International Journal of Plant Breeding *©2013 Global Science Books*

Genetic Analysis and Selection for Bread Wheat (*Triticum aestivum* L.) Yield and Agronomic Traits under Drought Conditions

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ABSTRACT

The climate is changing all over the world, particularly in semi-arid and arid regions. This changing climate could strongly affect wheat production worldwide. As the world population continues to grow, and water resources for crop production decline and temperature increases, so the development of heat- and drought-tolerant cultivars is an issue of global concern. In this context, two cycles of selection were employed in the F_2 generation of a cross between bread wheat (*Triticum aestivum* L.) 'Long spike 58' and 'Giza-168' to assess the impact of selection on grain yield in response to drought. Family selection and within-family selection were adopted in the second cycle of selection. The observed response to selection for grain yield was 64.66% in the F_3 generation and 18.14 and 12.39% in the F_4 generation for family and within-family selection, respectively. The mean grain yield of F_3 selections exceeded that of two standard cultivars ('Giza-168' and 'Sids 12') by 19.67 and 16.48%, respectively, while the mean of F_4 selections exceeded that of the two standard cultivars by 15.08 and 35.53%, respectively. Significant positive correlations were obtained for 1000-grain weight (32.34), number of kernels spike^{-1} (24.8) and spike length (12.55) in the F_3 generation but not in the second cycle of selection. Generally, the observed responses to selection were greater than the predicted responses indicating the presence of dominant gene effects for the traits studied.

Keywords: correlated response, family selection, observed response, predicted response

Abbreviations: CR, correlated responses; **F**, family selection; **GMP**, genotypic mean; **HSI**, heat stress susceptibility index productivity; **I**, within, family selection; **MP**, mean productivity

INTRODUCTION

Climate change is going to have a drastic impact on dryland ecosystems and its almost 2.5 billion inhabitants (Anderson and Morton 2008). All the climate models used by the IPCC suggest that the dry areas will become dryer and more water stressed (IPCC 2001, 2007) due to increasing temperature, decreasing rainfall and humidity. The dryland areas (40% of world land surface) are home to over 2 billion people, accounting for 35% of the world's population, some 55% of dryland inhabitants live in rural areas, more than 90% of dryland inhabitants are in the developing world and 70% in rural areas while approximately half of the poorest people in the world live in dry areas (Millennium Ecosystem Assessment 2005).

The direct effects of climate change will be through changes in temperature, rainfall, length of growing season and timing of extreme and critical threshold events relative to crop development. In the dryland of tropics and subtropics, where crops are near their maximum temperature tolerance level, yield will decline (El-Beltagy and Madkour 2012).

Desertification and climate change will greatly impact plant biodiversity. Traditionally, gene banks in different institutions have collected, evaluated and conserved plant germplasm under short- and long-term storage conditions (El-Beltagy and Madkour 2012). With the initiative of the Scandinavian countries and the Global Crop Diversity Trust, the conservation efforts have moved further to store germplasm in facilities created in the arctic permafrost (El-Beltagy and Madkour 2012). The idea is to have valuable and diverse genes of important species conserved for posterity and to provide resources for developing cultivars that might adapt to new eco-environments (El-Beltagy 2008). The development of new plant varieties with low-water requirements, better water-use efficiency and the production of drought-tolerant varieties can help increase food production.

Among the dryland countries, Egypt is the largest importer of wheat in the world, with Algeria not far behind. Together, they import more grain than all of South America (Stecker 2011). This is because most land in Egypt are deserts (Khieralla *et al.* 2011). Newly reclaimed soils in these deserts suffer from various stresses such as drought, salinity, nutrient deficiency, etc. (El-Fouly *et al.* 1984). On the other hand, population increase in Egypt is taking place at an alarming rate of 2.52-8%/annum (Khieralla *et al.* 2011). This tremendous increase in population is one of the most serious challenges the country now faces. Therefore, it is imperative to increase the yield per unit area of various crops by developing high-yielding cultivars suitable for sowing on poor soils and under stress conditions as well as the development and application of improved cultural practices.

Drought, the result of low precipitation or high temperature, is thus one of the main problems underlying the success of modern agriculture around the globe and is one of the most important environmental factors that affect the growth, development and production of plants (Hasanuzzaman *et al*. 2012; Hossain *et al*. 2012a, 2012b). Drought is a non-uniform phenomenon that influences plants differently depending on the development stage at the time of its occurrence (Martiniello and Teixeira da Silva 2011; Hossain

Received: 7 January, 2012. Accepted: 14 November, 2012.

