Genetic Divergence in Advanced Bread Wheat Genotypes for Yield and Its Attributes

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Abstract: Studying genetic divergence of quantitative traits and its attributes towards yield is important for developing high yielding varieties. Nine advanced bread wheat genotypes along with three check parental varieties; Sids1, Sakha 93 and Giza 168 were investigated at the Experimental Farm of the Faculty of Agriculture (Demo farm, new reclaimed sandy loam soil), Fayoum University, Fayoum Governorate, during two growing seasons (2017/2018 and 2018/2019). The research was laid out in randomized complete block design (RCBD) with three replications. The analysis of variance revealed highly significant differences among the studied genotypes for all investigated traits. Mostly high broad sense heritability 97.52 & 96.49, 91.63 & 93.70 and 95.24 & 97.38% accompanied with high genetic advance 70.33 & 61.23, 60.50 & 56.88 and 46.29 & 57.27 were observed for plant height, grains spike^{-1} and grain yield plant^{-1} in both seasons, respectively. In addition to, high broad sense heritability with low genetic advance were noticed for the rest of the studied traits. 100-grain weight, grains spike^{-1}, number of fertile tillers, spikelets spike^{-1} and spike length exhibited positive and significant effect on grain yield plant^{-1} in the 1nd season, while in the 2nd season its effected only with grains spike^{-1}, 100-grain weight and number of fertile tillers. Automatic multiple linear regression analysis was used to develop a fitted equation to a predicate. According to results forward stepwise regression was selected to predicate grain yield plant^{-1} in two seasons. 90.2% of the total variation in grain yield/plant could be explained by variation in SI =100-grain weight, NGS =grains spike^{-1}, NT = Number of fertile tillers, SS= Spikelets spike^{-1} and SL= spike length in first season. 85.3 % of the total variation in grain yield/plant could be explained by variation in SI =100-grain weight, NGS =grains spike^{-1}, and NT = Number of fertile tillers second season.

Keywords: Automatic regression, bread wheat, genetic divergence, genetic advance and heritability

INTRODUCTION

Wheat (*Triticum aestivum* L.) is the most broadly consumed cereal crop around the world. It provides food to 36% of the global population, and contributes 20% of food calories. With dynamic worldwide climatic change and declining eco-environment, wheat production is influenced enormously (Singh and Chaudhary, 2006). The Increasing yield potential has unquestionable importance in tackling world hunger issue. (Collaku, 1994). The genetic construction of yield can be resolved better by studying its component attributes, which embowers the plant breeders to improve for high yielding genotypes with desired combinations of characters (Khan and Dar, 2010; Ojha *et. al.,* 2018).

Broad-sense heritability is characterized as the proportion of genotypic variance to the phenotypic one. It plays a predictive role in breeding crops, expressing the reliability of phenotype as a guide to its breeding value (Firouzian, 2003; Songsri *et al.*, 2008; Ali *et al.,* 2009). Between heritability and response to selection there is a direct relationship, which is revealed as genetic progress. The expected response to selection is further called as genetic advance (GA). High heritability alone is not sufficient to make adequate improvement through selection generally in advance generations unless accompanied by considerable amount of genetic advance (Bhargava *et al.*, 2003; Kilic and Yağbasanlar 2010; Bhushan *et al.* 2013). High heritability estimates along with greater values of genetic advance for number of spikes per plant, number of grains per spike, 100 grain weight, grain yield and plant height were obtained by (Firouzian,

2003; Bhushan *et al.* 2013 Hamam 2014; Sharaan *et. al.* 2017).

Stepwise regression is a way that is utilized to determine the value of a quantitative variable with respect to its relation with one or some other quantitative variables. This relation is such that it is conceivable to anticipate other changes using one variable.this technique has used by many investigators on wheat such as (Mohamed, 1999; Pržulj and Momcilovic, 2011; Soleymanifard *et al.,* 2012). Investigators often collect a data set with a large number of independent variables and each of them is a potential predictor of the dependent variable (DV). The problem of deciding which subset (s) of the large pool of potential predictors to include in a linear regression model is; therefore, very common and arguably the hardest part of regression modeling (Ratner, 2012). As for popularity, the all-possible-subsets (Automatic linear model) method seems to be preferred by many researchers over the stepwise method. Perhaps, this is because researchers are no longer content with the selection of a single, final model based solely on an automatic variable selection method in statistics. Instead, the recommendation is to evaluate multiple, more promising subsets that are best according to the optimality criterion of choice (Kutner and Neter, 2004; Tamhane and Dunlop, 2000). The all-possible-subsets method is able to provide best subsets after evaluating all possible regression models and the researcher can then choose an appropriate final model from the most promising subsets after actoring in additional considerations beyond solely statistical ones.

