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Research Article

**Growth Performance, Heritability and Genetic Advance in
Bread Wheat (*Triticum aestivum* L.) Grown in the Sudan
Savanna of Nigeria**

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ABSTRACT

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Thirty bread wheat genotypes were taken up to evaluate their performance, heritability and genetic advance estimates. These genotypes were laid in a randomized complete design with three replications, plot size (3m x 2m) was measured and seeds were drilled at 30cm row to row. Fertilizer was applied at the rate of 100kg N, 40kg each P₂O₅ and K₂O per hectare. The experiment was conducted during the 2018/2019 cool harmattan season; seeds were sown on November 26th, 2018 and while the crop was harvested on March 2019 under irrigated condition. Results obtained from the experiment revealed significant variations for days to 50% heading, plant height, spike length, spikelets per spike, and grain yield. . Early heading genotypes were found to be Genos 21, 27, 25, 12, 24 and 28 with heading days ranging from 52 to 55 days. Similarly, high-yielding genotypes were detected in Genos 22, 18, 27, 12, 16 and 30, with the mean grain yield ranging from 5.90 to 7.91 tonnes per hectare. Heritability estimates were mostly moderate for some parameters ranging from 31.58% to 48.73% with spike length recorded the highest value of 63.55%. Similarly, genetic gain was low for some of the parameters ranged from 5.50% to 8.60%, while moderate values were observed for spike length (18.40%) and grain yield (18.40%).

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INTRODUCTION

Bread wheat (*Triticum aestivum* L.), an annual self-pollinating species of the family (*Gramineae*) and Tribe *Triticeae*, is the most widely grown cereal crop of the globe (Khan, 2013; Baloch *et al.*, 2016) It is a hexaploid crop ($2n = 6x = 42$) with a genome AABBDD (Shibeshi, 2019). Cultivation of wheat took place about 10000 years ago as part of the “Neolithic Revolution”. The earliest cultivated wheat forms were the diploids with genome “AA” which included “Einkorn” wheat and the tetraploids with genome “AABB” which also included the “Emmer” wheat (Shewry, 2009).

Recently, it was asserted that wheat was cultivated in Nigeria especially the Northern parts of the country since the sixteenth century (Rayar *et al.*, 1990) The wheat produced then was meagre and only consumed by the nobles during festive occasions (Aminu-Kano and Ikwelle, 1998). In Nigeria, wheat is cultivated entirely under irrigation during November to March and within latitudes 10 – 14°N at altitude of 240 – 360 meters above sea level (Masl). During these months, right temperatures are in the range of 10 – 15°C (Olugbemi, 1990). This favourable wheat production condition occurs within the Sudan–Sahel zones of the country (Falaki and Mohammed, 2011), with states of Borno, Yobe, Kano, Katsina, Zamfara, Sokoto, Kebbi, Bauchi, Gombe and Adamawa being the prominent wheat producers (Lagoke *et al.*, 1998; Wudu, 1998). Despite the number of acreage under production the output is very low, ranging from 60,000 to 90,000 tonnes (Anon, 2020; Anon, 2021). During 2018-2020, average wheat yield per hectare stood at 1368kg, while wheat consumption was 4760, 4900 and 4319 tonnes in these three years respectively; in fact, the consumption level grew from 3582 tonnes in 2010 to 4900 tonnes in 2019 (Anon, 2020). Wheat consumption in Nigeria is reportedly growing at the rate of more than 20% annually, leading to a wide gap between the domestic

It is produced worldwide on about 216 million hectares with production potential of about 650 million tonnes (FAO, 2012), thus being third in position after maize (785m. tonnes) and rice (652m. tonnes) (Shewry, 2009). The leading wheat producers today are China (126 million metric tonnes), India (95 million metric tonnes), Russia (60 million metric tonnes), USA (55 million metric tonnes), Germany (28 million metric tonnes), Pakistan (26 million metric tonnes), Australia (25 million metric tonnes) and Ukraine (24 million metric tonnes) (FAOSTAT, 2015).

production and consumption and, consequently, necessitating heavy import of the commodity (Shettima, 1998).

In order to meet the challenges of high wheat demand, breeders need to enhance their efforts to evolve and breed high-yielding, heat-tolerant, early maturing wheat varieties having resistance against pests and diseases, and a good baking quality. However, availability of improved, high-yielding wheat varieties is a major constraint towards successful wheat production in the country. Several wheat varieties have been evolved and released from time to time for cultivation in diverse climatic regions. However, yield and seed quality of these varieties need be improved to match the ever-growing demands (Deepak *et al.*, 2018). This can be achieved through the use of existing genetic variability (Deepak *et al.*, 2018). Improvement of several desirable traits is made possible through evaluation, and potential varieties are identified and selected as parental types. Hybridization combines desirable genes with target genotypes and further selection may result in identification of superior types for release as promising candidates obtained after multi locational trial. Important characters of wheat such as days to heading, plant height, spike length, number of spikelets per spike, 1000-seed weight, and maturity period, quality and quantity of grain are

often evaluated by experts (Baloch *et al.* 2016) Zeleke *et al.*2019; Gebrie *et al.* 2020).