Original Research Paper

et al. 2012a, 2012b).

Optimal crop growth requires a non-limiting supply of water, nutrients, and radiation; as temperatures rise, the demand for growth resources increases due to higher rates of metabolism, development, and evapotranspiration (Rawson 1988). When growth resources are limited by stress (drought and high temperature), the size of plant organs such as leaves, tillers, and spikes, is reduced (Martiniello and Teixeira da Silva 2011; Hossain *et al*. 2012c, 2012d, 2012e). The apparent sensitivity of metabolic processes to stress (drought and high temperature) in the field (Reynolds *et al*. 2000), coupled with the reduced length of the life cycle at high temperatures (Hakim *et al*. 2012; Hossain *et al*. 2012c, 2012d, 2012e), results in low grain yield with lower total plant biomass in hot environments.

However, the adverse effect of drought on a crop can be minimized by avoiding stress at the most sensitive stages of crop development such as reproductive and grain-filling periods (Hossain *et al*. 2012a). Abiotic stresses are unpredictable and the best way to cope with them is to develop tolerant varieties that perform well under stress and under optimum environments (Prasad *et al*. 2008; Nouri *et al*. 2011; Hossain and Teixeira da Silva 2012). For this purpose, however, a thorough understanding of genotypic and phenotypic responses of plants to drought stress, mechanisms of drought tolerance and possible strategies for improving crop drought tolerance is imperative.

Therefore, the aim of the present study was to identify wheat lines which are suitable for cultivation in drought conditions by understanding genotypic and phenotypic variation through genetic analysis and selection.

MATERIALS AND METHODS

Field trials

The experiment was conducted over two seasons (2009-2010 and 2010-2011) at the research farm of South Valley University, Qena, Egypt to observe the genotypic and phenotypic variation of spring wheat under drought stress. The plant material used in this study consisted of 100 F_2 plants derived from a cross established between 'Long spike 58' and 'Giza-168'. In the 2008-2009 season, seeds of 100 plants were sown on 30 November at the experimental farm of South Valley University. Stress conditions were imposed by 16.5% moisture deficient in sandy calcareous and infertile soil. Soil salinity before planting was 8.4 ds/m and after planting it was 4.2 ds/m. The pH of the soil was 8.4. Single plants were grown 30-cm apart, equally-spaced, with an inter-row distance of 50 cm. The eight highest yield segregates were selected because the predicted response to selection depends upon small selection intensity and high heritability; on the other hand, when selection intensity was small, the predicted response was greater to form F_3 selected families with a selection intensity of 8% (calculated by number of selected plants/all plants), and an equal number of seeds were pooled from plants so as to form the F_3 bulk. The 8 F_3 selected families, together with the F_3 bulk and two check varieties namely, 'Giza-168' and 'Sids 12', were sown on 30 November in the next season. Each family was represented in each block by 10 plants with a row-to-row spacing of 50 cm and a plant-to-plant distance within rows of 30 cm. Six highest families from 8 F_3 selected for grain yield were saved for the next season as family selection. Meanwhile, 5/240 plants were selected based on yield (individual selection) to form F_4 selected families in the next season (an intensity of 2.08%). In the 2010-2011 experimental season, seeds of the F_4 selected families along with their relevant F_4 bulk and two check varieties were planted on the sowing date, i.e., 29 November. Each family was represented in each block by 10 plants with a row–to-row spacing of 50 cm and plants within rows were 30 cm apart. Experiments were conducted by randomized complete block design (RCBD) with three replications, both two seasons.

Data collection

At full maturity, grain yield plant^{-1} (GYP), 1000-grain weight (1000-GW), number of kernels (NK) and spike length (SL) were recorded for each individual plant according to standard methods. To obtain the actual yield of all varieties, grain yield weight was adjusted at 12% moisture by the following equation (Hellevang 1995):

$$Y(M_2) = \frac{100 - M_1}{100 - M_2} \times 100$$

where Y (M_2) = weight of grain at expected moisture percentage (generally 12% for wheat); Y (M_1) = weight of grain at present moisture percentage; M_1 = present moisture percentage; M_2 = expected moisture percentage.