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The Present research was conducted with the following objectives:

1) To evaluate the heritability and genetic advance for grain yield and some of its related components in order to select the more desirable traits, which may contribute for the improvement of wheat.

2) To investigate the variation and identify important agronomic traits of utmost importance which may be used as selection criteria in a wheat breeding program and

3) To determine the automatic linear regression of important yield components on yield of wheat genotypes.

MATERIALS AND METHODS

Plant materials and experimental design:
A set of nine advanced bread wheat genotypes along with three check parental varieties; Sids1, Sakha 93 and Giza 168 (Table 1) were grown and evaluated at the Experimental Farm of Faculty of Agriculture, Fayoum University at Demo (new reclaimed sandy loam soil), Fayoum Governorate, during tow cropping seasons 2017/2018 & 2018/2019. The experiment was laid out in Randomized Complete Block design (RCBD) with three replications for each genotype. The experimental plot was 3 X 3.5 m. Seeds were planted in rows of 3m length, 25cm width, 5cm within and one plant was left hill[-1].

Table (1): List of investigated genotypes and their pedigree

No.	Genotypes	Pedigree	No.	Genotypes	Pedigree
1	**95*15-10**	Sids1 / Giza168-10	7	96*95-5	Sakha93 /Sids1-5
2	**95*15-2**	Sids1 / Giza168-2	8	95*15-4	Sids1 / Giza168-4
3	**96*95-1**	Sakha93 /Sids1-1	9	96*95-4	Sakha93 /Sids1-4
4	**95*15-8**	Sids1 / Giza168-8	1	Sakha-93	Sakha 92/TR 810328 S 8871- 1S-2S-0S
5	**96*95-7**	Sakha93 /Sids1-7	11	Seds-1	HD2172/Pavon"S"//1158.27/Maya74"S"Sd 46-4Sd-2Sd-1Sd-0sd
6	**96*95-9**	Sakha93 /Sids1-9	12	Giza-168	MIL/BUC//Seri CM93046 – 8M-0Y-0M-2Y-0B

Morphological data:

Five plants from each genotype and parental line per replication were selected at random for the study of yield and yield contributing traits. Data were recorded for plant height (cm), number of fertile tillers plant[-1], number of spikelets spike[-1], spike length (cm), number of grains spike[-1], grains weight spike[-1] (g), 100- grains weight (g) and grain yield plant[-1] (g).

Statistical analysis:

Statistical analyses were carried out using IBM® SPSS® (SPSS Inc., IBM Corporation, NY, USA) Statistics Version 25 (2017) for Windows. Data were subjected to analysis of variance (ANOVA) with P-value of <0.05 was considered to be statistically significant. Duncan post-hoc test was used to compare the genotypes means. The phenotypic and genotypic variances and coefficients of variation were estimated according to the methods suggested by Burton and Devane (1953). Heritability estimates in broad sense ($h^2_{b.s}$), environmental variance (Ve), genetic variance (Vg) and genetic advance (G.A) with a selection intensity of 5% were calculated following method suggested by Allard (1960).

The Automatic Linear Modeling was also carried out for the data obtained to test the significance of the independent variables affecting the grain yield according to the methods of IBM SPSS Inc. (2017).

RESULTS AND DISCUSSION

The analysis of variance of the nine bread wheat advanced lines and their parents revealed highly significant difference for all investigated traits (Table 2). The significant difference among genotypes for the traits implies the presence of substantial variation among all genotypes which is central to the study of both quantitative and qualitative traits and gives an opportunity to plant breeders for improvement of these characters through breeding. The amount of genotypic and phenotypic variability that exist in genotypes is of utmost importance in breeding better varieties and in initiating a breeding program. Genotypic and phenotypic coefficients of variation are used to measure the variability that exists in a given population. Estimated genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV), broad sense heritability (h^2_B) and genetic advance GA) of the traits studied are presented in Table (3).

