



Evaluation of Genetic Variability, Heritability and Genetic Advance for Yield and Components of Bread Wheat (*Triticum aestivum L.*) Genotypes grown under Saline and non - Saline Conditions

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ARTICLE INFO

ARTICLE HISTORY

Received: 08/04/2017

Accepted: 05/10/2017

Available online: December 2017

KEYWORDS:

Genetic variability,
heritability,
genetic advance,
bread wheat,
Salinity.

ABSTRACT

A field experiment was conducted during three consecutive winter seasons of the years 2008/09, 2009/10 and 2010/11 at Merowe Research Station Farm, Northern State, Sudan to estimate the genetic variability, heritability and genetic advance of grain yield and yield contributing traits in 16 bread wheat genotypes grown under saline and non – saline field conditions. The genotypes were arranged in a randomized complete block design with three replications. In both sites, the analysis of variance revealed highly significant differences among genotypes for all the traits studied. The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV), which indicates a slight effect of environment on the expression of the characters studied. In both sites, high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were recorded for number of spikes per m², plant height and number of grains per spike. In both sites, heritability exhibited wide range of variation. At non – saline site, the high heritability in broad sense was estimated for number of days to 50% heading (87.03), number of days to 90% maturity (85.13), plant height (83.79), 1000 – grain weight (62.78) and number of spikes per m² (58.87). On the other hand, at saline site high heritability estimates were recorded for number of days to 90% maturity (85.16) followed by number of days to 50% heading (84.29) and plant height (53.11). These traits also indicated high genetic advance except the plant height. In both sites, high heritability coupled with high genetic advance as percent of means were recorded for number of days to 50% heading, number of days to 90% maturity and plant height that indicated presence of additive gene action in the inheritance of these traits.

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INTRODUCTION

Wheat (*Triticum aestivum* L.) is a member of the family Poaceae, which includes major cereal crops such as sorghum, maize, wheat, rice, millet and barely (Briggle and Reitz, 1963). It is the staple food of about two billion people (36% of the world population), and provides nearly 55% of the carbohydrates and 20% of the food calories consumed globally (Breiman and Graur, 1995). Wheat is becoming increasingly popular and since 1960, its consumption has risen almost 5% per year in developing countries, faster than any other basic food crop (Bushuk, 1998).

Salinity is a major factor limiting plant growth and leads to lower agricultural production in arid and semi-arid regions (Bai *et al.*, 2011). Agricultural productivity is severely affected by soil salinity because salt levels harmful to plant growth affect large terrestrial areas. Damaging effects of salt accumulation in agricultural soils have influenced ancient and modern civilizations. It is estimated that 20% of the irrigated land in the world is presently affected by salinity (Yeo, 1999, Yamaguchi and Blumwald, 2005).

Land use the Sudan is geared towards achieving high and extensive agricultural production, pastures of natural grazing (ranching) and forest production for wood and charcoal (Alexander, 2001). Agricultural production is the most important system of land use, involving irrigated schemes as well as rain fed cropping (Conforti, 2011).

In recent years, the demand for more food dictated considerable expansion of cultivable land (Alexandratos, and Bruinsma, 2012). The efforts to maximize agricultural production encountered many constrains of which

soil salinity is a major element (Alexandratos, 2005, and Ali, 1990). Although the majority of agricultural crops are salt sensitive, there are differences in their ability to withstand salt stress among the various species (Wright *et al.*, 1992).

Heritability plays a predictive role in breeding, expressing the reliability of phenotype as a guide to its breeding value. It is understood that only the phenotypic value can be measured directly while breeding values of individuals are derived from appropriate analyses. It is the breeding value, which determines how much of the phenotype would be passed onto the next generation (Rehman, 1994). High genetic advance coupled with high heritability estimates offers the most effective condition for selection (Larik, *et al.*, 2000). Thus, genetic advance is yet another important selection parameter that aids breeder in a selection program (Shukla, *et al.*, 2004). Phenotypic and genotypic variance, heritability and genetic advance have been used to assess the magnitude of variance in wheat breeding material (Bhutta, 2006). Kumar *et al.*, (2003) reported high heritability coupled with high genetic advance for plant height, number of spikelets per spike, 1000 - grain weight and number of days to 50% heading in wheat.