Statistical procedures

Characters are often correlated, i.e., the phenotypic value of one character in an individual is correlated with the phenotypic value of another character on that individual. These correlations can also be due to environmental effects or genetic effects. The genetic causes of correlation are pleiotropy (genes affect more than one character) and genetic linkage. This needs not be constant across genes: some genes can cause positive pleiotropy and others negative pleiotropy; the balance determines the genetic correlation of two characters. These genotypic and phenotypic variations, due to the effect of the environment, can be identified by the following ways:

1. Expected response to selection

In our present research, expected response to selection (R_x) was estimated by the following equation, stated by Plomin *et al.* (1989):

$$R_x = i\,h^2\,\sigma\,p$$

where i = standardized selection differential; σ p = phenotypic standard deviation; h^2 = heritability.

For example, imagine that a plant breeder is involved in a selective breeding project with the aim of increasing the number of kernels/ear of corn. For the sake of argument, let us assume that the average ear of corn in the parent generation has 100 kernels. Let us also assume that the selected parents produce corn with an average of 120 kernels ear^{-1}. If h^2 equals 0.5, then the next generation will produce corn with an average of 0.5 (120-100) = 10 additional kernels/ear. Therefore, the total number of kernels/ear of corn will equal, on average, 110.

2. Correlated response to selection

Selection of one trait will often result in the response of another trait. This is genetic correlation. It is caused by changes in the breeding value of the selected trait being correlated with changes in the breeding value of the other trait. Selection of one trait can cause an apparent selection differential of another trait, because of both genetic and environmental correlations. This is a particularly huge problem when studying natural selection in natural conditions.

In our present research, the indirect response to selection (CR_x) was calculated accurately according to the formula of (Falconer 1989):

$$CR_x = i\,h^2\,\sigma\,p\,r_{xy}$$

where r_{xy} is the genetic correlation between the selected trait and unselected trait; i = standardized selection differential; σ p = phenotypic standard deviation; h^2 = heritability.

3. Heritability (broad sense)

Any particular phenotype can be modeled as the sum of genetic and environmental effects:

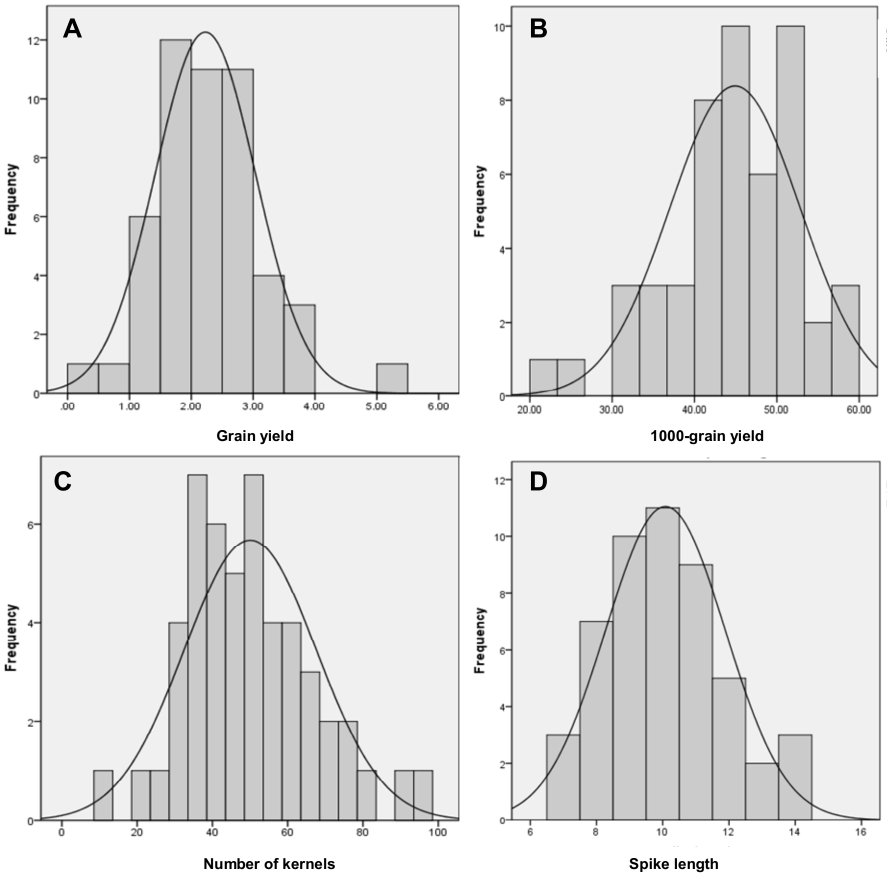

Fig. 1 Distribution of 100 F_2 plants for (**A**) grain yield, (**B**) 1000-grain weight, (**C**) number of kernels, (**D**) spike length. Mean = (**A**) 2.23; (**B**) 44.92, (**C**) 50.04, (**D**) 10.08. SD (standard deviation) = (**A**) 0.813, (**B**) 7.93, (**C**) 17.567, (**D**) 1.805. n = 50.