Table (2): Mean squares for various traits of the studied genotypes 2017/2018 and 2018/2019 seasons

Traits	Plant height (cm)	No. fertile tillers plant^{-1}	Spikelets spike^{-1}	Spike length (cm)	No. Grains spike^{-1}	Grains weight spike^{-1} (g)	100-Grain weight (g)	Grain yield plant^{-1} (g)
S.O.V				**First season 2017/2018**				
Rep	108.16	1.91	5.07	1.21	53.61	0.87	1.01	0.59
Genotype	1689.04**	11.79**	13.19**	10.52**	479.69**	4.95**	3.14**	188.08**
Error	39.38	1.27	2.49	1.41	32.80	0.31	0.27	0.39
				Second season 2018/2019				
Rep	97.24	3.11	0.03	2.04	77.46	0.02	0.55	21.45
Genotype	913.93**	5.05**	4.86**	4.66**	263.19**	3.55**	2.04**	109.49**
Error	83.90	1.96	2.00	1.79	42.38	0.39	0.30	3.99

**,* = Significant at 1 and 5% probability level, respectively

Plant height (cm):

Genotypes for plant height had high significant variability (P≤0.01) (Table 2). Mean values for plant height ranged from 92.93 & 107.19 to 129.47 & 136.29 cm with a general mean of 111.47 & 116.93 cm in the 1st and 2nd seasons, respectively (Table 3). Genotype 95*15-8was the tallest (136.29 cm) while genotype 96*95-5was the shortest (92.93& 107.19 cm) in 1st and 2nd season, respectively with highly significant differences with others. Variances due to genotypic and environmental factors were calculated as 1675.91 & 855.96 and 39.38 & 83.90 in both seasons (Table 4), respectively. The PCV values were slightly higher than GCV values. These results indicated that the environmental effect was small for the expression of this trait, which in line with the findings of Subhashchandra *et al.* (2009). High broad sense heritability estimates of 97.70 & 91.35 % and high genetic advance (GA) of 83.36 & 58.60 at 5% selection intensity in 1st and 2nd seasons, orderly (Table 4) indicating additive gene effect for plant height as obtained by (Singh and Narayanan, 1993). These results are in line with those of (Firouzian, 2003; Bhushan *et al.* 2013; Hamam, 2014; Sharaan *et. al.,* 2017).

Number of fertile tillers:

Analysis of variance revealed significant differences for No. of fertile tillers within investigated wheat genotypes (Table 2). It ranged from 3.5:6.2 & 3.4:5.4 with general mean of 4.4 & 4.34 in 1st and 2nd seasons, respectively (Table 3). These results are in agreement with the findings of different authors on wheat genotypes (Abd El-Mohsen *et al.,* 2012; Degewione *et al.*, 2013; Desheva and Cholakov, 2015). However, our results were in discrepancy with Bhutto *et al.* (2016) who detected non-significant differences among eight bread wheat genotypes for number of tillers plant^{-1}. Very high estimates of broad sense heritability of 89.95 & 69.17% accompanied by low

genetic advance of 6.59 & 3.59 indicates non additive genetic effect of variation and improvement of no. of fertile tillers through selection may not be effective in this population.

Number of Spikelets spike^{-1}:

Analysis of variance for Spikelets spike^{-1} showed highly significant differences (P≤0.01) among genotypes (Table 2). It ranged from 20.1: 23.7 & 21.17: 22.72 with general mean 22.33 & 21.74 1st and 2nd seasons (Table 3), respectively. This trait obtained a high heritability in both seasons 83.23 & 67.71% and low genetic advance 6.61 & 3.47, while it gained a high PCV and moderate GCV values. Results were in line with those of Sharaan *et al.* (2017).

Spike length (cm):

Studied genotypes showed highly significant differences for spike length (Table 2). General mean values of this trait were 13.3 & 13.01 cm and ranged from 11.4: 14.1 & 12.16: 18.8 cm in 1st and 2nd seasons, respectively (Table 3) as obtained by (Muhammad *et al.,* 2006; Sharaan *et al.,* 2017). The Genotype 95*15-10 had maximum spike length (14.1 cm) for both seasons. Results showed high estimates of broad sense heritability 87.70 & 69.42% and low genetic advance 6.12 & 3.40 for this trait with relatively higher PCV values 25.37 & 18.6 than GCV values 23.76 & 15.50 in 1st and 2nd seasons, respectively (Table 4) as stated by Deshmukh *et al.* (1986).

