SY) and harvest index (HI) while genotype G3 had the highest values for flag leaf length (FLL). The vertex genotype and other genotypes which fell in the related sector had good amounts of the above-mentioned traits. The other vertex cultivars (G1 and G13) and related sectors were not suitable performance for the measured traits

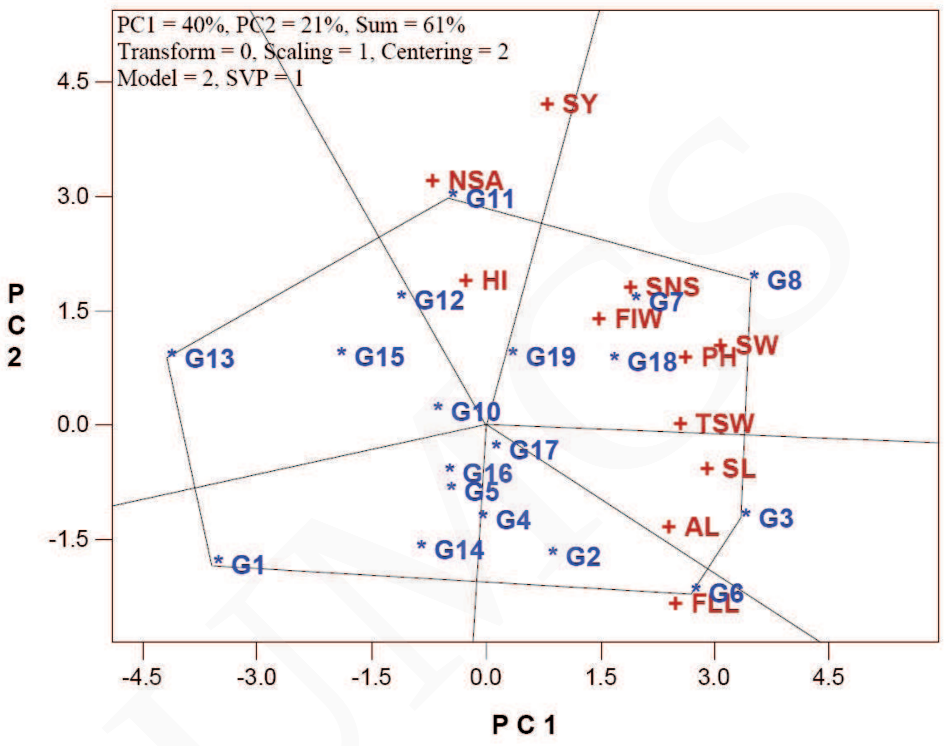

Fig. 1. Polygon view genotype by trait biplot, showing which genotype had the highest values for traits for 18 different rye genotypes

(Fig. 1). Different vertex genotypes and their related genotypes which are located in different sections of biplot are good candidates for examination heterosis (15) for hybrid production in rye using these genotypes or pure lines. Also, genotype G11 could be used for improving seed yield in the breeding program.

The most prominent relations by vector-view biplot at the first year (Fig. 2) are: a strong positive association between SW and PH; between TSW and SL; between FIW and SNS; between AL and FLL; and between HI and NSA; as indicated by the small obtuse angles between their vectors (r=cos 0=+1). There was a near zero correlation between FLL with FIW and SNS, between SY with TSW and SL, and between PH and SW with NAS and HI (Fig. 2) as indicated by the near perpendicular vectors (r=cos90=0). There was a negative correlation between FLL with NAS and HI as indicated by the near an angle of approximately 180 degrees (r=cos180=-1). Some above discrepancies of the biplot predictions and original data were expected because the biplot accounted for <100% of the total variation (Table 1).

