International Journal of Biosciences | IJB |
ISSN: 2220-6655 (Print) 2222-5234 (Online)
http://www.innspub.net
Vol. 3, No. 2, p. 234-240, 2013

RESEARCH PAPER OPEN ACCESS

Study of stability and adaptation on yield components of bread wheat (*Triticum aestivum* L.) genotypes

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Key words: Wheat, yield component, stability, adaptability.

doi: http://dx.doi.org/10.12692/ijb/3.8.234-240 Article published on August 22, 2013

Abstract

The development of genotypes, which can be adapted to a wide range of diversified environments, is the ultimate goal of plant breeders in a crop improvement programs. Therefore, this study was conducted to evaluate 25 durum wheat (*Triticum aestivum* L.) genotypes including 3 registered cultivars and 17 advanced breeding lines for their stability grown in three different locations of Iran and to select genotypes having desirable traits to be used in future bread wheat breeding program. Field trials were conducted in a randomized complete block design with three replications at each location. Combined analysis of variance across environments indicated that both environments and GE interactions influenced significantly the genotypes performance for number of spikes per square meter, number of kernels per spike, 1000 kernel weight and grain yield. The stability analysis method of Eberhart-Rusell was used to describe the GE interaction and to define stable genotypes in relation to yield components. The results showed for seed per spike number genotypes 18, Marvdasht and 13 were stable. Based on Eberhart and Russell's method in experiment for 1000 grain weight genotypes 15 and 19 having regression coefficient near to 1 was known as genotype with good adaptability to all environments. The results showed 1000 grain weight in comparison to other traits was more stable.

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Introduction

Bread wheat *(Triticum aestivum* L.*)* is the most importance for human diet. Sowing area of bread wheat in Iran is about 12 million hectares per year. The region also produces 14.3 million tons of wheat grain in 2005, in Iran, 4.3 million tons was harvested from rain fed (4.3 mha) and 10 million tons from irrigated (2.6 mha) wheat growing areas (Anonymous, 2008). The breeding strategies adopted during the last decades have contributed to reduce the interaction of genotypes with environments selecting genotypes with better stability across a wide range of locations and years and modern genotypes outperformed the old ones in all test environments with a strong adaptability to improved fertility.

The development of cultivars or varieties, which can be adapted to a wide range of diversified environments, is the ultimate goal of plant breeders in a crop improvement programs. Major goal of plant breeding programs is to increase stability and stabilize crop yield across environments. The study of the genotype × environment (GE) interaction may assist understanding of stability concept. Understanding the structure and nature of GE interaction is important in plant breeding programs because a significant GE interaction can seriously impair efforts in selecting superior genotypes relative to new crop introductions and cultivar development programs. It can help determine if they need to develop cultivars for all target environments or if they should develop specific cultivars for specific target environments. Phenotypic stability has been extensively studied by biometricians who have developed numerous methods to analyze it (Kafa and Kirtok, 1991; Ozberk *et al.,* 2004). Significant GEI results from the changes in the magnitude of differences between genotypes in different environments for changes in the relative ranking of the genotypes (Goeorge and Fernandez, 1991). Stable genotypes have the same reactions over the environments (Bjornsson, 2002).

Increasing genetic gains in yield is possible in part from narrowing the adaptation of cultivars, thus maximizing yield in particular areas by exploiting genotype × environment interaction (Roemer, 1917). According to Lin *et al.* (1988) there are three types of parametric stability of known as type 1, 2 and 3. In type 1, (Akcura *et al.,* 2006), a genotype is considered to be stable provided that the environmental variance is small; in Type 2, stability variance (Wricke, 1962) and ecovalence (1972), a genotype is considered to be stable if its response to environment is parallel to the mean response of all genotypes in the trial and in type 3, squared deviations from regression (Eberhart and Russell, 1966) and coefficients of determination (Shindin and Lokteva, 2000) a genotype is considered to be stable if the residual mean squares from the regression models on the environment index is small.
A genotype with a high bi and S2d reacts readily to change in the environment and possesses considerable variability, whereas cultivars with a bi < 1.0 and S^2d near to 0.0 react weakly to changes in growing conditions and are considered to be stable in yield (Pinthus, 1973). Finlay and Wilkinson (1963) regarded those genotypes with a bi near 1.0 and high mean yield as being well adapted to all environments.
In general, stability parameters are employed to figure out the adaptation behavior of genotypes in diverse environmental conditions. Stability is defined as the early prediction of environmental impacts on genotypes performances (Kang and Pham, 1991; Lin *et al,* 1986). Multivariate analysis methods are also useful tool to asses' stability and can be used to identify groups with desirable traits for breeding. Most studies on bread wheat have focused on stability characteristics of genotypes for grain yield (Kilic *et al.,* 2005; Budak and Yildirim, 2001; Akcura *et al.* 2005; Korkut and Baser, 1995). Tian *et al.* (2007) were analyzed Variation and Stability of Wheat genotype. The results showed that the coefficient of variation for the stability ranged from 24.29 to 49.60% across different varieties, locations, and years. Sial *et al.* (2000) studied stability for yield performance and G x E interaction in 12 wheat genotypes grown at 13 contrasting sites over two years. The results shown that stability in grain yield among genotypes can be described as the linear

response to environmental yield and deviation from that response.