Grains spike^{-1}:

Analysis of variance exhibited significant differences within genotypes for grains spike^{-1} (Table 2). Data ranged from 48.4: 69.9 & 51.8: 66.8 with a general mean value of 59.5 & 59.22 in 1st and 2nd seasons, in succession. Heritability estimates for number of grains spike^{-1} were 93.46 & 85.46% with high genetic advance 43.12 & 30.05 indicating additive gene effect for this trait (Table 4). These results are

similar to the findings of Memon *et al*. (2007) but are inversion with those reported byEid (2009), who reported low heritability for grains spike^{-1}.

Grain weight spike^{-1} (g):

Grain weight spike^{-1} showed highly significant differences (P≤0.01) within the 11 wheat genotypes (Table 2). Data varied from 2.3 to 4.2 g & 2.3 to 3.8 g in 1st and 2nd seasons, respectively (Table 3). Genotypes 96*95-1 & 96*95-9 had maximum grain weight spike^{-1} in 1st and 2nd seasons, respectively among all studied genotypes (Table 3). Broad-sense heritability estimate were high 93.99 & 89.76% with low 4.4 & 3.6 genetic advance (Table 4). High heritability is in lined with the findings of Asif *et al*. (2004) who also found high heritability for grain weight spike-1. PCV and GCV for grain weight spike^{-1} were 78.31 & 66.89 and 75.92 & 63.37 respectively. The present results are in accordance with those previously reported by (Hamam, 2014; Sharaan *et al.,* 2017) in wheat for this trait.

100-grain weight (g):

Significant differences (P≤0.01) were observed among genotypes for 100-grain weight (Table 2). Highest values of 100-grain weight were obtained for genotype 96*95-1 (6.2 & 5.9 g), while the genotype 95*15-8 exhibited lowest value for 100-grain weight (4.7 & 4.9 g) in both 1st and 2nd seasons, respectively (Table 3). 100-grain weight heritability estimate at broad-sense were 91.87 & 86.61 while the genetic advance values were 3.45 & 2.67. These results were in line with those of Sharaan *et al*. (2017). Phenotypic coefficient of variation were 34.68 & 28.04 and genotypic coefficient of variation were 33.24 & 26.10 in 1st and 2nd seasons, orderly (Table 4). 100-grain weight is one of the most imperative yield components and could be used as potential selection criteria for grain yield.

Grain yield plant^{-1}(g):

Analysis of variance of grain yield plant^{-1} showed highly significant differences among genotypes (Table 2). Data of grain yield ranged from 7.2 to 18.4 g and 8.25 to 18.49 g plant^{-1}in 1st and 2nd seasons, respectively (Table 3). Heritability estimates showed a very high broad-sense heritability for grain yield 99.79 & 96.44%, in addition to, a high genetic advance 28.21 & 21.04 (Table 4). The present findings are in agreement by those of (Khan and Dar, 2010; Sharaan *et al.,* 2017; Ojha *et al.,* 2018).

Table (3): Mean Performance of the studied traits of twelve bread wheat genotypes in 1st and 2nd seasons

