



Estimation of Genetic Parameters for yield and its components in bread wheat (*Triticum aestivum* L.) genotypes under pedigree selection

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Abstract

Grain yield is a complex trait and is greatly influenced by various environmental conditions. A 3-year field investigation was carried out to estimate genetic parameters for yield and its related traits of wheat under selection in reclaimed soils conditions. Three field experiments were executed at the Experimental Farm of the Faculty of Agriculture, Fayoum University at Demo (new reclaimed sandy loam soil), Fayoum Governorate, during 2012/2013, 2013/2014, 2014/2015 growing seasons in randomized complete block design (RCBD) with three replications. Results revealed that mean square values were highly significant for all studied traits in all seasons of the experiments, indicating the presence of sufficient variability among the investigated genotypes and gave several opportunities for wheat improvement. Great correspondence was observed between genotypic coefficients of variation and phenotypic coefficients of variation in every one of the traits. The coefficients of variation were high for no. fertile tillers plant⁻¹ (NFT), grains spike⁻¹ (GS), grains weight spike⁻¹ (GWS), grain yield plant⁻¹ (GYP), spikes m⁻² (NSM), grain yield (GY), and harvest index (HI). In addition to, Moderate were recorded for heading date (HD) and spike length (SL) in the all seasons, and low were obtained for days to physiological maturity (DPM) in all seasons. Heritability was greater than 80% for all studied traits whereas genetic advance as a percentage of mean (GAM %) ranged from 12.22 (SS) to 77.00 (GY) in the 1st season and from 15.42 & 12.69 (DPM) to 112.07 & 68.35 (GYP) in 2nd and 3rd seasons.

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Introduction

Wheat is one of the most important and strategic cereal crops over all the world and it is commonly known as king of cereals. The importance of wheat lays in the physical and chemical properties of its grain, which makes possible production of bread, a primary source of the staple diet for the poor population and rich one alike. Wheat provides over 20% of the calories and protein requirements for human nutrition, and is a staple food for over 41% of the world's population in more than 40 countries. Wheat also is one of the most important local cereal crops in terms of area and production. Egypt's total wheat production of grains in 2014/2015 season reached about 9,460 million t resulted from about 3.24 million faddan (FAO, 2013). Selection is the major feature using in plant breeding. Indeed, one of the ingredients of successful plant breeding is to recognize superior types in a limited or vast array of genetic variability. Abinasa *et al.* (2011), Bhushan *et al.* (2013), Tahmasebi *et al.* (2013), Zeeshan *et al.* (2014), Desheva and Cholakov (2015) and Khan *et al.* (2015) reported that the high phenotypic and genotypic coefficients of variability detected for most of the yield and yield components traits studied in wheat genotypes are indicators for their wide range of variation. The PCV values are close to the GCV values that indicated least influence of the environment on the traits and selection is more successful for this traits.

Heritability estimates provide the information about index of transmissibility of the quantitative traits of economic importance and are essential for an effective crop breeding strategy. The magnitude of heritability also helps in predicting the behaviour of succeeding generations by devising the appropriate selection criteria and assessing the level of genetic improvement. Similarly, genetic advance gives clear picture and precise view of segregating generations for possible selection. Higher estimates of heritability coupled with better genetic advance confirm the scope of selection in developing new genotypes with desirable characteristics. Ajmal *et al.* (1995), Singh *et al.* (1999), Ghimiray and Sarkar (2000), Kilic and Yağbasanlar (2010), Bhushan *et al.* (2013) and

Hamam (2014) found 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. However Afiah *et al.* (2000),

Abinasa *et al.* (2011) and Moustafa (2015) reported low to high estimates of heritability and genetic advance for these traits except plant height. The present study was carried out to evaluate the genetic variability and inheritance of yield and some related plant traits to develop desirable wheat genotypes in new reclaimed soils under pedigree selection.