The objectives of this study were to assess the variability, heritability and genetic advance as percent of mean of grain yield and some of its related components and to select more desired traits that may contribute for the improvement of bread wheat under saline and non - saline field conditions.

MATERIALS AND METHODS

Plant materials: Thirteen wheat genotypes (Table 1), plus three checks

namely, Sakha 93 and two Iranian cultivars, namely, Kavir and Sistan were evaluated under saline and non-saline field conditions over three consecutive years (2008/09, 2009/10 and 2010/11)

during the winter season at Fetna, Merowe locality (Latitude: 18° 27' 0" N, Longitude: 31° 49' 59" E, Elevation: 258 meters).

Table 1: List of 16 bread wheat genotypes used for genetic diversity studies

Genotype no.	Name of genotype
1	UP 301 / Son 64 // P160 / 3 / Debeira
2	PC 930 / Giza155 // BOW
3	Giza 155 / Nai 60 – 2
4	Kauz //Trap # 1 / Bow
5	Un known
6	Kauz / Pastor
7	Kavir (Irran variety used as check)
8	Sistan (Irran variety used as check)
9	Sakha 93 (Egypt variety used as check)
10	Super Seri # 2
11	VEE/MJI//2*TUI
12	Un known
13	Condor (released commercial cultivar)
14	EL Neilain (released commercial cultivar)
15	Wadi EL Neel (released commercial cultivar)
16	Sasareib (released commercial cultivar)

Land preparation, design and cultural practices:

Experimental land at the saline site was ploughed by a chisel plough and leveled. In the non-saline field, the land was pre-irrigated, disk ploughed, harrowed and leveled. The design used was a Randomized Complete Block with three replications. At the two sites, plots consisted of 6 rows, 4 m long spaced at 20 cm. Grain yield was assessed from a net area of 3.2 m². Planting dates were performed on 1 December 2008, 13 December 2009 and on 8 December 2010. Planting was done by hand at a seed rate of 120 kg ha⁻¹. In the saline field, experiment received the recommended dose of 43 kg P₂O₅ ha⁻¹ as triple super phosphate (TSP) during soil preparation, and the nitrogen fertilizer

was added at a rate of 86 kg N ha⁻¹ as urea in two split doses, three weeks after sowing and at heading stage. Weeds were controlled manually and chemically using the herbicide 2, 4-D three weeks after sowing for the control of broadleaf weeds species in non-saline site. No weeds were observed in the saline soil site. The experiment at the non-saline site (Karu) was irrigated every 13 to 15 days throughout the growing season, while in the saline site, irrigation was done at 9 to 11 days intervals.

In the three seasons soil samples were taken randomly from the saline site to determine the salinity level, exchangeable sodium percentage (ESP) and the soil pH (Tables 2, 3 and 4).

Table 2: Analysis of twelve soil samples from the saline site soil at Fetna, Merowe locality, season 2008/2009

Sample no.	Depth (cm)	PH	EC	ESP
1	0 – 20	7.8	12.6	54.4
2	20 – 40	8.2	23.6	73.2
3	0 – 20	8.2	5.0	35.0
4	20 – 40	8.3	9.8	33.9
5	0 – 20	8.3	19.3	80.3
6	20 – 40	8.4	28.1	71.0
7	0 – 20	8.2	16.8	59.5
8	20 – 40	8.0	27.0	55.0
9	0 – 20	8.5	14.8	58.2
10	20 – 40	8.0	76.7	93.6
11	0 – 20	8.2	18.6	50.0
12	20 – 40	8.0	21.7	74.7

Table 3: Analysis of ten soil samples from the saline site soil at Fetna, Merowe locality, season 2009/2010

Sample no.	Depth (cm)	PH	EC	ESP
1	0-20	6.4	168.2	30
2	20-40	6.5	170.8	24
3	0-20	7.5	14.2	18
4	20-40	7.6	6.1	16
5	0-20	7.6	17.1	31
6	20-40	7.6	11.3	20
7	0-20	6.5	235.0	88
8	20-40	7.2	95.6	35
9	0-20	6.7	144.6	22
10	20-40	7.1	135.8	21