Genotypes	Season	Plant height (cm)	No. fertile tillers plant^{-1}	Spikelets spike^{-1}	Spike length (cm)	No. Grains spike^{-1}	Grains weight spike^{-1} (g)	100-Grains weight (g)	Grain yield plant^{-1} (g)
95*15-10	2017/18	114.40^{de}	4.00^{ab}	22.33^{bc}	14.13^{b}	61.33^{c}	2.63^{abc}	5.01^{ab}	15.04^{e}
	2018/19	119.40^{de}	3.60^{ab}	21.67^{ab}	13.87^{c}	58.73^{cd}	2.69^{a}	5.19^{bc}	14.61^{c}
95*15-2	2017/18	129.47^{h}	5.80^{de}	22.33^{bc}	14.00^{b}	63.13^{c}	2.79^{bc}	5.10^{b}	16.08^{f}
	2018/19	136.29^{f}	4.71^{bcd}	21.18^{a}	13.59^{bc}	59.72^{cd}	2.75^{a}	5.29^{bc}	15.49^{cde}
96*95-1	2017/18	117.00^{ef}	4.13^{ab}	22.87^{cd}	13.93^{b}	69.87^{d}	4.23^{d}	6.20^{d}	18.41^{h}
	2018/19	115.33^{bcd}	4.20^{abc}	22.47^{b}	12.58^{abc}	66.87^{cd}	3.71^{b}	5.92^{e}	18.49^{g}
95*15-8	2017/18	122.93^{g}	4.53^{bc}	22.73^{cd}	13.53^{b}	61.60^{c}	2.89^{c}	5.02^{ab}	15.01^{e}
	2018/19	118.88^{de}	4.40^{abcd}	22.72^{b}	13.48^{bc}	63.65^{cd}	2.74^{a}	5.18^{bc}	15.28^{cde}
96*95-7	2017/18	98.93^{b}	4.07^{ab}	23.00^{cd}	13.40^{b}	61.40^{c}	2.62^{abc}	5.07^{ab}	15.15^{e}
	2018/19	109.52^{ab}	4.71^{bcd}	21.64^{ab}	13.54^{bc}	60.32^{cd}	2.72^{a}	5.37^{bce}	14.73^{cd}
96*95-9	2017/18	115.20^{ef}	4.07^{ab}	23.67^{d}	13.60^{b}	60.00^{c}	3.85^{d}	5.62^{c}	16.97^{g}
	2018/19	112.77^{abcd}	4.26^{abcd}	22.50^{b}	12.88^{abc}	61.16^{cd}	3.83^{b}	5.79^{de}	16.47^{ef}
96*95-5	2017/18	92.93^{a}	4.13^{ab}	22.60^{cd}	13.33^{b}	60.73^{c}	2.91^{c}	5.86^{cd}	17.07^{g}
	2018/19	110.28^{bc}	4.46^{abcd}	22.06^{ab}	12.16^{a}	61.83^{cd}	3.52^{b}	5.74^{de}	17.61^{fg}
95*15-4	2017/18	110.27^{cd}	5.33^{cd}	22.33^{bc}	13.33^{b}	59.67^{c}	2.65^{abc}	5.57^{c}	14.27^{d}
	2018/19	107.19^{a}	4.06^{abc}	21.28^{a}	13.02^{abc}	60.04^{cd}	2.78^{a}	5.24^{bc}	16.56^{ef}
96*95-4	2017/18	119.67^{fg}	6.2^{e}	22.87^{cd}	14.13^{b}	61.47^{c}	2.99^{c}	5.12^{b}	17.15^{g}
	2018/19	117.08^{cd}	5.37^{d}	21.28^{a}	13.36^{bc}	56.55^{ab}	2.67^{a}	5.50^{cde}	16.24^{def}
Sakha-93	2017/18	99.73^{b}	3.87^{ab}	22.07^{bc}	12.00^{a}	51.13^{ab}	2.42^{ab}	5.05^{ab}	11.03^{c}
	2018/19	124.92^{e}	5.07^{cd}	21.17^{a}	12.61^{abc}	56.44^{ab}	2.78^{a}	5.28^{bc}	14.62^{c}
Seds-1	2017/18	110.33^{cd}	3.40^{a}	21.13^{ab}	13.33^{b}	54.93^{b}	2.53^{abc}	4.79^{ab}	8.71^{b}
	2018/19	117.31^{cd}	3.38^{a}	21.68^{ab}	12.25^{a}	53.59^{a}	2.55^{a}	4.94^{ab}	12.00^{b}
Giza-168	2017/18	106.80^{c}	3.53^{a}	20.07^{a}	11.40^{a}	48.40^{a}	2.31^{a}	4.65^{a}	7.15^{a}
	2018/19	114.18^{abcd}	3.84^{ab}	21.19^{a}	12.74^{abc}	51.78^{a}	2.29^{a}	4.6^{a}	8.26^{a}

Table (4): Genetic parameters of the studied traits of bread wheat genotypes 2017/2018 and 2018/2019 seasons

