RELATIVE RESPONSE OF SELECTION FOR GRAIN YIELD AND ITS COMPONENTS ON ONE BREAD WHEAT CROSS (*Triticum aestivum* L.)

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ABSTRACT

The present work was performed at the Faculty of Agriculture, Cairo University, Agriculture Experiment and Research Station over three seasons (2010/2011, 2011/2012 and 2012/2103) in Egypt to study the variability and relative response to selection in one bread wheat cross (L-53 X V99/17) for two cycles started in the F_2 using the pedigree selection procedure in improving grain yield and its components. Result of analysis of variance revealed significant ($p \leq 0.05$) and highly significant ($p \leq 0.01$) differences among genotypes (families + parents) for all studied traits across the three generations (F_2, F_3 and F_4), so a great response to selection can be expected. Results of variability for grain yield plant^{-1} revealed that the magnitude of phenotypic and genotypic variances were decrease through generations. However, for grain yield plant^{-1} the actual gain as percentage of cross mean was higher than the predicted one, through cycle 1 and 2 suggest that the gene action involved in cycle 1 and 2 largely additive.

Keywords: Triticum aestivum L., heritability in broad sense, phenotypic and genotypic coefficient of variability, predicted and actual gain of selection, yield and its components.

INTRODUCTION

Wheat is the world's most important and most widely grown cereals crops. Its importance is derived from many properties and uses of its grains, which makes it staple food for more than one third of world's population (Poehlman, 1987).

Egypt retains the pride of place as the world's largest importer of wheat ahead of Brazil, the EU-27 and Indonesia. Egypt is now the world's 7th largest consumer of wheat and also the world's 17th largest producer. (Analyzing Agriculture, Egypt Wheat Data Analyses: May 2012).

Increasing grain of cereal crops is an important national goal to face the increasing food needs of Egyptian population. Wheat production in Egypt increased from 2.08 million ton in 1982/1983 to 9.42 million ton in 2012/2013 seasons. This increase was done by both increasing wheat area (from 554,400 to 1,291,000 hectares) and the continuous rise in grain yield ha^{-1}. However, increase in area planted to wheat in Egypt meet with difficulties; but increasing the production per unit area appears to be the applicable solution to reducing the wheat gap. This can be done through continuous developing high-yielding and early maturing genotypes and these genotypes must be directed into intensive cropping system practiced in Egypt.

Individual plant selection in early segregating generations for grain yield has meet with low achievements due to several factors such as low heritability, high environmental effects, linkage and dominance gene effects. The most frequent reasons given for this failure in wheat include the inability to identify useable genetic variation and a large environment effect (Rezqui, 1993).

The high heritability associated with high genetic advance for main quantitative traits in wheat offer better scope of selection of genotypes in early segregating generations (Memon et al., 2005). In this regard heritability estimates plays an important role for planning the breeding strategy. The heritability of the trait determine the extent to which it is transmitted from one generation to the next and it is most valuable tool when used in conjunction with other parameters in predicting genetic gain that follows in the selection for that character (Baloch et al., 2003, Ansari et al., 2004, El-Ameen et al., 2013). The heritability values become a measure of the genetic relationship between parents and progeny; hence considerable research work has been carried out to

incorporate the desirable genes in present wheat varieties to increase the productivity of the crop (Gale and Youssefian 1985; Rebetzke and Richards 2000; Sial et al., 2002). Tammam and Abd EL -Rady (2010) found that Broad sense heritability values varied from intermediate to high for plant height and yield and its components.

Numerous methods have been proposed for wheat selection. Pedigree methods of selection are very common selection techniques in wheat crop. However, pedigree method has drawbacks due to high costs of record keeping, utilization of manpower, genetic drift and loss of desirable genes (Borghi et al., 1998). Results of Verma et al. (1997) and El-Ameen et al. (2013) showed that pedigree method of selection was more effective in improving grain yield and its components.

The present investigation was design to study the variability and relative response to selection in one bread wheat population for two cycles started in the F_2 using the pedigree selection procedure in improving grain yield and its components.

MATERIALS AND METHODS

Genetic materials and its culture

The experiment was conducted over three seasons (2010/2011, 2011/2012 and 2012/2103) at Faculty of Agriculture, Cairo University, Agriculture Experiment and Research Station, in Giza governorate (30.029°N 31.207°E), Egypt to study the relative response to selection in one bread wheat cross for two cycles started in F_2 using pedigree selection procedure for improving grain yield and its components. Also, identify genotypic and phenotypic variation of wheat cross through three generations. The plant material used in this study consisted of 300 F_2 plants derived from a cross established between 'Line 53 and V99/17. The pedigree and origin of the studied genotypes are listed in Table (1).