Materials and methods

Three field experiments were carried out at the Experimental Farm of the Faculty of Agriculture, Fayoum University at Demo (new reclaimed sandy loam soil), Fayoum Governorate, during 2012/2013, 2013/2014, 2014/2015 growing seasons.

The 1st experiment (2012/2013) was designed to study thirty six wheat genotypes (*Triticum aestivum*. L) of hybrid origin and subjected to selection among and within them. In addition to these genotypes there were four check parental varieties namely; Sids1.

Sakha 93, Giza 168 and Gemmiza 5. In the 2nd experiment (2013/2014) the selected genotypes became thirty eight together with the same parental varieties, were evaluated and selection was again practiced. In the 3rd experiment (2014/2015) the selected promising lines, those became sixteen, together with the four check varieties were evaluated.

Wheat genotypes (G)

The genetic materials used in the first season consisted of forty genotypes of bread wheat (*Triticum aestivum* L.), which involved thirty-six promising lines of hybrid origin (in their F₄ generation) developed in Argon. Dep., Fac of Agric., Fayoum Univ. by Ghallab (2006) and four commercial varieties, namely; Sids1, Sakha93, Giza 168 and Gemmiza 5 obtained from wheat Dept., Agric. Res. Cent., Giza, Egypt. Varieties and lines names and their pedigree are presented in Table (1).

Experimental design and agricultural practices

The experimental work was laid out in Randomized Complete Block design (RCBD) with three replications for each experiment. The experimental plot was 3 X 3.5m. Seeds were planted in rows of 3m length and 25cm width. Seeds spaced at 5cm within each row and one plant was left hill⁻¹. Total nitrogen fertilization was applied at the rate of 140 kg feddan⁻¹ N as Urea (46.5%) in two equal doses, before the first and second irrigations. The other agricultural practices recommended for growing wheat were followed to obtain a healthy crop.

Selection procedures

In 2012/13 season, the F₄ bulk seeds of thirty six genotypes plus the four checking varieties were planted in RCBD with three replications at the experimental farm (Demo) on 23th November. Pedigree selection was practiced on the basis of visual phenotypic performance and yield components. The selection was done in two ways; the first one, between genotypes and the second way of selection was done within each genotype. Then, thirty-eight advanced F₅ lines were selected on the basis of previous selection criteria. At harvesting time, *in vivo*, the best 10 plants were selected from each genotype.

Among them, after lab. work and measurements *in vitro*, 5:7 plants from each genotype were selected, to form seeds of F₆ lines.

In 2013/14 season, F₆thirty-eight selected lines were planted in RCBD with three replications at the experimental farm (Demo) on 23th November together with four check varieties. During this second selection cycle, only sixteen advanced F₆ lines were selected on the basis of previous selection criteria. In 2014/15 season, the selected sixteen F₆ advanced lines plus four checking varieties were planted in RCBD with three replications.

Agronomic traits

At flowering, measured heading date, day (HD) and at maturity recorded physiological maturity, day (PM). At harvest, ten representative plants were randomly taken from each plot and data of the following traits were recorded: Plant height, cm (PH), Fertile tiller number (NFT), Spike length, cm (SL), Number of spike lets for the main stem spike, (SS), Grains weight spike⁻¹, g (GWS), 100-grain weight, g (HSW), Grain yield plant⁻¹, g (GYP), Number of spikes m⁻² (NSM), Grain yield t/fad, (GY), Harvest index %, (HI).

Statistical analysis

The collected data were subjected to analysis of variance using GENSTAT version 12th software package (VSN International, Hemel Hempstead, UK) to determine least significant difference (LSD) at 1% and 5% probability level among our genotypes according to Payne *et al.* (2009).

Table 1. Code number, Genotypes and pedigree of wheat genotypes used, in the study.