The objective of this study was: to identify what genotypes that have high yield and stable performance across different locations.

Materials and methods

Plant materials

Twenty bread wheat genotypes, including 3 registered cultivars and 17 advanced breeding lines, were used as plant material in this study. Data analyzed in this study obtained from sets of wheat yield trials conducted at three different research stations in Iran included Esfahan, Kermanshah and Varamin. Planting was done in experimental plots of 6 m length and 1.2 m width each. The experiments were carried out using randomized complete block design (RCBD) of 3 replications each.

Statistical analysis

Bartlett's test was used to determine the homogeneity of variances between environments to determine the validity of the combined ANOVA on the data. Pooled analysis of variance for G×E interaction on grain yield and yield component were done according to Eberhart-Russell model was computed for classification of genotypes and environments. Eberhart and Russel developed Finlay and Wilkinson's regression concept of stability and suggested the use of two stability parameters. They proposed that the regression of each cultivar on an environmental index and a function of the squared deviations from regression would provide more useful estimates of yield stability parameters. Stability analysis was performed whenever the genotype x environment interactions for grain yield component were determined as statistically significant ($P < 0.01$). The regression coefficient (bi) and mean square of deviation from regression (S^2d) values were used as the stability parameters. Wheat genotype demonstrating a higher value than the overall mean with a bi value of 1 or close to 1 and an S^2d value of 0 or close to 0 in grain yield was judged as a stable genotype. Additionally, graphical adaptation classifications, developed by Finlay and Wilkinson using the overall mean and bi value, were employed for the assessment of stability parameters for grain yield of wheat genotypes.

Statistical analysis of variance (ANOVA) combined over locations and years was done on a plot mean basis and pooled over locations using the generalized linear model procedures of the statistical analytical system SAS (2000).

Results and discussion

Combined analysis

The results analysis of variance combined for number of spikes per square meter, number of kernels per spike, 1000 kernel weight, and grain yield are given in Table 1. Analysis of variance was conducted to determine the effect of environment (E), genotype (G) and interaction among these factors, on grain yield and yield components (Table 3). Analysis of variance indicated significant genotype × environment interaction ($p<0.01$) and showed the influence of changes in environment on the yield performance of the genotypes evaluated. The environment effect was significant ($p<0.01$). Highly significant environment also showed that the response of genotype to changes in the environments was under genetic control. G effects also were significant ($p<0.01$).

Effects from G and E that showed highly significant MS reflected genotypic differences towards adaptation to different environments, thus the highly significant G×E effects suggests that cultivars may be selected for adaptation to specific environments. High variability was observed among cultivars as indicated by the range of their mean performance (Table 2). The highly significant differences ($P<0.01$) of the combined analysis across locations indicate the fluctuation of genotypes in their responses to the different environments. There are also tremendous changes in yield ranks of the genotypes across locations. Pham and Kang (1988) indicated that a G×E interaction minimizes the usefulness of genotypes by confounding their yield performance. Thus, it is important to study in depth the yield levels, adaptation patterns and stability of genotypes in multiplication trials.

Table 1. Results of mean of square of combined ANOVA on grain yield and component yield.

SOV	df	Grain yield	No. spike per m2	No. kernel per spike	1000 kernel weight
Environment	2	115.47**	1668160**	1249**	2099.4**
Rep in Env.	6	1.74 ns	11831ns	31.61ns	31.9**
Varieties	19	3.69**	35362**	248.2**	107.6**
Var x Env.	38	1.62**	76337**	90.21**	46.37**
Error	114	0.61	979819	37.74	6.64
CV (%)	-	12.84	19.73	12.81	7.63

*and** significant at probability level of less than 0.05 and 0.01

Table 2. Mean of traits at three locations by Duncan test.

Genotype	1000 kernel weight	No. kernel per spike	No. spike per m²	Grain yield (kg ha⁻¹)
Marvdasht	25h	58a	797ba	5380dc
Crossalborz	30.8efg	40ef	786ba	4733ed
Azar	37.1ba	36f	811ba	4343e
4	35.7bc	44ced	863ba	5855bac
5	34.9bcd	52b	777b	6255ba
6	33.1efcd	48cbd	789ba	6092bac
7	31.5efg	50cd	802ba	6677ba
8	35bcd	46cbd	750b	5706bac
9	33.4ecd	46cebd	752b	6173bac
10	37.1ba	42ed	958a	6159bac
11	35.5bc	49cbd	736b	6384ba
12	30.4fg	58a	802ba	5806bac
13	39a	45ced	886ba	6297ba
14	39.2a	47cbd	716b	6670ba
15	35.2bcd	49cbd	845ba	6330ba
16	35.6bc	44ced	856ba	6540ba
17	32.5efd	49cbd	722b	6298ba
18	32.1efg	49cbd	708b	6064bac
19	29.5g	51cb	838ba	6736a
20	30.3efg	49cbd	763ba	6147ba

Researchers also indicated that assessment of stability across many sites and years could increase both reliability and heritability of important traits. Sakin *et al.,* (2011), Aina *et al.* (2009) reported that linear response of a genotype is associated with mean performance.