Table 1. Names, pedigree and origin of the studied parental genotypes

No.	Genotypes	Pedigree	Origin*
1	Line 53 (P$_1$)	KUZ*2/MNV//KAUZ	Egypt
2	V99/17 (P$_2$)	Not Available	Yemen

*Source: Plant Genetic Resources Research Department (Bahteem Gene Bank), FCRI, ARC-Egypt

Experiments layout

In 2010- 2011, 300 F_2 plants of cross L-53 X V99/17 with their parents were in a randomized complete block design with two replications on 20 November. Single plants were grown in rows 3 m long and 30-cm apart, equally-spaced, with an inter row distance of 10 cm. The 96 highest yield segregates plants were selected to form F_3 plants. At maturity, plants were individually harvested and threshed. Data were recorded for six characters (plant height, spike length, spikelets spike^{-1}, number of kernels spike^{-1}, number of spikes plant^{-1}, and grain yield plant^{-1}).

In 2011/2012, F_3 progenies of the selected F_2 plants for the cross L-53 X V99/17 with their parents were planted in single row plots in a randomized complete block design with two replications in rows 1.30 m long and spaced 30 cm apart and 10 cm between plants within rows. Within each F_3 row, 4 random guarded plants were measured for the studied traits.

In 2012/2013, for the cross L-53 X V99/17 a sample of 48 families (a family is the progeny of an individual F_2 plant), each represented by two lines (a line is the progeny of an individual F_3 plant) were they grown in a randomized complete block design with three replications, single rows plots were as in the previous year.

Biometrical procedures

Keeping in view the objectives set out for the study, the following statistical tools and methods have been deployed.

Analysis of variance (ANOVA)

Analysis of variance (Table 2) were conducted for the cross L-53 X V99/17 in F_2, F_3 and F_4 generations to determine the differences among genotypes according to the methods outlined by Snedecor and Cochran (1967). The data were statistically analyzed by MSTAT-C V.2.1 (Russell, 1994).

Table 2. The analysis of variance (ANOVA) showing expected mean squares.

Source of variation	df	Mean Squares (MS)	Expected mean Squares (EMS)
Replication	r – 1	M$_3$	$\sigma^2_e + g\,\sigma^2_r$
Genotypes	g – 1	M$_2$	$\sigma^2_e + r\,\sigma^2_g$
Familles	f-1		
Parents	p-1		
Parents Vs Familles	1		
Error	(r –1) (g –1)	M$_1$	σ^2_e

Where σ^2_g and σ^2_e are the genetic and environmental variances, respectively.

Estimation of heritability in broad sense (h^2_{bs})

Heritability in broad sense (h^2_{bs}) was estimated using the components of variation according to the formulae outlined by Weber and Moorthy (1952) as following:

$$h_{bs} = \frac{\sigma^2_g}{\sigma^2_{ph}}$$

Where: $\sigma^2_g = (M_2-M_1)/r$ and $\sigma^2_{ph} = (\sigma^2_e/r) + \sigma^2_g$ are the phenotypic and genotypic variances.

Estimation of Phenotypic (PCV) and Genotypic (GCV) Coefficient of variability

Phenotypic (PCV) and genotypic (GCV) Coefficients of variation for the studied traits of each cross were calculated as described by Burton (1952) using the following formulae.

$$PCV = \frac{\sigma_{ph}}{\bar{x}} . 100 \qquad GCV = \frac{\sigma_g}{\bar{x}} . 100$$

Where: $\bar{x}$ is the general mean, σ_{ph} and σ_g are the phenotypic and genotypic standard deviations in the same rank and they estimated according to the following formula:

$$\sigma_{ph} = \sqrt{\sigma^2_g + \frac{\sigma^2_e}{r}} \qquad \sigma_g = \sqrt{\frac{(M_2 - M_1)}{r}}$$

Where: M_2 and M_1 are the mean square of genotypes and error, respectively.

Predicted and Actual gain of selection

The predicted and actual genetic gains were estimated using the method outlined by Frey and Horner (1955) as follow:

In cycle 1 the predicted gains of F_3 progenies derived from selected F_2 lines were obtained by multiplying the differential between the F_2 cross and parental sample means by the heritability percentage. The actual gain represented by the differential between the progeny of the selected parents and the F_2 cross mean.

In cycle 2 the predicted gains of F_4 progenies derived from selected F_3 lines were obtained by multiplying the differential between the F_3 cross and parental sample means by the heritability percentage. The actual gain represented by the differential between the progeny of the selected parents and the F_4 cross mean.