Heritability is a measure of phenotypic variance attributable to genetic cause, which has a predictive function in breeding crops (Songiri *et al.*,2008). Estimates of heritability provide information about the traits that transmit from parents to their offsprings, hence has a crucial role in selection criteria to improve quantitative traits of crops (Saleem *et al.*, 2016). Varying heritability estimates have been obtained for several quantitative characters in bread wheat and used in predicting selection of important characters (Al-Sayaydeh *et al.*, 2019; Destaw *et al.*, 2020; Prasad *et al.*, 2021). However, Dergicho *et al.* (2015) reported high heritability estimates for days to heading, number of spikelets per spike, spike length, 1000 grain weight and grain yield. High, moderate or low genetic advance has been reported for several quantitative characters of wheat. Yadav *et al.* (2015), Dergicho *et al.* (2015) and Prasad *et al.*(2021) reported high genetic advance for characters such as tillers per plant, number of spikelets per plant, spike length, 1000-seed weight, days to heading and grain yield. However, Arega *e al.* (2010) and Saleem *et al.* (2016) reported moderate genetic gain for spike length, days to heading, plant height and spikelets per spike.

The present study was undertaken to evaluate the performance of bread wheat genotypes for yield and yield components, their heritability in broad sense, and the genetic gain.

MATERIALS AND METHODS

The present experiment was conducted at the Experimental Garden of the Biological Sciences Department, University of Maiduguri, Maiduguri, Borno State [lat. 11°.50'N, long. 13°09'E, 359 meters above sea level (Masl)]. The whole experiment was set up on 26th November 2018 under irrigated condition. Harvesting was done on 10th March 2019. The experiment used 30 bread-wheat genotypes, including two

Checks; Reyna28 and Norman, obtained from Lake Chad Research Institute(LCRI), Maiduguri, Nigeria (Table 1). A randomised complete block design (RCBD) was used with three replications. Statistix 0.8 was the statistical software used for the analysis. All the 30 genotypes were source from LCRI gene bank originated from Cimmyt, Mexico after series of selections and hybridizations. Plot size measured 3m x 2m with seeds drilled at 30cm apart within plots. A seed rate of 100kg ha⁻¹ was used and dressed with seed-dressing chemical (Apron plus). Similarly, standard fertilizer rate of 100kgN, 40kg K₂O and 40kg ha⁻¹ was supplied. All plots received 50kgN, 40kg each of P₂O₅ and K₂O per hectare as basal application and incorporated. The balance of the 50kgN was applied 4 weeks after sowing. Immediately after sowing, irrigation was carried out at the frequency of 4 – day intervals. At full maturity, irrigation was stopped 10 to 14 days before harvest to allow proper drying and mellowing of crops for easy harvest and thresh. Weeding was carried out to keep plots and surrounding field weed-free and clean. All other recommended cultural practices for wheat production were carried out.

Data were collected from 10 randomly selected plants from the net plot for each genotype, following the standard agronomic data-collection procedure.

Data were collected on the following parameters:

1. **Days to 50% heading:** this was recorded from the day of sowing to when 50% of plants in the net plot produced heads.
2. **Plant height:** this was the measurement (in cm) from the base (ground level) of the plant to the top of the spike (excluding awns) at maturity.
3. **Spike length:** this was the measurement (in cm) from the base to the tip of the spike, excluding awns, at maturity.

4. **Number of spikelets per spike:** this was counting of spikelets of each genotype on the rachis of the main mature plant.
5. **1000-seed weight:** this was the weight of 1000 seeds collected from individual genotypes from each plot at maturity and weighed (in g), using a sensitive weighing balance.
6. **Grain yield per hectare:** this was the weight of each net plot (in kg) expressed in tonnes per hectare (t/ha).

The morphological characters were analysed using randomized complete block design analysis following Gomez and Gomez (1984). “F” test was applied to determine the significance of treatments at 5% level of probability. LSD at 5% was used to separate the means, using the statistics’ 8.0 software. Broad sense heritability was estimated using variance components as described by Falconer (1989)

$$h_b^2 = \frac{\delta_g^2}{\delta_{ph}^2} \times 100$$

Similar genetic gain as a percentage of mean was obtained, assuming selection differential of superior 5% genotypes, as described by Johnson *et al.* (1955)

$$GA = K \delta_{ph} h^2$$

$$GAM = \frac{(GA)}{\bar{x}} \times 100$$

Where: δ_g^2 , δ_{ph}^2 , are genotypic and phenotypic variances, GA= genetic advance in absolute unit, K standardized differential at 5% selection intensity (K=2.063), δ_{ph} = phenotypic standard deviation and h^2 = heritability in broad sense.