Phenotype (*P*) = Genotype (*G*) + Environment (*E*).

Likewise, the variance in the trait – Var (P) – is the sum of genetic effects as follows:

Var (*P*) = Var (*G*) + Var (*E*) + 2 Cov (*G*,*E*).

Heritability is defined as, according to the following equation (Mather and Jinks 1971):

$$h^2 = \frac{Var(G)}{Var(P)}$$

h^2 is broad-sense heritability. This reflects all the genetic contributions to a population's phenotypic variance including additive, dominant, and epistatic (multi-genic interactions), as well as maternal and paternal effects, where individuals are directly affected by their parents' phenotype (such as with milk production in mammals).

4. Genetic correlation and phenotypic correlation

The phenotypic correlation (r_p) is an expression of the observed relationship between the phenotypic performances of different traits while the degree of association between genes responsible for the additive variance of different traits is measured through genetic correlation (r_g). Genetic correlations inform that genes affecting one trait also affect other traits. The effectiveness of selection and net genetic progress can be measured when selection is made for more than one trait (Javed *et al*. 2004).

r_g and r_p were estimated according to Miller *et al*. (1958):

$$r_g = {}^{\sigma g1.2}\sqrt{\sigma^2\ g_1 \times \sigma^2 g_2}$$

where $\partial g1.2$ is the genetic covariance between traits 1 and 2 and $\sigma^2 g_1 \times \sigma^2 g_2$ are the genetic variation of 1 and 2, respectively.

$$rp = {}^{\partial p1.2}\sqrt{\partial^2\ p1 \times \partial^2\ p2}$$

where $\partial p1.2$ is the phenotypic covariance between traits 1 and 2 and $\partial^2 p1 x\ \partial^2 p2$ are the phenotypic variation of 1 and 2, respectively.

5. Student's t-test

A student's *t*-test (*t*) was calculated according to the following formula stated by Gosset (1876):

$t = X^{-} - \mu / s_{x^-}$.

RESULTS

Variation in agronomic characters

1. Grain yield plant^{-1}

Based on GYP of 100 F_2 plants, the distribution was continuous and normal, indicating the quantitative and polygenic nature of the system controlling that character (**Fig. 1A**). The range of GYP of the F_2 plants ranged from 0.41 to 5.00 g with an average of 2.23 g. However, the *t*-test (**Table 1**) was highly significant indicating that genetic variation among F_2 plants was operating. The phenotypic correlation between GYP and SL was positive and significant but rather weak (r = 0.35).

2. 1000-grain weight

The distribution of 100 F_2 plants was continuous with skewness to the right indicating an abundance of very high 1000-GW among that array (**Fig. 1B**). The 1000-GW of the F_2 plants ranged from 23.25 to 59.09 (g). The differences between F_2 plants were significant according to the *t*-test (**Table 1**). The phenotypic correlation between 1000-GW and GYP was weak (r = 0.18).

Table 1 *t* values for studied traits of F_2 plants.

Traits	t	df	Standard error	significant
Spike length	60.94	99	0.17	0.00
Number of kernel	33.59	99	1.61	0.00
Grain yield	25.98	99	.009	0.00
1000-grain weight	66.95	99	.68	0.00

3. Number of kernels spike^{-1}

The distribution of the 100 F_2 plants for NKS was continuous and normal indicating a polygenic type of genetic control for this character (**Fig. 1C**). NKS ranged from 11 to 96 with an average of 50.04. The *t*-test revealed highly significant differences between F_2 plants (**Table 1**).

4. Spike length

The distribution of 100 F_2 plants for SL was continuous and normal indicating a polygenic type of genetic control (**Fig. 1D**). The mean of SL ranged from 7 to 14 cm with an average of 10.08 cm. According to the *t*-test, differences among entries were highly significant (**Table 1**).