Table 4: Analysis of eight soil samples from the saline site soil at Fetna, Merowe locality, season 2010/2011

Sample no.	Depth (cm)	PH	EC	ESP
1	0 – 20	7.5	24.5	42
2	20 – 40	7.6	11.6	38
3	0 – 20	7.5	15.5	29
4	20 – 40	7.5	10.0	27
5	0 – 20	7.5	26.3	43
6	20 – 40	7.4	17.9	31
7	0 – 20	7.8	15.6	29
8	20 – 40	8.0	17.6	33

Parameters measured: During the three seasons and in both sites, observations were taken on ten plants randomly selected in a plot. Data were collected on

the following vegetative and reproductive characters:

Days to 50% heading: it was recorded when 50% of the heads merged from leaf sheath.

Days to 90% maturity: it was recorded as number of days from planting to 90% of spikes lost green color from the glumes.

Plant height (cm): it was measured from the ground level to the tip of the spike at the physiological maturity stage.

Number of spikes / m²: it was counted in each sample taken from an area of 0.2 m². Then the total number of spikes from this area was multiplied by 5.

Number of grains/spike: Seeds of 10 randomly taken spikes were counted to estimate grains / spike.

Thousand grain weight (g): it was determined from a sample of 10 spikes taken from the central rows.

Harvest index (HI %): it was calculated as the ratio of the grain yield to biomass yield.

Grain yield (kg ha⁻¹): Excluding the two boarder rows, a net area of 3.2 m² (four rows by 4 m long) was hand harvested from the ground level. The harvested material was bundled and left to sun-dry, then threshed manually and the grains were weighed to give the grain yield.

Statistical analysis: The data were analyzed using the MSTAT statistical package. Combined analyses of variance were carried for the all data and means were tested for significant difference by Duncan's Multiple Range Test (DMRT).

Genetic parameters estimates: Heritability in broad sense (H²) was estimated according to Falconer (1989) using eq. 1:

$$\text{Heritability (H}^2\text{)} = (\sigma^2_g / \delta^2_{ph}) \times 100 \quad (1)$$

H²: Heritability; δ^2_g : genotypic variance and δ^2_{ph} : phenotypic variance. Genotypic (δ^2_g) and phenotypic

variances (δ^2_{ph}) were obtained from the analysis of variance table according to Comstock and Robinson, (1952) using eq. 2 and eq. 3:

$$\delta^2_g = (MS1 - MS2) / r \times s \quad (2)$$

$$\delta^2_{ph} = (MS1) / r \times s \quad (3)$$

Where

r: replication,

s: season

MS1: Mean square for cultivar,

MS2: Mean square for genotype \times season).

The mean values were used for genetic analyses to determine Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV), according to Singh and Chaudhury (1985) using eq. 4 and eq. 5: Phenotypic coefficient of variation

RESULTS AND DISCUSSION

In both sites, the analysis of variance showed that the mean squares for genotypes were highly significant ($P \leq 0.001$) for all traits studied (Tables 5 and 6). This indicated the existence of a high degree of genetic variability in the material to be exploited in a breeding

Table 5: Mean squares of yield and some yield components for 16 bread wheat genotypes grown during three seasons 2008/09, 2009/10 and 2010/11 under non – saline field conditions

Traits	Season (d.f= 2)	Genotype (d.f= 15)	Seas. X geno. (d.f= 30)	Pooled error (d.f = 90)
Days to 50% heading	316.3331***	148.681***	6.696**	1.036
Days to 90% maturity	2700.1111***	163.6571***	8.4301***	1.842
Plant height (cm)	1236.2721**	327.4931***	16.1821*	11.737
No. of spikes/m ²	370173.911**	46102.279***	7373.113*	4935.474
No. of grains/spike	2752.654***	135.014***	51.366*	32.648
1000-grain weight	155.647*	118.678***	18.250***	4.698
Grain yield	25963788.088***	2460395.731***	1070360.365n.s	1364416.158

*, ** and *** Significant at 0.05, 0.01 and 0.001 levels of probability, respectively.

n.s = non - significant difference at 5% probability level.