No	Genotypes	G.	Pedigree	No.	Genotypes	G.	Pedigree
1	96x42-2	G1-2	Sakha93 / Gimmeiza5 - 2	20 S	95x15-7 Short	G4-7 short	Sids1 / Giza168 -7- 1SS
2	96x42-3	G1-3	Sakha93 / Gimmeiza5 - 3	21	95x15-8	G4-8	Sids1 / Giza168 -8
3	96x42-4	G1-4	Sakha93 / Gimmeiza5 - 4	22	95x15-10	G4-10	Sids1 / Giza168 -10
4	96x42-5	G1-5	Sakha93 / Gimmeiza5 - 5	23	96x95-1	G5-1	Sakha93/ Sids1 -1
4 T	96x42-5 Tall	G1-5 Tall	Sakha93 / Gimmeiza5 - 5- 1 ST	24	96x95-2	G5-2	Sakha93/ Sids1 - 2
4 S	96x42-5 Short	G1-5 Short	Sakha93 / Gimmeiza5 - 5- 1SS	25	96x95-3	G5-3	Sakha93/ Sids1 - 3
5	96x42-6	G1-6	Sakha93 / Gimmeiza5 - 6	25 T	96x95-3 Tall	G5-3 Tall	Sakha93/ Sids1 - 3- 1ST
6	96x42-7	G1-7	Sakha93 / Gimmeiza5 - 7	25S	96x95-3 Short	G5-3Short	Sakha93/ Sids1 - 3- 1SS
7	96x42-9	G1-9	Sakha93 / Gimmeiza5 - 9	26	96x95-4	G5-4	Sakha93/ Sids1 - 4
8	42x15-1	G2-1	Gimmeiza5 / Giza168 - 1	27	96x95-5	G5-5	Sakha93 /Sids1 - 5
9	42x15-4	G2-4	Gimmeiza5 / Giza168 - 4	28	96x95-7	G5-7	Sakha93/ Sids1 - 7

No	Genotypes	G.	Pedigree	No.	Genotypes	G.	Pedigree
10	42x15-5	G2-5	Gimmeiza5 / Giza168 - 5	29	96x95-8	G5-8	Sakha93/Sids1 - 8
11	42x15-7	G2-7	Gimmeiza5 / Giza168 - 7	30	96x95-9	G5-9	Sakha93/ Sids1 - 9
12	42x15-9	G2-9	Gimmeiza5 / Giza168 - 9	31	96x15-1	G6-1	Sakha93/ Sids1 - 6
13	42x15-10	G2-10	Gimmeiza5 / Giza168 - 10	32	96x15-4	G6-4	Sakha93/Giza168 - 1
14	95x42-7	G3-7	Sids1 / Gimmeiza5- 7	33	96x15-6	G6-6	Sakha93/ Giza168 - 4
15	95x42-8	G3-8	Sids1 / Gimmeiza5- 8	34	96x15-7	G6-7	Sakha93/ Giza168 - 7
16	95x15-2	G4-2	Sids1 / Giza168 - 2	34 T	96x15-7 Tall	G6-7 Tall	Sakha93/ Giza168 - 7-1ST
17	95x15-3	G4-3	Sids1 / Giza168 - 3	34 S	96x15-7 Short	G6-7Short	Sakha93/ Giza168 - 7-1SS
18	95x15-4	G4-4	Sids1 / Giza168 - 4	35	96x15-8	G6-8	Sakha93/ Giza168 - 8
19	95;8x15-6	G4-6	Sids1 / Giza168 - 6	36	96x15-10	G6-10	Sakha93/ Giza168 - 10
19; T	95x15-6 - Tall	G4-6 Tall	Sids1 / Giza168 - 6-1 ST	37	Sids 1	P1	HD2172/Pavon"S"//1158.27/Maya74"S"Sd46-4Sd-2Sd-1Sd-osd
19 S	95x15-6 Short	G4-6 short	Sids1 / Giza168 - 6-1SS	38	Sakha 93	P2	Sakha 92/TR 810328 S 8871- 1S-2S-oS MIL/BUC//Seri
20	95x15-7	G4-7	Sids1 / Giza168 - 7	39	Giza 168	P3	CM93046 - 8M-oY-oM-2Y-oB
20 T	95x15-7 Tall	G4-7 Tall	Sids1 / Giza168 - 7-1 ST	40	Gemmeiza 5	P4	Vee "S"/SWM 6525 CGM 4017-1GM-6GM-3GM-oGM