The results of the combined analysis of variance for yield component (Table 1) showed a strong influence of the locations on number of spikes per square meter, number of kernels per spike, 1000 kernel weight. Genotypic effects were mainly observed for 1000 kernels weight.

The genotypes 10, 14, 15 and 16 favored higher values of number of spikes per square meter; spike weight and grain yield, but had less number of kernels per spike (table 2). Grain yield was influenced both by genotype and by environment. Because the GE interaction was significant for grain yield, stability analyses were performed by using linear regression techniques.

Stability analysis

The stability parameters, determined by the regression coefficient (bi) of Finlay and Wilkinson and mean square of deviation from regression (S^2d) of Eberhart and Russell were presented in table 4.

Table 3. Partitioning of G×E into linear and nonlinear component for 1000 kernel weight of 20 wheat genotypes evaluated across 3 environments.

Source of variation	df	Mean squares
Environments	2	36.43 ns
Genotypes (G)	19	205.5
G x Env.	38	15.5*
Environments(linear)	1	1411.35
G x Env.(linear)	19	6.72
Pooled deviations	20	22.57*
Marvdasht	1	11.03
Crossalborz	1	3.87
Azar	1	4.73**
4	1	36.63**
5	1	0.88
6	1	38.82**
7	1	13.02*
8	1	106.85**
9	1	5.9
10	1	40.72**
11	1	1.26
12	1	1.4
13	1	93.26**
14	1	3.38
15	1	0.09
16	1	46.44**
17	1	31.44**
18	1	0.26
19	1	0.94
20	1	6.84
Pooled error	114	2.62

* and ** are significant at P<0.05 and 0.01, respectively.

Regression coefficients ranged from 0.48 to 1.55 for 1000 kernel weight. This variation indicates differences in responses to environmental changes. Lines 6, 15, 19 and Marvdasht can be considered as judged by their bi values and adaptation classifications, whereas lines 15 and 19 can only be considered stable by the S2d value (Table 4).

The result of combined ANOVA, by Eberhart-Russell model for 1000 kernel weight showed that, the majority of the tested genotypes (Table 3) were non-significantly different from a unit regression coefficient (bi=1). Finlay and Wilkinson and Eberhart and Russell stated that genotypes with high mean yield, regression coefficient equal to unity (bi=1) and deviation from regression as small as possible (S2di=0) are considered a stable. Accordingly, genotypes 15 and 19 were the most stable genotypes since the regression coefficients almost unity and had one of the lowest deviations from regression and also have above average mean yield. In contrast, varieties such as 9, 10, 11 and 12 with regression coefficients greater than one were regarded as sensitive for environmental change. Romagosa and Fox (1993) indicate that the common breeding strategy for variable environments is generally to develop widely adapted varieties by testing over a rage of diverse conditions covering representative samples of special and temporal variations.

Table 4. Parameters of Eberhart-Russell model for 1000 kernel weight.

Genotype	bi	S^2di
Marvdasht	0.48	8.4
Crossalborz	1.1	1.26
Azar2	1.03	2.06
4	0.88	35
5	0.56	0
6	1.08	36.2
7	1.16	10.37
8	0.42	10.04
9	1.37	3.29
10	1.41	38.03
11	1.55	0
12	0.8	1.37
13	1.01	7.09
14	1.19	0.76
15	0.98	0
16	0.68	43.8
17	1.23	28.7
18	1.27	0
19	1.01	0
20	0.81	4.24

Among the joint regression stability measures, S^2di was largely used to rank the relative stability of cultivars (Peterson *et al.*, 1989). The indication was that bi could be used to describe the general response to the goodness of environmental conditions, whereas, S^2di actually measures the yield stability.

Other genotypes were not stable indicated by the employed stability parameters (bi and S^2d) for 1000 kernel weight. Stability parameters of line 4, Line 5, Line 12 and 20 were less than unit (bi = 1.0) and had low 1000 kernel weight. Therefore, these genotypes were considered to be adapted to poor environments. Regression coefficients of Line 4 and 16 were less than unit (bi = 1.0), however, they had higher 1000 kernel weight. Thus, these genotypes could be considered as progenitors in breeding programs for high grain yield.

The result for number of spike per square meter showed that, lines 10 and 13 had highest number of spike (958 and 888 spike per square) and lines 14 and 18 had low number of spike (708 and 716 spike per square meter). The results between number of spike per square meter and grain yield had not related (not shown). Various method of stability apple for study of number of kernel per spike that result showed, genotypes 18, Marvdasht and 13 had regression coefficient near to one and genotypes 4, 6 9 and 19 could be suggest for cultivation in special location.

Negative correlation between grain yield and this trait was observed, while based on result by Garcia Del Moral (2003) positive correlation obtained between these traits.

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