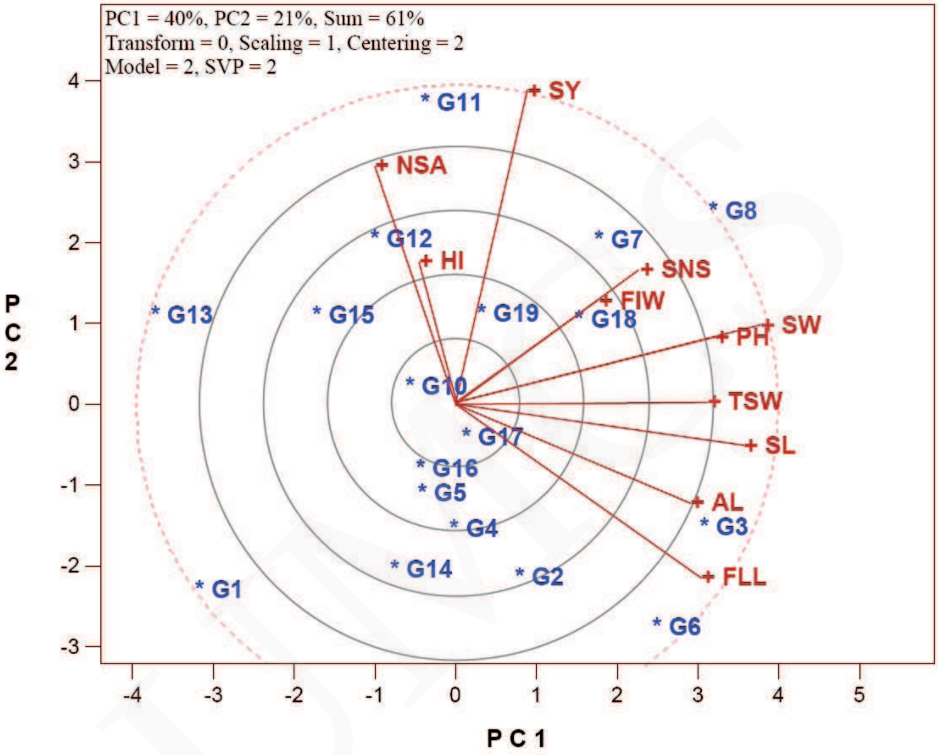

Fig. 2. Vector view genotype by trait biplot, showing the interrelationship among all measured traits for 18 different rye genotypes

The mean effects of the measured across genotypes were examined by defining an average tester coordinate (ATC) axis and an average or virtual genotype is indicated by a circle and shows the positive end of the ATC axis. An ideal genotype is the one that should have large PC1 scores (high traits' means) and small (absolute) PC2 scores (low variability). Genotypes with above-average means were selected, whereas the rest were discarded. Genotype G8 was the most favorable genotype regarding all of the measured traits due to its low distance from horizontal axis (Fig. 3). Ranking of the best genotypes based on the ideal genotype was G7> G18 > G3 > G19 > G6> G11 > G17 and the ranking of the most unfavorable genotypes based on the ideal genotype was G1 and G13 (Fig. 3). The requirement for the use of site regression based GT biplots in the identification of most superior genotypes is to facilitate the identification of such genotypes (2). The present research has clearly shown that the site regression model can analyze patterns and relationships of genotypes and traits successfully as well as provide a valuable prediction.

Table 1. Pearson correlation coefficients of rye seed yield and some morphologic traits

	PH	SL	AL	SNS	FIW	SW	FLL	NSA	SY	TSW
SL	0.68									
AL	0.39	0.66								
SNS	0.23	0.47	0.28							
FIW	0.17	0.30	0.13	0.42						
SW	0.68	0.70	0.48	0.73	0.45					
FLL	0.54	0.67	0.56	0.16	0.11	0.55				
NSA	0.25	-0.26	-0.29	-0.16	-0.09	-0.21	-0.48			
SY	0.39	0.01	-0.07	0.42	0.27	0.40	-0.32	0.70		
TSW	0.68	0.49	0.52	0.06	0.23	0.69	0.53	-0.11	0.25	
HI	-0.27	-0.05	-0.20	0.29	0.08	0.07	-0.29	-0.02	0.26	-0.12

Critical values of correlation $P < 0.05$ and $P < 0.01$ (df 16) are 0.40 and 0.47 respectively.

Traits are: plant height (PH), spike length (SL), awn length (AL), seed number per spike (SNS), first internode weight (FIW), spike weight (SW), flag leaf length (FLL), number of spike per area (NSA), seed yield (SY), thousand seed weight (TSW) and harvest index (HI)

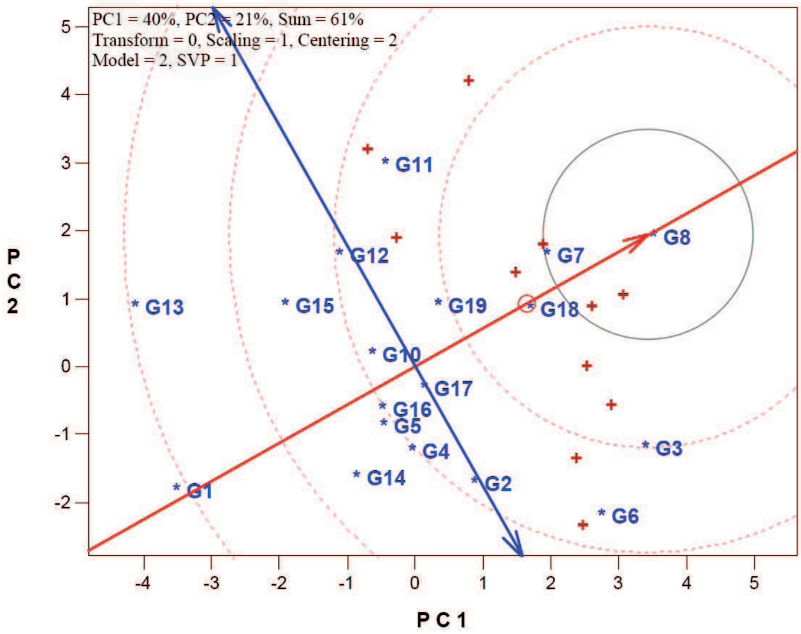

Fig. 3. Ideal entry view of genotype by trait biplot, showing the relationships of rye genotypes with ideal entry