The phenotypic and genotypic variances and coefficients of variation were estimated according to the methods suggested by Burton and Devane (1953). Heritability in broad sense ($h^2_{b.s}$) and genetic advance was computed using the formula adopted by Allard (1960). Genetic advance as percent of mean (GAM) was computed to compare the extent of predicted genetic advance of different traits under selection using the following formula:

$$GAM\% = \frac{GA}{\bar{X}} * 100$$

Results and dissection

Analysis of variance

Analysis of variance is important to the plant breeder that acceptable levels of genetic variability really exist in breeding populations. A successful selection depends upon the information on the genetic variability and association of morpho-agronomic traits with grain yield. Therefore, analysis of variance was applied in order to test the significance of genotypic differences in yield and yield components traits. Mean squares of analysis of variance for the thirteen investigated traits of the wheat genotypes tested in the three seasons are given in Table (2).

Results revealed that mean square values were highly significant for all studied traits in all seasons of the experiments, indicating the presence of sufficient variability among the investigated genotypes and gave several opportunities for wheat improvement.

Genotypic differences were reflected also in the broad ranges of all investigated traits. In addition to a high coefficient of variation (C.V%) and standard error (SE) values for most of the traits studied, particularly in the first year, which confirmed the results of genotypic mean square values. In the first season, C.V% and SE values were mostly high for PH: 4.98 & (121.12±3.485), NFT: 23.15 & (5.34±0.714), GWS: 25.80 & (2.83±0.420), and GYP: 30.37 & (10.70±1.876), respectively. All of them confirmed the existence of sufficient genetic variability within the studied genotypes to be exploited in the breeding programs. Thus, selection for these traits would be effective for wheat improvement. Many investigators found significant differences among wheat genotypes which support our results (Khan *et al.*, 2011; Abd El-mohsen *et al.*, 2012; Gulnaz *et al.*, 2012; Degewione *et al.*, 2013; Tahmasebi *et al.*, 2013; Abd El-mohsen and Abd El-shafi, 2014; Desheva and Cholakov, 2015; Khan *et al.*, 2015; Raza *et al.*, 2015; Mahdi, 2015 and Bhutto *et al.*, 2016). However, our results are inversion with those reported by Ali *et al.*, 2007, Shah *et al.*, 2007 and Khan *et al.*, 2013.

In the second season, the selected genotypes became thirty eight ones in addition to the four parental varieties due to exclusion of the unfavorable genotypes and dividing each of the segregated genotypes to new two distinctive classes "Tall and Short".

So that, almost all C.V% and some SE values were lower than the corresponding values of the 1st season due to the effect of selection as shown in Table (2). It is interesting to note, due to selection, 10 general trait means of the 3rd season were advantage over the corresponding means of the 1st season (Table 2). Phenotypic plant selection resulted in reduced 10 C.V, 9 SE and 12 ranges out of 13 traits studied in 3rd season compared with those of 1st one. All these results, showed that our selection procedure was going in the wright way.

Phenotypic and genotypic coefficients of variation Genotypic (Vg), phenotypic (Vp) and environmental (Ve) variances, genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV), heritability and genetic advance for thirteen traits are presented in Tables (3). In the present examination, mostly, phenotypic coefficients of variation were equivalent to their relating genotypic coefficients of variation, showing few impact of environment on the declaration of these traits. Nevertheless, great correspondence was observed between genotypic coefficients of variation and phenotypic coefficients of variation in every one of the traits.

