

Investigation of Genetic Variation for Agronomic Traits among the Recombinant Inbred Lines of Wheat from the Norstar × Zagross Cross under Water Stress Condition

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Abstract—Determination of genetic variation is useful for plant breeding and hence production of more efficient plant species under different conditions, like drought stress. In this study a sample of 28 recombinant inbred lines (RILs) of wheat developed from the cross of Norstar and Zagross varieties, together with their parents, were evaluated for two years (2010-2012) under normal and water stress conditions using split plot design with three replications. Main plots included two irrigation treatments of 70 and 140 mm evaporation from Class A pan and sub-plots consisted of 30 genotypes. The effect of genotypes and interaction of genotypes with years and water regimes were significant for all characters. Significant genotypic effect implies the existence of genetic variation among the lines under study. Heritability estimates were high for 1000 grain weight (0.87). Biomass and grain yield showed the lowest heritability values (0.42 and 0.50, respectively). Highest genotypic and phenotypic coefficients of variation (GCV and PCV) belonged to harvest index. Moderate genetic advance for most of the traits suggested the feasibility of selection among the RILs under investigation. Some RILs were higher yielding than either parent at both environments.

Keywords—Wheat, genetic gain, heritability, recombinant inbred lines.

I. INTRODUCTION

THE development of high yielding wheat cultivars is a major objective in breeding programs [6]. The genetic variation for the trait under selection and a higher heritability are necessary to have response to selection [7]. Breeding programs depend on the knowledge of key traits, genetic systems controlling their inheritance, genetic and environmental factors that influence their expression [11], [1], [15]. The study of statistical parameters like mean, variance, CV%, habitability and genetic advance is a measure to evaluate genetic potential, diversity and stability performance of any genotype for effective selection of particular traits in that genotype [8], [1].

Risk management is crucial in the investment and financing decisions for farmers in developing countries and in transition economies. Basic risk management in agriculture includes choosing plant varieties against adverse weather events [17]. The optimum variety should have superiority in environments with different stress intensities. Some genotypes are only

favorable in a specific environment, like landraces which have been adapted for severe local stresses or inbred cultivars which have been genetically modified for high yield in full irrigation conditions. The plant performance in diverse environments depends on efficiency of developed varieties which should be matched to the production area. Multi-environment testing is the main tool for understanding varietal responses to the environments, although the process is time-consuming and expensive.

The main objectives of this study were to determine genotype by environment interaction, estimate heritability and genetic advance in recombinant inbred lines with winter habit, developed from the cross of Norstar and Zagross varieties. The main objectives of this study were to determine genotype by environment interaction, estimate heritability and genetic advance in recombinant inbred lines with winter habit, developed from the cross of Norstar and Zagross varieties.

II. MATERIALS AND METHODS

A. Plant Material and Experimental Design

The field experiments were conducted at Agricultural Research Station of Islamic Azad University of Tabriz, located in the northwest of Iran (38° 5' N and 46° 27' E, 1360 m altitude) during two cropping seasons (2010-2011 and 2011-2012). Some climatic parameters during the experiment are given in Table I. The soil texture was clay-loam with less than 1% of organic matters.

In each year, 28 recombinant inbred lines of wheat randomly sampled from a larger population, together with their parental varieties, Norstar (a winter type variety developed in Canada) and Zagross (a spring type and relatively drought tolerant variety developed in Iran), were evaluated under two irrigation conditions, using a split plot design based on randomized complete blocks with three replications. Main plots included irrigation treatments at two levels: 70 and 140 mm evaporation from Class A pan for normal and drought stress conditions, respectively. Plots were arranged in three rows of two- meters long and 15 cm apart. Cultural practices were carried out according to the existing standards. During the growing season, spike length, biomass, kernel number per spike, 1000-grain weight, harvest index, and grain yield were recorded in each experiment.

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Analysis of variance was carried out by combining the data from two years of experimentation. Normality of experimental errors was checked by the Shapiro-Wilk's normality test. Where the normality assumption was not fulfilled, a log

transformation was performed. Furthermore, based on residual plots, weighted least squares method was carried out for the analysis of 1000-grain weight and kernel number per spike due to heteroscedasticity.