Response to selection of the F_3 families for grain yield

The means of grain yield of the F_3 selected families, F_3 random families and the two check varieties with observed response to selection are described in **Table 2**. ANOVA revealed significant differences between the 11 entries as well as significant differences between F_3 selected families. A significant positive response to selection was obtained in the F_3 selected families for GYP (**Table 3**). The observed response to selection was 64.66%. The observed response to selection for GYP was greater than the predicted response (1.03), indicating that dominance gene effects are involved in the inheritance of that trait. The means of the high selections exceeded those of 'Giza-168' and 'Sid 12' by 19.67 and 16.48% on average, respectively. The heritability in broad sense estimate was 0.73.

Correlated response to selection for grain yield

1. 1000-grain weight

Generally, the correlated response to selection for GYP in 1000-GW, NKS and SL was positive and significant (**Table 2**). The observed correlated response was 32.34% on average. The significant positive correlated response in the F_3 generation could be attributed to the positive genetic correlation between GYP and 1000-GW (r = 0.96). The observed correlated response in 1000-GW was greater than the predicted correlated response indicating that dominance gene effects were operating (**Fig. 1B**). For 1000-GW, the F_3 selections exceeded those of 'Giza-168' and 'Sids 12' by 9.33 and 1.56%, respectively. The heritability estimate was 0.073.

2. Number of kernels spike^{-1}

The observed correlated response for NKS was positive and significant (24.8). In contrast, the observed correlated response in NKS was equal to the predicted response indicating that additive gene effects are involved in the inheritance of NKS. For NKS, the F_3 selections exceeded those of 'Giza-168' and 'Sids 12' by 10.22 and 14.38%, respectively. The significant positive correlated response in the F_3 generation of NKS could be attributed to the positive genetic correlation between GYP and NKS (r = 0.97). The heritability estimate was 0.78.

3. Spike length

Here too, a significant positive correlated response to selection for GY in SL was obtained, 12.25% (**Table 2**). Dominant gene effects were operating since the observed correlated response (12.25) was greater than the predicted response (2.60) (**Table 2**). The genotypic correlation between GYP and SL was high and positive (r = 0.94). The heritability estimate was 0.80.

Response to selection of the F_4 families for grain yield

The means of GYP of the F_4 selected families, random families and the two check varieties with observed correlated responses are given in **Table 4**. The data in **Table 5** reveals significant differences between the 14 entries, while between F_4 selected families, differences were not significant. The observed response to selection for GYP was positive but not significant. Moreover, the observed response to selection for GY was 18.14 in the F_4 family selection, while in the F_4 individual selection, it was 12.39 (**Table 4**). Generally, the observed response to selection was greater than the predicted response, confirming the predominance of dominant gene effects. In our research, F_4 family selection of 'Giza-168' and 'Sids 12' was exceeded by 15.08 and 35.53%, respectively, while individual selection was exceeded by 9.48 and 28.93%. These findings indicate that family selection might be more profitable in effecting a direct response for GY. Broad sense heritability was 0.46.

Correlated response to selection for grain yield (second cycle)

1. 1000-grain weight

The CR of 1000-GW for selection of GYP was positive (**Table 4**). In the second cycle, for the family selection, the observed correlation response was 14.51, but within family

Table 2 Means of grain yield 1000-grain weight, number of kernels and spike length of F_3 selected and random and two check cultivars with heritability.

Generation	Grain yield			1000-grain weight			Number of kernel			Spike length		
	Mean	obs %	P %	Mean	C.R %	P %	Mean	C.R %	P %	Mean	C.R %	P %
Giza-168	1.83			39.74			45.66			10.33		
Sids-12	1.88			42.78			44.0			10.33		
F_3 random	1.33			32.83			40.33			9.00		
F_3 selected	2.19	64.66	1.03	43.45	32.34	6.11	50.33	24.8	22.04	10.13	12.55	2.60
H^2		0.73			0.66			0.78			0.80	

Table 3 The analysis of variance of F_3 random and selected families in the 2009-2010 season.