In the 1st and 2nd seasons, phenotypic variance ranged from 0.68 (100- grains weight (HGW)) to 8927.24 (spikes m⁻² (NSM)) and from 1.02 (grain yield, t/f (GY)) to 7103.68 (NSM), orderly.

In addition, genotypic variance ranged from 0.63 (HGW) to 8679.95 (NSM) and from 0.99 (GY) to 6941.52 (NSM) in both seasons, in succession.

Environmental variance of the 1st and 2nd seasons ranged from 0.04 (GY) to 247.29 (NSM) and from 0.03 (GY) to 162.16 (NSM), respectively. However, in the 3rd season, phenotypic variance, estimates ranged from 0.42 (HGW) to 6985.66 (NSM). Genotypic variance ranged from 0.37 (HGW) to 6796.12 (NSM), although, the environmental variance extended from 0.05 (HGW) to 189.54 (NSM).

Phenotypic coefficient of variation (PCV) exhibited a wide range for all the studied traits, which ranged from 7.20 (days to physiological maturity, day (DPM)) to 52.34% (grain yield plant⁻¹, g (GYP)) and from 7.57 (DPM) to 52.34% (GYP). However, genotypic coefficient of variation (GCV) ranged from 6.69 (spikelets spike⁻¹ (SS)) to 42.63% (GYP) and from 7.53 (DPM) to 55.52% (GYP) in 1st and 2nd seasons, respectively. However, in the 3rd season, the values of PCV ranged from 6.21 and 6.09% (DPM) to 35.87 and 36.05% (GYP), in addition, values of GCV ranged from 6.18 and 6.07% (DPM) to 34.50 and 32.12% (GYP). According to Deshmukh *et al.* (1986), PCV and GCV can be categorized as low (<10%), moderate (10-20%) and high (>20%). So that, in the 1st, 2nd and 3rd seasons, the high PCV and GCV were recorded for no. fertile tillers plant⁻¹ (NFT), grains spike⁻¹ (GS), grains weight spike⁻¹ (GWS), grain yield plant⁻¹ (GYP), spikes m⁻² (NSM), grain yield (GY), and harvest index (HI). In addition to, high PCV and GCV for plant height and 100- grains weight (HGW) in 2nd season and moderate in 1st season.

Table 2. Mean square values and dispersion measurements of the studied traits of forty bread wheat genotypes in three seasons (2012/13 to 2014/2015).

	S.V. d.f	1 st Season					C.V %
		Reps	Genotypes	Error	Mean ± SE	Range	
		2	39	78			
Traits	Heading Date (day)	6.83	267.93**	2.53	99.75±0.918	83 –118.7	1.6
	Days to Physiological Maturity(day)	2.06	115.55**	1.37	149.79±0.68	138 – 163	0.78
	Plant height (cm)	154.98	474.79**	36.44	121.12±3.49	96.1– 149.9	4.98
	No. fertile tillers plant ⁻¹	1.01	3.29**	1.53	5.34±0.714	3.20 – 8.93	23.1
	Spike length (cm)	0.63	2.85**	0.65	12.45±0.465	10.3 –15.1	6.47
	Spikelets spike ⁻¹	3.61	2.29**	0.57	21.66±0.44	20.3–23.8	3.5
	Grains spike ⁻¹	30.92	199.83**	61.81	58.05±4.54	36.5–74.5	13.5
	Grains weight spike ⁻¹ (g)	1.31	1.23**	0.53	2.83±0.420	1.5 – 4.8	25.8
	100- Grains weight (g)	0.03	0.65**	0.05	4.80±0.129	3.9 – 5.8	4.78