TABLE I
Rainfall AND MEAN TEMPERATURE DURING 2010-2012 GROWTH SEASONS AT TABRIZ AGRICULTURAL RESEARCH STATION OF ISLAMIC AZAD UNIVERSITY

Climatic parameters	Year	Oct	Nov	Dec	Jan	Feb	Mar	Apr	May	June	Total
Rainfall	2010-11	7.0	0.0	1.1	7.8	18.3	42.4	85.7	35.0	0.7	198
	2011-12	13.7	26.7	7.9	25.2	42.1	20.0	26.7	27.5	15.8	205.6
Mean temp. (°C)	2010-11	17.1	8.8	4.4	-0.7	1.7	6.5	12.8	17.9	24.9	
	2011-12	13.7	2.9	-0.8	0.0	2.5	3.2	14.8	19.8	25	

B. Formulas of Genetic Parameters

Heritability estimates were obtained using variance components as:

$$h^2 = \frac{\sigma_g^2}{\left(\sigma_g^2 + \frac{\sigma_e^2}{ry}\right)}$$

where, σ_g^2 = genetic variance; σ_e^2 = environmental variance; r = number of replications; y = number of environments

Genetic advances for the characters under study were calculated as [3]:

$$GA = \sigma_p \times h^2 \times k$$

where, σ_p = standard deviation of the phenotypic variance; h^2 = narrow sense heritability; k = standardized selection intensity (regarding 10% selection intensity k = 1.755).

Genotypic coefficient of variation (CV_g) and phenotypic coefficient of variation (CV_p) were calculated by the:

$$CV_g = \frac{\sqrt{\sigma_g^2}}{X_{00}} \times 100 \quad CV_p = \frac{\sqrt{\sigma_p^2}}{X_{00}} \times 100$$

where, X_{00} is the grand mean for each character.

Data were analyzed by MSTAT-C and SPSS computer packages.

III. RESULTS AND DISCUSSION

A. Analysis of Variance for Agronomic Characters

Combined analysis of variance showed the significant effects of year, genotype, year × water regime, genotype × year, genotype × water regime and genotype × water regime × year for all of the characters under study (Table II). The results indicate considerable genetic variability among the recombinant inbred lines of wheat under study for all of the characters including grain yield, suggesting that the parents used in the cross were genetically different. Environmental conditions were not also similar in two years, specially, in terms of rainfall distribution and temperature. Significant interaction of genotypes with water regimes and years suggest that the differences among genotypes were not stable across water regimes and years. Genotype by environment interaction (GEI) has been observed in many studies. GEI is important in

crop breeding and production [10]. GEI confounds with the genotypic effects if the experiment is carried out in only one environment. GEI has a negative impact on heritability. The lower the heritability of a trait, the greater the difficulty in improving that trait via selection is [19]. Knowledge about GEI is important because a significant GEI can seriously impair selecting superior genotypes in plant breeding programs [18]. Information about GEI is useful to plant breeders in deciding whether to develop a cultivar for all environments or to develop specific genotypes for specific environments [5].

B. Estimates of Genetic Parameters

Estimates of genotypic and phenotypic variances, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), narrow sense heritability among lines, and genetic advance per se and expressed as percentage of the mean for the studied attributes are presented in Table III. In all characters, the PCV was larger than GCV; however, in some cases the differences were negligible. Highest genotypic and phenotypic coefficients of variation belonged to harvest index (%). Although significant differences were observed among the recombinant inbred lines for spike length, the values for PCV, GCV, and also genetic advance were low; indicating that improvement for these characters may not be effective in this population. Similar results for days to heading were observed by [6], [4] and [14]. High heritability estimates were obtained for 1000 grain weight (0.87). The estimate was relatively high for the number of kernels per spike (0.71). High heritability estimates in wheat have been reported in most studies for 1000 grain weight [2], [6], [12]-[14], and kernels per spike [6], [13], [14], [16]. 1000 grain weight is less sensitive to environmental effects and therefore showed high heritability in most studies. Biomass and grain yield had the lowest heritability values (0.42 and 0.50, respectively) among the traits studied. Moderate to low heritability estimates for grain yield were also reported by others [9], [6]. Lower heritability values for grain yield as compared with the estimates for the yield components in our study and other researches [6], [4], [13], [14] indicate the important contribution of environmental effects to the phenotypic variance of this trait. Therefore, selection for grain yield per se in the segregating generations would not be fruitful and emphasis must be put on the components such as 1000 grain weight and number of kernels per spike. Moderate genetic