Items	Grain yield	1000-grain weight	Number of seeds	Spike length
Among entries	0.55 *	49.46 **	200.13 **	2.60 **
Among F_3 selected	0.48 **	25.07 **	233.71 **	3.14 **
F_3 selected vs F_3 random	1.95 **	300.442 **	266.60 **	3.37 **
Error	0.09	8.50	38.60	0.49

* significant at 5% level of probability
** significant at 1% level of probability

Table 4 Means of grain yield, 1000-grain weight, number of kernel and spike length of F_4 selected random and two check varieties with heritability.

Generation	**Grain yield**			**1000-grain weight**			**Number of kernel**			**Spike length**		
	Mean	**O%**	**P %**	**Mean**	**C.R %**	**P %**	**Mean**	**C.R %**	**P %**	**Mean**	**C.R %**	**P %**
F_4 Random	2.26			41.82			50.00			10.33		
F_4 selected (F)	2.67	18.14	0.25	47.89	14.51	4.35	56.50	13.00	8.23	11.50	11.33	0.53
F_4 selected (i)	2.54	12.39	0.76	47.10	12.62	13.18	55.80	11.60	24.91	12.20	18.10	1.45
Giza-168	2.32			42.96			54.33			10.33		
Sids-12	1.97			36.16			54.60			10.31		
H^2		0.46			0.61			0.59			0.42	

Table 5 Pertinent Ms of the different items of the analysis of variance of the F_4 families with two varieties in the 2010-2011 season.

Items	**Grain yield**	**1000-grain weight**	**Number of kernel**	**Spike length**
Among entries	0.70*	88.50*	341.30*	4.80**
Among F_4 selected (F)	0.51 ^{NS}	103.78*	401.96*	0.23 ^{NS}
Among F_4 selected (i)	0.73 ^{NS}	51.54 ^{NS}	593.93*	2.43 ^{NS}
F_4 selected vs F_4 bulked (F)	0.48 ^{NS}	94.90 ^{NS}	108.65 ^{NS}	3.50
F_4 selected vs F_4 bulked (i)	0.06 ^{NS}	17.95 ^{NS}	31.50 ^{NS}	0.07 ^{NS}
Error	0.26	29.10	123.40	1.00

* significant at 5% level of probability
** significant at 1% level of probability
Ns non significant

selection it was 12.62% (**Table 4**). The observed selection response was higher than the predicted response (4.35) in the family selection indicating the presence of non-additive gene effects, but the reverse was true within family selection. The F_4 selections (family selection) exceeded those of 'Giza-168' and 'Sids 12' by 13.32 and 32.65%, respectively while the selections in the F_4 generation within family selection exceeded those of 'Giza-168' and 'Sids 12' by 9.63 and 30.47%, respectively. The heritability estimate was 0.61.

2. Number of kernels spike^{-1}

A positive CR to selection for GY was obtained for NKS (**Table 5**). The observed correlated response in NKS ranged from 11.60 for within-family selection to 13.00% for the family selection in the F_4 generation (**Table 4**). Generally, the observed response (O) was higher than the predicted response (P), indicating than non-additive gene effects were operating. In the F_4 generation, the F_4 selection exceeded that of 'Giza-168' and 'Sids 12' by 3.99 and 3.47%, respectively with the family selection while the individual selection was exceeded by 2.76 and 2.19%, respectively. The heritability estimate was 0.59%.

3. Spike length

The observed CR in SL was neither significant, nor positive (**Table 5**). In the F_4 generation, the observed response was 11.50% with family selection and 12.20% with individual selection. Across the board, the observed response was greater than the predicted response confirming the presence of non-additive gene effects. Broad sense heritability was 0.42%. Genetic improvement of GYP was obtained after two cycles of selection.

DISCUSSION

Genetic variation for different agronomic traits

The distribution of F_2 plants was continuous and normal for GY, NKS. While for 1000-GW with skweness to the right indicating the abundance of very high 1000-GW. Significant and high genetic variation was observed between F_2 plants for all studied traits. The findings of our present study are similar to the following previous studies: Dere *et al.* (2006) showed that the genetic dominance variance was significant for GY. Sing and Rana (1989) and Mostafavi (2005) reported that inheritance of grain yield GY spike^{-1} in bread wheat controlled genetically by additive and non additive gene. The diallel analysis revealed that non additive gene effects were important than additive gene effects in the inheritance of GYP, NG and 1000–GW (Motowea 2006). Amein (2007) found that the additive gene effects was significant positive in magnitude confirmed, it play the major role in controlling the genetic variance in NKS and SL, but the dominance gene effects was for GY and 1000-GW. He also revealed the highly significant differences of the recombinant inbred lines for all studied traits. Wang *et al.* (1997) found that 1000-GW fitted and additive dominance model with dominant genes in positive effects and recessive genes having negative effects and such trait exhibited mainly dominant effects. The genetic system controlling GY is dominance gene effects reported by Hassan (2006). Significant genotypic differences were manifested in for all studied traits, indicating a considerable amount of variation among genotypes. High heritability estimates were recorded for SL, NSS and days to 50% flowering (Ullah *et al.* 2011). Heat or salt tolerance genotypes can be improved by genetic variation between genotypes through selection under stress (Yildirm and Bahar 2010). The analysis of variance has indicated that there are significant differences between genotypes in order to use in improvement plants (Ahmadizadeh 2011).