		1 st Season					
S.V.	Reps	Genotypes	Error	Mean ± SE	Range	C.V %	
d.f	2	39	78				
Grain yield plant ⁻¹ (g)	42.02	24.33**	10.56	10.70±1.88	6.7 – 17.8	30.3	
Spikes m ⁻²	522.16	8762.38**	247.2	264.73±9.0	172 – 428	5.94	
Grain yield (t/f)	0.02	0.81**	0.04	2.33±0.15	1.38–3.43	8.62	
Harvest index (HI) (%)	9.88	52.70**	4.89	22.21±1.277	11.1 – 29.4	9.95	
		2 nd Season					
Heading Date (day)	6.6	285.28**	2.49	97.67±0.911	80.7 - 118.0	1.62	
Days to Physiological Maturity(day)	0.34	124.88**	1.46	148.15±0.69	136 - 161	0.81	
Plant height (cm)	8.22	938.25**	6.82	114.4±1.508	88.9 - 156.8	2.28	
No. fertile tillers plant ⁻¹	0.04	3.00**	0.24	4.87±0.283	3.17 – 7.00	10.1	
Spike length (cm)	1.73	4.02**	0.58	13.14±0.440	10.7 - 15.4	5.79	
Spikelets spike ⁻¹	0.07	10.19**	0.75	22.78±0.50	17.8 - 26.6	3.8	
Grains spike ⁻¹	2.3	291.65**	8.33	56.45±1.666	29.9 - 72.5	5.11	
Grains weight spike ⁻¹ (g)	0.0026	1.25**	0.07	2.761±0.153	1.5 - 4.1	9.23	
100- Grains weight (g)	1.64	1.09**	0.05	4.69±0.129	3.3 - 5.8	4.62	
Grain yield plant ⁻¹ (g)	0.45	32.83**	0.67	10.39±0.473	4.2 - 18.2	7.87	
Spikes m ⁻²	803.88	6995.57**	162.16	253.64±7.35	179.3-357.3	5.02	
Grain yield (t/f)	0.02	1.00**	0.03	2.08±0.100	1.05 - 3.47	8.51	
Harvest index (HI) (%)	23.3	115.13**	21.88	28.7±2.701	16.7 - 44.7	16.3	
		3 rd Season					
Heading Date (day)	1.85	184.09**	1.57	95.50 ±0.723	81.7-113.3	1.31	
Days to Physiological Maturity(day)	2.47	82.33**	0.68	146.53±0.476	140.0- 158.3	0.56	
Plant height (cm)	22.11	352.96**	13.09	101.2±2.09	83.1- 121.33	3.58	
No. fertile tillers plant ⁻¹	1.8	2.75**	0.43	6.19 ±0.379	3.98 - 8.20	10.58	
Spike length (cm)	0.15	2.46**	0.54	12.47 ±0.424	10.8 - 14.07	5.9	
Spikelets spike ⁻¹	2.72	9.00**	0.91	20.05 ±0.551	16.7 - 22.87	4.77	
Grains spike ⁻¹	89.71	208.69**	15.58	60.97 ±2.279	42.3 - 73.40	6.47	
Grains weight spike ⁻¹ (g)	0.14	0.65**	0.08	2.86 ±0.163	2.1 - 3.88	9.69	
100- Grains weight (g)	0.08	0.39**	0.05	4.42 ±0.129	3.8 - 5.09	4.86	
Grain yield plant ⁻¹ (g)	2.25	14.31**	1.13	10.82 ±0.614	7.6 - 14.52	9.84	
Spikes m ⁻²	28.43	6642.28**	71.36	255.5±4.877	183.0- 362.0	3.31	
Grain yield (t/f)	0.17	0.53**	0.11	3.09 ±0.191	2.1 - 3.7	10.48	
Harvest index (HI) (%)	1.86	32.82**	12.97	30.33 ±2.079	23.2 - 36.9	11.87	

Where: * and ** denote significant at 0.05 and 0.01 levels of probability, respectively, SE = Standard error of mean.