RESULTS AND DISCUSSION

Analysis of variance

Result of analysis of variance for the studied cross (L-53 X V99/17) is presented in Table 3. These results revealed significant ($p \leq 0.05$) and highly significant ($p \leq 0.01$) differences among genotypes (families + parents) for all studied traits across the three generations (F_2, F_3 and F_4). These results showed that a great response to selection can be expected. These results were similar to those obtain by McNeal et al. (1978), Ahmadi-zadeh et al. (2011) and El-Ameen et al. (2013). However, McNeal et al. (1978) reported that higher response to selection can be expected by selection in crosses with high phenotypic and genotypic variances and vise versa.

Mean values

Mean values of F_2 plants, F_3 and F_4 lines selected for yield and its components are shown in Table 4. The differences between the high and low mean values, in the F_2 generation ranged from 3.3 cm for spike length to 34.00 cm for plant height; whereas, in the F_3 generation, these values ranged from 3.45 cm for spike length to 38.00 for plant height. Mean while, in the F_4 generation, the differences between the high and low mean value ranged from 1.91 for No. of spikes plant^{-1} to 35.44 cm for plant height. These percentages were higher for grain yield than for any yield components in the F_2 generation. On the contrary, grain yield plant^{-1} was lower than any yield components in the F_3 and F_4 generations.. The presence of the differences between high and low suggested that selection would be effective in this cross. These findings were agreed with those obtained by Loffler and Busch (1982) and El-Ameen et al. (2013).

Variability

The most important item control the efficiency of selection and breeding methods is variances. Results of phenotypic variance (σ^2_p), genotypic variance (σ^2_g), broad sense heritability (h^2), phenotypic coefficient of variation (PCV %) and genotypic coefficient of variation (GCV %) are shown in Table 5. Results of plant height showed different values of phenotypic, genotypic variances and variability of PCV % and GCV % according to generations with high values for all variances in F_3. Similar results are obtained by Ortiz-Ferrara (1981) and Tammam (2004) .The importance of genetic components of variability controlling plant height rather than the environmental effects were obvious due to small differences between PCV % and GCV% as mentioned by Tammam (2004). Broad sense heritability estimates for plant height (Table 5) were 36.95, 95.00 and 15.22 and for F_2, F_3 and F_4, respectively. These results confirm that plant height was less affected by environmental factors especially in F_3.

Results of variances and variability for spike length and spikelets spike[-1] (Table 5), show that less values were detected through generations. These results are in harmony with the results obtained by Tammam (2004). Estimate of broad sense heritability for spike length was intermediate for spike length and spikelets spike[-1] through generations.

Variances and variability for No. of kernels spike[-1] and No. of spikes plant[-1] revealed that different values of variances and variability according to generations with high values for all variances in F_4. Similar results are obtained by Tammam (2004) .The importance of genetic components of variability controlling plant height rather than the environmental effects were obvious due to small differences between PCV % and GCV% as mentioned by Tammam (2004) and Tammam and Abd EL-Rady (2010). Broad sense heritability estimates for plant height (Table 5) were 49.11, 49.37 and 91.03 for F_2, F_3 and F_4, respectively. These results confirm that No. of kernels spike[-1] and number of spikes plant[-1] were less affected by environmental factors especially in F_4.

Results of grain yield plant[-1] (Table 5), revealed that the magnitude of phenotypic and genotypic variances were decrease through gereations. Similar results were reported by Tammam (2004). The variability of PCV % and GCV % were decrease of variability. These results revealed that selection reduce the range and variability for grain yield plant[-1] in the F_4. Difference between phenotypic, genotypic variances were high indicate that grain yield plant[-1] were affected by environmental factors and this is clearing in the high values of broad sense heritability for the two generations F_2 and F_3. At the other hand the values of variances, variability and heritability were low in F_4. These results are in agreement with those reported by Tammam 2004 and Tammam and Abd EL-Rady (2010).

High and low heritability across generation may be explained by Salem et al., 1983, where they reported that magnitude of heritability percentage appeared to be affected by four relevant factors a- methods of estimation b- cross and generation c- nature of measured traits and d- the magnitude of environmental variation. Also, Weber and Moorthy 1952 found that heritability for grain yield in the crosses was very erratic and average near zero. Such results indicate the need for better control of environmental variance and/or genotypic-environmental interaction.

Frey and Horner 1955 reported that heritability percentages calculated by the components of variance methods are usually based on data from one generation and year and then are applied to the next generation. Under such circumstances a great deal of discrepancy would be expected between the gain obtained in the F_5 and that predicted on the basis of the F_4 because of genotype-year interaction. Baker et al., 1968 mentioned that heritability is a measure of the effectiveness of the selection procedure. It is possible to visualize a situation where the heritability or effectiveness is high but because of little potential for improvement (i.e. low σ_{ph}) little response can be expected.