Traits	Season	Mean ± SE	Vg	Ve	Vp	PCV %	GCV %	h^2_b %	GA
Plant height (cm)	2017/2018	111.47±0.89	1675.91	39.38	1715.29	37.15	36.72	97.70	83.36
	2018/2019	116.93±0.87	885.96	83.90	969.86	26.63	25.46	91.35	58.60
No. fertile tillers plant[-1]	2017/2018	4.42±0.10	11.37	1.27	12.64	80.39	76.24	89.95	6.59
	2018/2019	4.34±0.10	4.40	1.96	6.36	58.12	48.34	69.17	3.59
Spikelets spike[-1]	2017/2018	22.33±0.13	12.36	2.49	14.85	17.25	15.74	83.23	6.61
	2018/2019	21.74±0.10	4.19	2.00	6.19	11.45	9.42	67.71	3.47
Spike length (cm)	2017/2018	13.34±0.10	10.05	1.41	11.46	25.37	23.76	87.70	6.12
	2018/2019	13.01±0.10	4.06	1.79	5.85	18.60	15.50	69.42	3.46
No. Grains spike[-1]	2017/2018	59.47±0.58	468.76	32.8	501.56	37.66	36.40	93.46	43.12
	2018/2019	59.22±0.56	249.06	42.38	291.44	28.83	26.65	85.46	30.05
Grains weight spike[-1] (g)	2017/2018	2.90±0.06	4.85	0.31	5.16	78.31	75.92	93.99	4.40
	2018/2019	2.92±0.06	3.42	0.39	3.81	66.89	63.37	89.76	3.61
100- Grains weight (g)	2017/2018	5.25±0.05	3.05	0.27	3.32	34.68	33.24	91.87	3.45
	2018/2019	5.34±0.05	1.94	0.30	2.24	28.04	26.10	86.61	2.67
Grain yield plant[-1] (g)	2017/2018	14.34±0.26	187.95	0.39	188.34	95.73	95.63	99.79	28.21
	2018/2019	15.03±0.24	108.16	3.99	112.15	70.46	69.19	96.44	21.04

Where: Vp = phenotypic variance, Vg = genotypic variance, Ve = Environmental variance, PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, $h^2_{b.s}$ = heritability in broad sense, GA = genetic advance

Automatic Linear Regression:

The data obtained from automatic linear regression analysis for grain yield plant[-1] are presented in Fig. (1 a, b) for 1st and 2nd seasons, respectively. The results showed that 100-grain weight (SI), grains spike[-1] (NGS), number of fertile tillers (NT), Spikelets spike[-1] (SS) and spike length (SL) in the 1st season Fig.1 and grains spike[-1] (NGS), 100-grain weight (SI) and number of fertile tillers (NT) in the 2nd season (Fig. 1) had a positive regression coefficient, which, justified the maximum of yield changes. Existence of significant positive regression coefficient by automatic regression indicates the effectiveness of these traits to increase grain yield. Therefore, these traits were considered as the main grain yield components. Our findings are in line with those illustrated by Nasri *et al*. (2014).
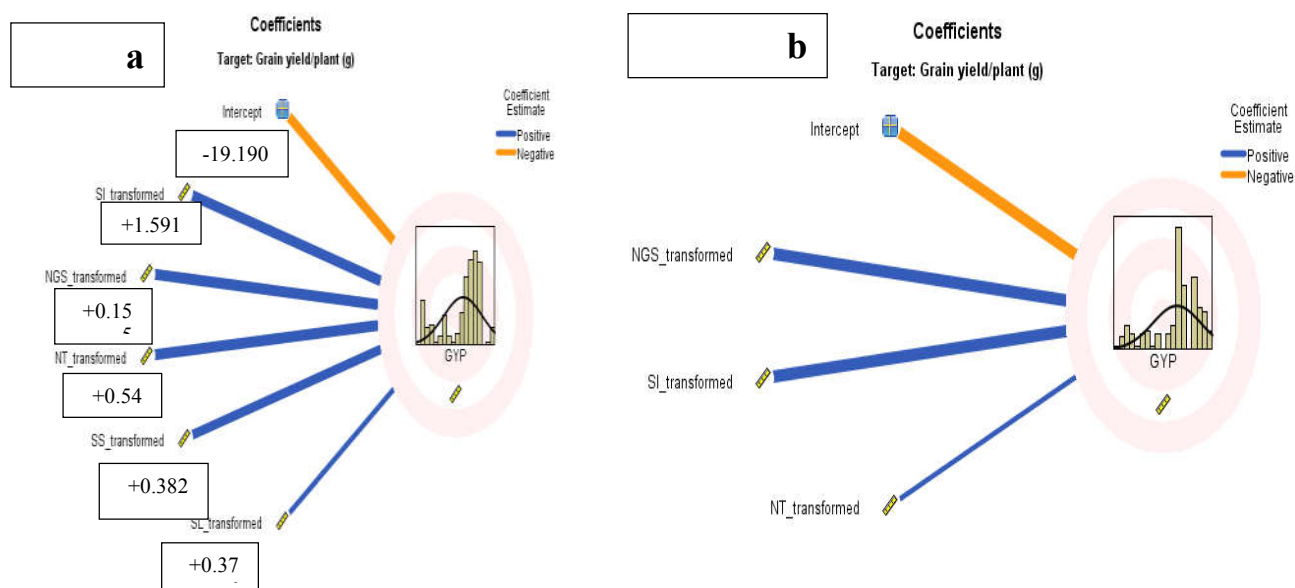
Fig. (1): Automatic Linear regression for grain yield plant[-1] and its attributes 2017/2018 (a) and 2018/2019 (b) seasons
While: SI =100-grain weight, NGS =grains spike[-1], NT = Number of fertile tillers, SS= Spikelets spike[-1] and SL= spike length