Table 6: Mean squares of yield and some yield components for 16 bread wheat genotypes grown during three seasons 2008/09, 2009/10 and 2010/11 under saline field condition

Traits	Season (d.f= 2)	Genotype (d.f= 15)	Seas. X geno. (d.f= 30)	Pooled error (d.f = 90)
Days to 50% heading	703.938***	155.052***	8.678***	1.307
Days to 90% maturity	315.438***	158.033***	8.119***	1.806
Plant height (cm)	3210.173***	174.098***	36.565***	11.747
No. of spikes/m ²	532237.194***	19467.748***	12090.935**	5688.547
No. of grains/spike	1393.761***	187.398***	40.443*	21.798
1000-grain weight	268.072***	32.761***	21.231***	4.655
Grain yield	57420952.333***	1213834.800***	675913.015**	336086.583

*, ** and *** Significant at 0.05, 0.01 and 0.001 levels of probability, respectively.

$$(PCV) = (\sqrt{\delta^2_g} / \bar{x}) \times 100 \quad (4)$$

Genotypic coefficient of variation

$$(GCV) = (\sqrt{\delta^2_{ph}} / \bar{x}) \times 100 \quad (5)$$

Where:

δ^2_g = genotypic variance.

δ^2_{ph} = phenotypic variance.

\bar{x} = sample mean.

Genetic advance (GA) was calculated with the method suggested by Allard (1960); Singh and Chaudhary (1985) using eq. 6:

$$GA = K. \sigma_{ph}. H^2 \quad (6)$$

Where:

GA: genetic advance.

K: constant = 2.06 at 5% selection intensity.

σ_{ph} : square root of phenotypic variance.

H²: Heritability.

GA as % of mean (GAM) = (GA / mean value) \times 100

program, and also reflected the broad ranges observed for each trait. These results confirmed the results of (Yousaf *et al.*, 2008; Kalimullah *et al.*, 2012 and Kumar *et al.*, 2014), who reported considerable variation among wheat genotypes tested.

Genetic parameters at non - saline soil:

The mean, genotypic variance, phenotypic variance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (%) in broad sense, genetic advance and genetic advance as percent of the mean are presented in (Table 7). The phenotypic coefficients of variation were generally higher than the genotypic coefficients of variation for all traits studied, indicating the influence of growing environments. These findings were in agreement with those reported by (Panwar and Singh, 2000); (Bergale *et al.*, 2001); (Pawar *et al.*, 2002); (Dwivedi *et al.*, 2004) and (Kumar *et al.*, 2014). The estimates of GCV were high for number of spikes / m² followed by plant height, days to 50% heading and days to 90% maturity and number of grains per spikes; these results are similar to those of (Sharma and Garg, 2002) and (Kumar *et al.*, 2002). The remaining traits recorded moderate to low GCV estimates. The PCV values were higher than GCV values for all the traits which reflect the influence of environment on the expression of traits. High estimates heritability associated with high estimates of genetic advance was observed for days to 50 % heading,

Table 7: Genetic parameters for some characteristics in 16 bread wheat genotypes grown during three seasons 2008/09, 2009/10 and 2010/11 under non – saline field conditions

Characters	Mean	δ^2g	δ^2ph	GCV (%)	PCV (%)	h^2 (%)	GA	GAM (%)
Heading	66	15.77	18.12	24.81	26.60	87.03	7.64	11.57
Maturity	106	17.24	20.25	25.95	28.12	85.13	7.89	7.44
Plant height	82	34.59	41.28	36.75	40.15	83.79	11.09	13.52
Spikes/m ²	536	4303.24	7309.32	409.99	534.34	58.87	103.69	19.34
Grains/spike	52	9.29	30.04	19.04	34.25	30.92	3.49	6.71
1000-grain weight	39	11.15	17.76	20.86	26.33	62.78	5.45	13.97

δ^2g = Genotypic variance, δ^2ph = Phenotypic variance, PCV = Phenotypic coefficient of variance, GCV = Genotypic coefficient of variance, h^2 (%) = Broad sense heritability, GA = Genetic advance, GAM = Genetic advance as percent of mean.