Response to selection

The actual versus predicted gains obtained with selection are given in Table 6 for the studied traits. For plant height spike length, spikelets spike[-1] and kernels spike[-1] the selected parental sample in the F_2 of the cross was (1.40, 4.82, 1.17 and 9.03 %, respectively) higher than the cross mean, and was higher than the actual one (0.25, 0.01, 0.98 and 1.26%, respectively) with mean plant height of their progenies of the F_3. The previous results suggest that the gene action involved in cycle 1 largely additive (Frey and Horner, 1954). However, the trend of the predicted (0.60, 1.85, 0.43 and 1.34%, respectively) was lower than the actual gains (2.49, 2.26, 1.88 and 2.92%, respectively) in cycle 2 from F_3 and F_4 generation. Cycle 2 results of higher values of actual than predicted indicate that dominance gene effects are involved in the inheritance of that trait (Frey and Horner, 1954 and El-Ameen et al., 2013).

For No. of spikes plant[-1] the predicted gain as percentage of cross mean was higher than the actual one, through cycle 1 and for cycle 2 the two values almost identical. These results confirming the predominance of dominance gene effects (El-Ameen et al., 2013).

All previous results of dominance gene effects may explain as mentioned previously by Salem et al., 1983, Weber and Moorthy, 1952 and Frey and Horner, 1955. Also, Frederickson and Kronstad 1985 reported that the nature of selfing drastically reduces the opportunities for new genetic recombination with each generation. Avey et al., 1982 comparing the C_o and C_1 data at both locations for cycle 1 from that the C_o had higher values than C_1. This may indicate that the genetic effects being selected in this cycle showed a relatively high degree of dominance and epistatic variances. However, when one considers, that this is a mean and that about half of the population of plant is higher than the mean, it can be seen that considerable progress has been made.

However, Khader et al., 1972, reported that testing progenies in F_3 generation in a replicated experiment would not give similar values of heritability and genetic advance as those obtained in F_4 generation unless the contribution of non additive gene action to the trait variation is significant. These findings are in harmony with those obtained by Islam 1985, Ismail, 1995 and Saad, 1999.

For grain yield plant[-1] the actual gain as percentage of cross mean was higher than the predicted one, through cycle 1 and 2 for the studied cross. The previous results suggest that the gene action involved in cycle 1 and 2 largely additive (Frey and Horner, 1954 and El-Ameen et al., 2013). Saad, 1999 found that predicted response exceeded the observed for grain yield plant[-1], it is possible that significant discrepancies did exit however, experimental design is not sensitive enough to detected the differences. Same results were found also by Pesek and Baker, 1971 and Mc-Ginnic and Shebeski, 1968.

Table 3. Pertinent analysis of variance of wheat cross across three generations (F$_2$, F$_3$ and F$_4$) for the studied traits.

Traits		Genotypes		Families		Parents		Parents vs. Families	
								SOV	
Plant height	F$_2$	195.86	*	182.83	*	441.00	*	706.16	*
	F$_3$	310.60	**	314.60	**	441.00	**	4.29	**
	F$_4$	431.75	*	445.39	*	477.56	*	47.72	*
Spike length	F$_2$	1.23	**	1.06	**	0.01		12.67	**
	F$_3$	1.69	**	1.72	**	0.01	**	2.00	**
	F$_4$	5.48	**	1.52	**	11.51	**	0.98	*
Spikelets spike^{-1}	F$_2$	1.81	**	1.55	**	11.56		7.31	**
	F$_3$	13.43	*	2.81	**	11.56	**	323.77	**
	F$_4$	5.85	*	4.39	*	4.22	**	27.34	*
Kernels spike^{-1}	F$_2$	98.18	**	92.66	*	14.41		502.06	**
	F$_3$	195.77	**	178.69	**	14.44	**	1128.71	**
	F$_4$	221.42	**	95.14	*	334.18	**	555.06	**
No. of spikes plant^{-1}	F$_2$	26.71	**	25.98	**	2.10		93.83	*
	F$_3$	16.59	**	17.29	**	1.82	**	0.74	**
	F$_4$	4343.45	**	2997.44	*	6833.28	**	172.52	*
Grain yield plant^{-1}	F$_2$	212.93	**	150.69	**	7.95		4027.71	**
	F$_3$	143.97	**	114.81	**	14.73	**	1556.34	**
	F$_4$	21.79	*	12.81	*	15.28		132.65	**

*,** significant at 5% and 1% levels of probability, respectively

Table 4. Mean values of wheat cross across three generations (F$_2$, F$_3$ and F$_4$) for the studied traits..