gain for most of the characters suggests that selection for superior genotypes would be effective among the recombinant inbred lines obtained from the cross of Norstar and Zagross varieties.

TABLE II
ANALYSIS OF VARIANCE OF DIFFERENT AGRONOMIC CHARACTERS FOR 28 RECOMBINANT INBRED LINES OF WHEAT AND TWO PARENTAL VARIETIES UNDER TWO WATER REGIMES DURING 2010-11 AND 2011-12 GROWING SEASONS

SOV	df	Mean squares					
		Based on log transformation				Based on weighted least squares	
		Spike length	Biomass	Grain yield	Harvest index	Kernel number per spike	1000-grain weight
Year (Y)	1	0.054**	18798.4**	29831.6**	0.115*	761.4*	1610.0**
Replication/Y	4	0.005**	241.9**	230.2**	0.035**	293.3**	34.4**
Water regime (W)	1	0.175 ^{ns}	59.3 ^{ns}	48.4 ^{ns}	^{ns} 0.017	5733.4 ^{ns}	988.9 ^{ns}
W × Y	1	0.008**	136.8**	235.3**	0.003**	223.3**	24.8**
Error A	4	0.003	4.9	135.8	0.005	93.2	71.3
Genotype (G)	29	0.003**	78.2**	782.8**	0.016**	261.5**	330.8**
G × Y	29	0.003**	96.5**	302.6**	0.008**	374.7**	93.7**
G × W	29	0.001**	13.47**	82.16**	0.008**	127.29**	44.56**
G × W × Y	29	0.001**	9.63**	62.13**	0.007**	224.52**	94.46**
Error B	232	0.001	6.98	30.85	0.004	38.40	19.67

ns, * and **: Non-significant and significant at 5% and 1% levels of probability, respectively.

TABLE III
GENETIC VARIANCE (σ_g^2), PHENOTYPIC VARIANCE (σ_p^2), GENOTYPIC COEFFICIENT OF VARIATION (GCV), PHENOTYPIC COEFFICIENT OF VARIATION (PCV) NARROW SENSE HERITABILITY AMONG LINES (h^2), AND EXPECTED GENETIC ADVANCE (GA) FOR THE TRAITS UNDER STUDY FOR 28 RECOMBINANT INBRED LINES OF WHEAT AND TWO PARENTAL VARIETIES EVALUATED AT TWO WATER REGIMES AND TWO YEARS

Trait	σ_g^2	σ_p^2	GCV%	PCV%	h^2	GA	GA (% of the mean)
Spike length	0.08	0.13	3.22	4.28	0.57	0.36	4.23
Kernel number per spike	3.62	5.10	5.62	6.87	0.71	2.81	8.29
1000-grain weight	8.19	9.39	7.32	7.84	0.87	4.66	11.92
Grain yield	699.71	1397.39	6.91	9.76	0.50	32.71	8.54
Biomass	3912.81	9362.64	5.87	9.08	0.42	71.12	6.66
Harvest index (%)	6.93	12.35	7.32	9.78	0.56	3.44	9.57

IV. CONCLUSION

Evaluation of 28 recombinant inbred lines of wheat developed from the cross of Norstar and Zagross varieties at normal and water stress conditions over two years showed significant genetic variation and genotype by environment interaction for all traits. Moderate genetic gain for most of the characters indicated the possibility of selection among the lines under study.

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