Effect of drought stress on genotypic and phenotypic characters of wheat

Combined analysis variance indicated that there were significant differences among the genotypes in their GY, 1000-GW, peduncle length, plant height, number and weight grain spike^{-1} and harvest index (Nouri-Ganbalani *et al.* 2009). Under normal irrigation no significant correlation was observed between the GY and other morphological characters, but under the drought stress conditions there were positive highly significant correlations between the GY and the 1000-GW and number of tillers plant^{-1} (Nouri-Ganbalani *et al.* 2009). Results showed that in comparison with other drought stress treatments, imposing drought stress at the start of stem elongation stage through the ripening stage (1) had most impact on reducing the yield of wheat cultivars. In different growth stages, different genotypes respond to moisture stress and irrigation discontinuance differently (Shamsi and Kobrace 2011). In another study, 1000-GW, grains spike^{-1} and GY were decreased by water limitation. Despite of their significant differences ($P < 0.05$) in 1000-GW, spikelets spike^{-1} and grains spike^{-1}, but GY of wheat cultivars was not significantly different. Bahar Bilge *et al.* (2008) studied the effect of canopy temperature depression (CTD) on GY and yield components in bread and durum wheat. Their results revealed that CTD of bread wheat ranged from 0.22 to 0.57°C. On the other hand, CTD average values of durum wheat genotypes changed 0.63 to 1.23°C. This study showed that durum wheat was cooler than bread wheat in high temperature conditions. In addition, CTD was positively correlated with GY spike^{-1} and grain numbers spike^{-1} and CTD can successfully as a selection in breeding programs.

Response to selection

1. Direct response to selection

Significant positive response to selection for grain yield under drought stress was 64.66 in F_3 generation, 18.14 in F_4 generation of family selection and 12.39% within family selection. These results were in agreement with those obtained by Geber-Martin and Latter (1996) who found that simultaneous improvement of grain yield in F_3 and F_4 populations' spring wheat and Gadio (2010) using recurrent selection for improving grain yield. Genotypes Toos and 4057 were selected for higher GY both in stress and non stress conditions and they were identified as the most tolerant genotypes to drought (Mollasadeghi and Dadbakhsh 2011).

The observed response to selection for GY was greater than the predicted response indicating that dominance gene effects are involved in the inheritance of that trait. Apparently, the additive genetic variation for GY was not depleted after the two cycles of selection. The fact that the observed responses were greater than expected response in grain yield indicated that the genes with dominance effects were involved in the genetic controlling of GY. The above finding of our present study was similar to Manoochehr *et al.* (2010), who stated that the plant breeding selection has increased grain yield through decrease of plant height and the increase number of grains spike^{-1} was high in modern varieties than older ones. Pedigree selection for the two cycles (F_3 and F_4 generations) in each environment showed a 25 and 25.54% increase in GY over the bulk samples for normal and drought stress conditions, respectively, as compared to 22.6% for selection over environments (Ali 2011). Response to selection was evaluated in two crosses under drought stress (Venuprasad 2011). Who found that stress selected lines had a yield advantage of 25 to 34% over random lines when evaluated at stress levels similar to those in which they were selected. Yield gains under very severe stress occurred only in population derived from highly tolerant parent. Direct selection usually gave greater response under stress than indirect selection under non-stress conditions. In wheat selection for large size and visual head selection produced later heading, tall or high yielding plants than other selection methods. Larger number of F_4 selected lines in top yielding 5 and 25% within each cross was chosen by visual selection and by selection for large size (Nass 1987).