Traits	F$_2$	Range	L-53	V99/17	F$_3$	Range	L-53	V99/17	F$_4$	Range	L-53	V99/17
Plant height	93.11	34.00	93.45	105.4	85.30	38.00	93.7	108.82	105.38	35.44	103.53	104.84
Spike length	13.19	3.30	8.74	13.83	10.89	3.45	9.65	8.72	13.25	2.89	11.72	11.65
Spikelets spike^{-1}	23.24	3.90	20.95	23.25	21.04	4.00	14.55	14.10	19.30	2.44	19.50	19.55
Kernels spike^{-1}	74.07	32.8	49.10	60.19	67.26	37.80	47.34	48.47	49.19	24.22	56.39	55.98
No. of spikes plant^{-1}	19.00	15.84	12.35	25.17	18.11	10.50	17.65	15.45	19.12	1.91	11.85	11.76
Grain yield plant^{-1}	49.17	33.78	48.93	57.21	41.16	28.82	20.84	19.72	15.27	7.22	18.75	18.37

Table 5. Phenotypic (σ^2p), genotypic (σ^2g) variances, phenotypic (PCV %), genotypic (GCV %) coefficients of variability and heritability in broad sense (h^2) of wheat cross across three generations (F$_2$, F$_3$ and F$_4$) for the studied traits.

Traits	Generation	σ^2p	σ^2g	h^2%	PCV %	GCV %
Plant height	F$_2$	97.93	36.19	36.95	9.81	5.59
	F$_3$	155.30	147.54	95.00	14.62	14.25
	F$_4$	47.97	7.30	15.22	6.57	2.56
Spike length	F$_2$	0.62	0.33	53.04	6.09	4.10
	F$_3$	0.85	0.57	67.46	8.46	6.94
	F$_4$	0.61	0.27	44.18	5.89	3.92
Spikelets spike^{-1}	F$_2$	0.90	0.40	44.14	3.91	2.30
	F$_3$	6.72	3.03	45.12	12.44	8.36
	F$_4$	0.65	------+	--------+	4.18	--------+
Kernels spike^{-1}	F$_2$	49.09	22.50	45.83	11.12	7.26
	F$_3$	97.89	60.34	61.64	14.87	11.67
	F$_4$	24.60	11.44	46.49	10.08	6.88
No. of pikes plant^{-1}	F$_2$	13.35	6.56	49.11	19.09	13.18
	F$_3$	8.30	4.10	49.37	15.48	10.87
	F$_4$	33.53	30.52	91.03	0.51	0.48
Grain yield plant^{-1}	F$_2$	106.46	79.91	75.06	16.76	13.49
	F$_3$	71.99	50.25	69.81	21.05	17.59
	F$_4$	2.42	0.10	4.03	10.19	2.05

+ Genotypic variance was negative

Table 6. Predicted vs. actual gain in studied traits with selection through two cycles starting F_2 generation.

Items of cycle 1	Plant height		Spike length		Spikelets Spike^{-1}		Kernel spike^{-1}		No. of spi plant^{-1}
	F_2	F_3	F_2	F_3	F_2	F_3	F_2	F_3	F_2
Population mean	97.32	85.08	11.92	10.89	22.48	20.84	61.12	66.43	18.84
Selected sample mean	93.11	85.30	13.19	10.89	23.24	21.04	74.07	67.26	19.00
Difference (D)	4.21	0.22	1.27	0.00	0.76	0.20	12.95	0.83	0.16
Predicted gain	1.37	-----	0.57	-----	0.26	-----	5.52	-----	0.08
Actual gain	-----	0.22	-----	0.00	-----	0.20	-----	0.83	-----
Gain as % of population mean	1.40	0.25	4.82	0.01	1.17	0.98	9.03	1.26	0.40
Items of cycle 2	F_3	F_4	F_3	F_4	F_3	F_4	F_3	F_4	F_3
Population mean	85.08	102.82	10.89	13.32	20.84	19.68	66.43	50.92	18.61
Selected sample mean	84.54	105.38	10.59	13.25	20.64	19.30	64.99	49.19	20.28
Difference (D)	0.54	2.56	0.30	0.31	0.20	0.38	1.44	1.77	1.67
Predicted gain	0.51	------	0.20	------	0.09	------	0.89	------	0.82
Actual gain	-----	2.56	-----	0.31	-----	0.38	-----	1.77	-----
Gain as % of population mean	0.60	2.49	1.85	2.26	0.43	1.88	1.34	2.92	4.43

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