Moderate PCV and GCV were recorded for heading date (HD) and spike length (SL) in the all seasons, in addition to 100- grains weight (HGW) in the 3rd season. Although, low PCV and GCV were obtained for days to physiological maturity (DPM) in all seasons and for spike lets spike⁻¹ (SS) only in 1st season. The phenotypic coefficient of variation was somewhat higher than genotypic coefficient of variation for all these traits. Notwithstanding, the magnitude of the differences between both were low for all traits. This proposed that the influence of environmental factors on the phenotype expression of the genotypes was low and there is a high chance for improvement of these traits through selection based on the phenotypic performance of these genotypes.

Heritability and genetic advance

Heritability is a critical parameter for executing an efficient improvement strategy. Single plant selection may be more effective for a trait that is highly heritable as compared to a trait which is less heritable.

Furthermore, environment may also interact with the genotypic constitution to influence heritability.

Heritability estimates for the thirteen studied traits are given in Table (3) and it was watched that in the 1st season high heritability was distinguished for heading date (99.06%) followed by DPM (98.82%), NSM (97.23%), GY (95.22%), PH (92.70%), HGW (92.68%), HI (91.26%), and SL (80.20%). Moderate heritability values were recorded for SS (78.65%), GS (74.36%), GWS (66.53%), GYP (66.34%) and NFT (64.50%). However, in the 2nd season (2013/2014) the highest heritability values were obtained for PH (99.28%) followed by HD (99.13%), DPM (98.84%), GYP (97.99%), NSM (97.72%), GS (97.20%), GY (97.06%), GFP (96.56%), HGW (95.55%), GWS (94.60%), SS (92.98%), NFT (92.41%), SL (86.84%) and HI (83.13%).

In the 3rd season (Table 3), the highest heritability values were recorded for DPM (99.18%) followed by HD (99.15%), GFP (97.21%), PH (96.38%), GS

(92.89%), GYP (92.50%), SS (90.53%), HGW (88.19%), NFT (85.84%), GY (81.71%) and SL (80.85%). Moderate heritability values were recorded for HI (68.72%).

These results revealed that environment had low influence on the expression of these traits which suggested that direct selection for them as major contributors of yield components would be improved yield of the study materials.

The estimates of genetic advance help in understanding the type of gene action involved in the expression of various polygenic traits. High values of genetic advance are indicative of additive gene action whereas low values are indicative of non-additive gene action (Singh and Narayanan, 1993). Thus, the heritability estimates will be reliable if it accompanied by high genetic advance.

The expected genetic advance values (GA) for thirteen studied traits of the evaluated genotypes are presented in Tables (3).

These values are also expressed as percentage of the genotypes mean (GAM) for each trait so that comparison could be made among various traits, which had different units of measurement. Genetic advance as a percent of mean (GAM %) was ranged from 12.22 (SS) to 77.00 (GY) in the 1st season and from 15.42 & 12.69 (DPM) to 112.07& 68.35 (GYP) in 2ndand 3rdseasons, respectively.

GAM results revealed that selecting the top 5% of the genotypes could be resulted in an advance of 12.22 to 77.00% and from 15.42 to 112.07% over the respective population mean. In this investigation almost all traits obtained a high genetic advance in 1st, 2ndand 3rdseasons, respectively.

Table 3. Genetic parameters of the studied traits of bread wheat genotypes 2012/2013, 2013/2014 and 2014/2015 seasons.