Direct selection for GYP in F_2 was carried out and yield per line in F_3 was evaluated under contrasting environmental conditions in France, Syria and Tunisia. Results revealed that some F3 lines were higher yielding than improved durum wheat varieties Chan1 and ONrabis under both stressed (Aleppo) and favorable (Montpellier) environmental conditions. Results indicated the use of modified bulk breeding method is promising not only for increasing durum wheat yield in drought prone environments, but also for improving durum wheat yield stability across contrasting environments (Alhakimi *et al.* 1998). A 15% increase in yield was observed after 2 cycles of recurrent selection for grain yield. Despite the fact that harvest index was not used in the selection protocol, there was a significant increase 11.4% in c_2 with respect to c_0 (Maich *et al.* 2000).

2. Indirect response to selection

The positive CR in number of NKS, 1000-GW and SL by selecting for GY could be attributed to the strong positive correlations found between GY and NKS, 1000-GW and SL. The results of Mostafa Ahmadizadih (2011) showed the GY's positive and significant correlation with number of grains spike^{-1}, 1000-GW and harvest index. The positive correlated response was 25.23% in 1000-GW. The mean of 1000-GW of recombinant inbred lines selected for high grain protein percentage exceeded that of Giza-168 and Saha 69 by 11.05 and 25.74 g (Amein *et al.* 2007). Selection for cell membrane thermostability (CMS) in F_3 generation did not produce correlated response in GYP under either favorable or drought stress conditions. Positive and significant correlated responses to selection for high CMS in the F_4 were obtained in 1000-GW in the five populations under combined drought + heat stress condition, which was ranged from 5.01 to 7.53% with an average 6.45% (El Rawy *et al.* 2010). GY was positively correlated with spike weight, grain number spike^{-1} and biological yield under non stress and heat stress conditions (Mehmit Yildirin and Bahar 2010). The results obtained by Khliq (2004) showed that SL, number of grain spike^{-1} appeared to contribute to the GY, therefore direct selection for higher GY may be effective for improving these characters. Accordingly to the results of Bhutta (2006) the correlation and path analysis of GY and its component in promoting wheat lines revealed that there is strong positive association of GY with number of tillers and number of spikes plant^{-1}. Dogan (2009) found that the grain number spike^{-1}, 1000-GW, plant height and test weight had significant direct effect on GY. It was concluded that these characters could be important selection criteria in durum wheat breeding for GY. GY was positively correlated genetically with days to maturity, tillers m^{-2} and number of grains spike^{-1}. Negative correlation of GY was observed with plant height, SL, peduncle length and 1000-GW. The characters such as days to maturity, tillers m^{-2}, number of grains spike^{-1} having positive direct effect along with positive genotypic correlation on GY are considered to be suitable selection criteria for the development of high yielding genotypes (Khan *et al.* 2010). Wicrsma *et al.* (2001) studied the recurrent selection for kernel weight in spring wheat. About 20 F_2 plants, with the highest kernel weight were selected (2% of the population) and about of three of their F_3 progeny were intermated to form the next cycle. This procedure was repeated for eight cycles, with an average of 60 crosses per cycle. The observed gain from selection and heritability estimates point to control by several genes with smallest effects. Kernel weight increased linearly at about 4.5% cycle^{-1}. Cycle mean did not differ for plant height and grain yield, but tillers m^{-2} and NKS decreased 2.4 and 1.6% cycle^{-1}, respectively. Heat or salt tolerance genotypes can be improved by selection breeding due to genetic variation among genotypes (Yildirim and Bahar 2010). Correlation between the GY spike^{-1} was positive and significant with 1000-GW in normal condition ($r = 0.562$). On the other hand an increase of substance weight in grain filling time causes decrease in the amount of substances transfer to the productive part of the plant, consequently it results in yield decrease in drought stress conditions (Dadbakhsh *et al.* 2012). Okuyama *et al.* (2005) revealed that yield per spike correlated positively with SL. Path coefficient analysis indicated that under irrigated and non-irrigated conditions, yield per spike had a positive direct effect and a positive correlation with SL.

CONCLUSION

From the results obtained in this work, it can be concluded that selection was effective in improving the grain yield under drought conditions has always been important target for enhancing productivity. Also selection was effective to produce new lines with highest yield resistant to drought.

ACKNOWLEDGEMENTS

This work was supported by the experimental farm of South Valley University by means of technical assistance with agricultural practices and yield measurements in the lab.

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