CONCLUSION

It could be concluded that highly significant differences were obtained among advanced bread wheat genotypes evaluated for all investigated traits which gives the opportunity to plant breeders for the improvement of these traits. Mostly high broad sense heritability coupled with high genetic advance for Plant height, no. Grains spike[-1] and Grain yield plant[-1] warrant effective selection. However, all other traits observed high broad sense heritability with low genetic advance ($\geq$10). Based on the results genotypes 96*95-5 and 96*95-9 performed better than the check parental varieties in yield and its studied attributes. A positive regression coefficient of automatic linear regression for 100-grain weight, grains spike[-1], number of fertile tillers, spikelets spike[-1] and spike length in 1st season and grains spike[-1], 100-grain weight and number of fertile tillers in 2nd one indicates the effectiveness of these traits to increase grain yield plant[-1].

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التنوع الوراثي في بعض التراكيب الوراثية المتقدمة لقمح الخبز للمحصول ومكوناته

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تعد دراسة الاختلافات الوراثية للصفات الكمية وخصائصها لصفة المحصول ومكوناته هامة للغاية لإنتاج أصناف عالية المحصول. أقيمت تجربة لتقييم تسعة تراكيب وراثية متقدمة لقمح الخبز إلى جانب ثلاثة أصناف أبوية (سدس١، وسخا ٩٣، وجيزة ١٦٨) في المزرعة التجريبية لكلية الزراعة (مزعة دمو)، جامعة الفيوم، محافظة الفيوم، خلال موسمي النمو ٢٠١٨/٢٠١٧ و ٢٠١٩/٢٠١٨ في تصميم قطاعات كاملة العشوائية في ثلاثة مكررات. أظهر نتائج تحليل التباين وجود اختلافات كبيرة بين التراكيب الوراثية محل الدراسة في جميع الصفات التي تمت دراستها. أظهرت صفات طول النبات، عدد حبوب السنبلة ومحصول الحبوب للنبات نسب عالية لمعامل التوريث بالمعنى الواسع ٩٧.٥٢ ، ٩٦.٤٩ ، ٩١.٦٣ ، ٩٣.٧٠ ، ٩٥.٢٤ ، ٩٧.٣٨ ٪ مصحوبة بالتقدم الجيني العالي ٧٠.٣٣ ، ٦١.٢٣ ، ٦٠.٥٠ ، ٥٦.٨٨ ، ٤٦.٢٩ ، ٥٧.٢٧ في كلا الموسمين على التوالي. هذا بالإضافة إلى وجود نسب مرتفعة لمعامل التوريث بمعناه الواسع، ولكن مع تقدم وراثي منخفض لبقية الصفات المدروسة. وفقا لنتائج اختبار الانحدار التدريجي إلى الأمام للتنبؤ بصفة محصول الحبوب للنبات في الموسمين، فقد وجد أن ٩٠.٢٪ من إجمالي التباين في صفة محصول الحبوب للنبات يمكن تفسيره بالتباين في وزن ١٠٠ حبة، عدد حبوب السنبلة، عدد الأفرع الخصبة، عدد السنيبلات وطول السنبلة في الموسم الأول. في حين وجد أن ٨٥.٣٪ من إجمالي التباين في محصول الحبوب للنبات يمكن تفسيره بالتباين في وزن ١٠٠ حبة، عدد حبوب السنبلة، عدد الأفرع الخصبة في الموسم الثاني.