Genetic parameters at saline soil: The mean, genotypic variance, phenotypic

days to 90% maturity and plant height, which in fact demonstrate the presence of additive genes effect indicating effectiveness of selection for the improvement of these trait. Such results showed similarity with findings of (Atta *et al.*, 2008) and (Bhoite *et al.*, 2008). Broad sense heritability was highest for days to 50 % heading followed by days to 90% maturity, plant height; similar results were published by (Atta *et al.*, 2008). Heritability and genetic advance are important selection parameters. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone (Johnson *et al.*, 1955). Broad sense heritability was highest for days to 50 % heading followed by days to 90% maturity, plant height, similar results were published by (Atta *et al.*, 2008). High heritability accompanied with high genetic advance in case of plant height, days to 90% maturity and days to 50% heading, number of spikes / m² indicates that most likely the heritability is due to additive gene effects and selection may be effective in early generations for these traits. Similar findings have been reported by (Sharma and Garg, 2002).

variance, genotypic coefficient of variation (GCV), phenotypic coefficient

of variation (PCV), heritability, genetic advance and genetic advance as percent of mean are given in (Table 8). From the observed results the phenotypic coefficient of variation was ranged from 462.75% (number of spikes per m²) to 27.45% (number of days to 50% heading). Although broad-sense heritability estimates suggested much greater phenotypic than genetic variation in salinity tolerance among wheat genotypes. The substantially greater phenotypic variance indicated a strong masking effect of the environment (Singh and Narayanan, 2000). Reduction in genetic variability under stress, which

has been reported previously in wheat (Singh and Chatrath, 1992); (Ashraf, 1994) and sorghum (Azhar and McNeilly, 1989), suggests rigorous and careful selection of salt tolerant accessions. The heritability values in a broad-sense are useful as first approximations but not as definitive values for the improvement of salinity tolerance in wheat. Genetic grains that expected from selecting the top 5% of the genotypes, as a present of mean were varied from 3.03% for 1000 – grain weight to 18.50% for number of grains per spike.

Table 8: Genetic parameters for some characteristics in 16 bread wheat genotypes grown during three seasons 2008/09, 2009/10 and 2010/11 under saline field conditions

Characters	Mean	δ^2_g	δ^2_{ph}	GCV (%)	PCV (%)	h^2 (%)	GA	GAM (%)
Heading	59	16.26	19.29	25.20	27.45	84.29	7.62	12.91
Maturity	92	16.65	19.55	25.50	27.63	85.16	7.75	8.42
Plant height	50	15.28	28.77	24.43	33.52	53.11	5.87	11.74
Spikes/m ²	383	819.64	5482.01	178.93	462.75	14.95	22.80	5.95
Grains/spike	32	16.32	32.22	25.24	35.47	50.65	5.92	18.50
1000-grain weight	29	1.28	8.87	7.07	33.09	14.43	0.88	3.03

δ^2_g = Genotypic variance, δ^2_{ph} = Phenotypic variance, PCV = Phenotypic coefficient of variance, GCV = Genotypic coefficient of variance, h^2 (%) = Broad sense heritability, GA = Genetic advance, GAM = Genetic advance as percent of mean

CONCLUSION

The analysis of variance revealed highly significant differences among the genotypes for all parameters measured. Phenotypic coefficients of variation were generally higher than genotypic coefficients of variation for all traits studied, indicating the influence of growing environment. At saline site, the result of genetic advance as percent of mean showed an increase of 3.03% to 18.50% magnitude made by selection. In both sites, the characters days to 50% heading, days to 90% maturity and plant height exhibited high heritability coupled with high genetic progress indicating that most likely the heritability is due to additive gene

effects and selection may be effective in early generations for these traits. The high genetic variability, heritability and genetic advance as percent of mean for the traits viz: days to 50% heading, days to 90% maturity and plant height could be the appropriate selection criteria for better grain yield in bread wheat under saline and non - saline field conditions.

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