In rye, improvement for achieving high seed yield as an important desirable character is the purpose of many breeding programs. In Figure 4, seed yield (SY) was compared with other measured traits and the ranking of measured traits based on the SY was NSA > HI > SNS > FIW > PH > SW following TSW > SL > AL > FLL. In other words, the most important traits for producing high yielding rye cultivars are the number of spike per area, harvest index and seed number per spike while the least important trait on rye yield were flag leaf length and awn length. It is noticeable that the NSA, HI and SNS are important for improving seed yield and so it seems that defining breeding strategies for genetic improvement of seed yield must be performed based on them. The relative contributions of different traits of economical crop yield to the identification of desirable genotype found in this study by the traits comparing biplot procedure of the GT biplot are similar to those found in other crop studies; soybean (16), white lupin (10), and rapeseed (11).

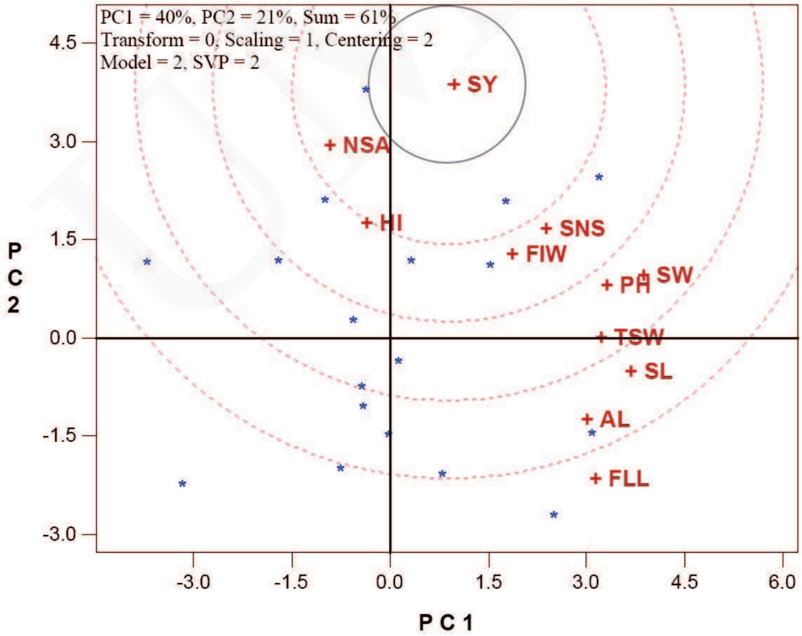

Fig. 4. Vector view genotype by trait biplot, showing the interrelationship among all measured traits for 18 different rye genotypes

Potential sources of genetic variation are important to allow rye breeders to deal with changing environmental condition but large collections do not exist for rye while there are some local landraces available to breeders but variation values for most traits have not been investigated. The data obtained in this study could be useful for rye breeders in efforts to increase yield. The correlation coefficients between the seed yield and yield components showed good variation, and the results suggest that the seed number per spike, first internode weight, the number of spike per area and harvest index are the primary selection criteria for higher seed yield in rye.

It is clear that the GT biplot method is an excellent tool for visual genotype by trait data analysis because it is a powerful tool and can be used to graphically address research questions (17). Compared with conventional methods, the GT biplot approach has some advantages: (i) graphical presentation of the data, which greatly enhances our ability to understand the patterns of the data, (ii) more interpretative and facilitates pair-wise genotype or trait comparisons and effectively reveals the interrelationships among the rye traits, (iii) it facilitates identification of possible which-won-where patterns or which-lost-where patterns, and (iv) it can be used in independent culling based on multiple traits and in comparing selection strategies (15, 18).

In conclusion, based on the GT biplot, seed number per spike (SNS), first internode weight (FIW), the number of spike per area (NSA), and harvest index (HI) were identified as traits suitable for selection for yield improvement in rye. Thus, selecting for these traits is expected to lead to improved yield and this suggests that selection index that incorporates these traits will not only result in the development of high yielding cultivars but also other desirable agronomic traits. From my observations, it appears possible to improve exotic rye landraces by selecting for genotypes with higher values of the above-mentioned traits. Also, almost half of the studied genotypes including G3, G7, G6, G11, G17, G18 and G19, are good candidates for improving most of the measured traits due to existence of good genetic variability in the plant materials.

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