Parameters	Seasons								
		Vp	Vg	Ve	PCV%	GCV%	h ² _{bs} %	GA	GAM %
Traits									
Heading Date (day)	2012/13	269.62	267.09	2.53	16.46	16.38	99.06	33.51	33.59
	2013/14	286.94	284.45	2.49	17.34	17.27	99.13	34.59	35.42
	2014/15	185.14	183.57	1.57	14.25	14.19	99.15	27.79	29.10
Days to Physiological Maturity(day)	2012/13	116.46	115.09	1.37	7.20	7.16	98.82	21.97	14.67
	2013/14	125.85	124.39	1.46	7.57	7.53	98.84	22.84	15.42
	2014/15	82.78	82.10	0.68	6.21	6.18	99.18	18.59	12.69
Plant height (cm)	2012/13	499.08	462.64	36.44	18.44	17.76	92.70	42.66	35.22
	2013/14	942.80	935.98	6.82	26.84	26.74	99.28	62.79	54.89
	2014/15	361.69	348.60	13.09	18.80	18.46	96.38	37.76	37.33
No. fertile tillers plant ⁻¹	2012/13	4.31	2.78	1.53	38.88	31.22	64.50	2.76	51.66
	2013/14	3.16	2.92	0.24	36.50	35.09	92.41	3.38	69.48
	2014/15	3.04	2.61	0.43	28.15	26.08	85.84	3.08	49.78
Spike length (cm)	2012/13	3.28	2.63	0.65	14.56	13.04	80.20	2.99	24.05
	2013/14	4.41	3.83	0.58	15.98	14.89	86.84	3.76	28.58
	2014/15	2.82	2.28	0.54	13.47	12.11	80.85	2.80	22.43
Spikelets spike ⁻¹	2012/13	2.67	2.10	0.57	7.54	6.69	78.65	2.65	12.22
	2013/14	10.69	9.94	0.75	14.35	13.84	92.98	6.26	27.49
	2014/15	9.61	8.70	0.91	15.46	14.71	90.53	5.78	28.83
Grains spike ⁻¹	2012/13	241.04	179.23	61.81	26.74	23.06	74.36	23.78	40.97
	2013/14	297.20	288.87	8.33	30.54	30.11	97.20	34.52	61.15
	2014/15	219.08	203.50	15.58	24.28	23.40	92.89	28.32	46.45
Grains weight spike ⁻¹ (g)	2012/13	1.58	1.05	0.53	44.54	36.33	66.53	1.72	61.04
	2013/14	1.30	1.23	0.07	41.24	40.11	94.60	2.22	80.37
	2014/15	0.70	0.62	0.08	29.32	27.61	88.63	1.53	53.54
100- Grains weight (g)	2012/13	0.68	0.63	0.05	17.22	16.58	92.68	1.58	32.88
	2013/14	1.12	1.07	0.05	22.60	22.09	95.55	2.09	44.48
	2014/15	0.42	0.37	0.05	14.72	13.82	88.19	1.18	26.74
Grain yield plant ⁻¹ (g)	2012/13	31.37	20.81	10.56	52.34	42.63	66.34	7.65	71.53
	2013/14	33.28	32.61	0.67	55.52	54.96	97.99	11.64	112.07
	2014/15	15.06	13.93	1.13	35.87	34.50	92.50	7.40	68.35
Spikes m ⁻²	2012/13	8927.2	8679.9	247.29	35.69	35.19	97.23	189.3	71.49
	2013/14	7103.7	6941.5	162.16	33.23	32.85	97.72	169.7	66.89
	2014/15	6906.9	6835.5	71.36	32.52	32.36	98.97	169.4	66.31
Grain yield (t/f)	2012/13	0.84	0.80	0.04	39.26	38.31	95.22	1.79	77.00
	2013/14	1.02	0.99	0.03	48.56	47.84	97.06	2.02	97.08
	2014/15	0.60	0.49	0.11	25.14	22.73	81.77	1.31	42.34
Harvest index (HI)	2012/13	55.96	51.07	4.89	33.68	32.18	91.26	14.06	63.32

Parameters	Seasons								
	Vp	Vg	Ve	PCV%	GCV%	h ² _{bs} %	GA	GAM %	
Traits (%)	2013/14	129.72	107.84	21.88	39.68	36.18	83.13	19.50	67.96
	2014/15	41.47	28.50	12.97	21.23	17.60	68.72	9.12	30.06

Where: Vp = phenotypic variance, Vg = genotypic variance, Ve = Environmental variance, PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, h²_{b.s} = heritability in broad sense, GA = genetic advance, GAM (%) = Genetic advance as percent of mean.

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