RESULTS

The result of analysis of variance (ANOVA) for grain yield and other yield-related traits showed highly significant differences with the exception of 1000-seed weight (Table 2). The means and their ranking of the measured characters are given in Table 3. Days to 50% heading significantly varied from 52 days for genotypes 21 and 27 to 65 days for genotype 3. These were the early and latter heading genotypes. Early-heading genotypes were also observed for genotypes 25 and 12, with mean heading days being 52 and 53 days, respectively. The overall mean heading days was 58.36 days, and a coefficient of variation of 6.99 percent. Plant height significantly varied from 73.63cm for genotype 5 to 92.50 cm for genotype 20. However, genotype 1 (92.27cm) was the second tallest plant, and together with genotype 20 recorded non-significant plant heights. Similarly, genotypes 11, 12, 19, 21, 22 and 29

appeared to be among the shortest. The overall mean value for this character was observed to be 82.95cm, with coefficient of variation of 4.83 percent. Spikelet number as a component of yield varied significantly from 14.33 for genotype 25 to 19.33 for genotype 1. Also, genotypes 4, 6, 13, 16, 23, 26 and 30 provided superior members for spikelets per spike, which did not differ significantly among them, (Table 3). The overall mean value for the character was 16.88, with a coefficient of variation of 7.06 percent. Spike length, a component of high yield, also varied significantly from 6.43cm for genotypes 24 to 9.337cm for genotype 29. Also, genotypes 5, 16 and 17 recorded long spike length values, e.g., 9.00cm and 9.17cm for the latter two, respectively, which were not significantly different from each other. The overall mean value for this character was 8.18cm, with a coefficient of variation of 8.50 percent. The grain yield being the most important of all characters also varied significantly. However, it varied from 3.60 tonnes for genotype 6 to 7.91 tonnes for genotype 22, the two being the lowest and highest yielders. Genotypes 12 (6.00 tonnes), 16 (6.40 tonnes), 18 (6.40 tonnes) and 27 (6.02 tonnes) were also among the top yielders.

Genotypes 6 (3.60 tonnes), 7 (4.17 tonnes) and 24 (4.22 tonnes) recorded the lowest yields. The overall mean grain yield was 5.22 tonnes with a coefficient of variation of 14.78 percent. Heritability (broad sense) and genetic advance of all significant characters are presented in Table 4. Heritability estimates ranged from high to moderate (63.55%) for spike length and (31.58%) for days to 50% heading. Similarly, moderate heritability estimates were recorded

for plant height (48.73%), number of spikelets per spike (44.36%) and grain yield (43.54%). The estimated genetic advance showed mostly low to moderate values. Moderate genetic advance was recorded for spike length (18.40%) and grain yield (17.62%). However, days to 50% heading (5.50%), plant height (6.78%) and number of spikelets per spike (8.00%) recorded a low genetic advance (Table 4).

Table 1: Names of Genotypes/Lines Used

S/No	Genotypes/Lines	Treatment Number
1	Reyna 28 (check 1)	Geno 1
2	Norman (check 2)	Geno 2
3	Qafzah-19//Vee 7/Kauz	Geno 3
4	Kauz//Altar 84/Aos 3/Kauz/3/Katila-1/4/Chen/Aegilopes Squarrosa (Taus)//BCN/3/Kauz	Geno 4
5	Seri/B*2/3/Kauz *2/Bow//Kauz/4/Kauz/Florkwa-1/5/Pl.861/Rdwg//Naama-6	Geno 5
6	YMI#6/Gen//Tia.1/3/Vee #5//Dove/Bud 4/Milan/Pastor /S/Attila *2/3/Kauz *2/Trap//Kauz	Geno 6
7	Vee/Pjn//2* Kauz/3/Milan/Pastor/4/Kauz//Trap#1/Bow	Geno 7
8	Goumria – 8//Milan/Pastor/3/Tnmu/Milan	Geno 8
9	Kauz//Altar 84/ Aos 3/Kauz/3/Catbird – 10/4/Milan Ducula	Geno 9
10	Giza – 168/4/Attila *2/3/Kauz *2/Trap//Kauz	Geno 10
11	Seri.1B//Kauz/Hevo/3/Amad/4/Kauz/GYS//Kauz	Geno 11
12	Seri.1B//Kauz/Hevo/3/Amad/4/Pfau/Milan	Geno 12
13	Vee/Pjn//2* Kauz/3/Shuha -4/Fow2	Geno 13
14	Hubara – 7/4/Chen/Aegilops Squarrosa (Taus)//Ben/3/ Kauz	Geno 14
15	Seri.1B//Kauz/Hevo/3/Amad/4/Milan/Pastor/5/Icarda – srrl – 6	Geno 15
16	Hubara – 7//Milan/Pastor	Geno 16
17	Seri.1B *2/3/Kauz *2/Bow///Kauz/4/Milan/Pastor	Geno 17
18	Attila *2/P6w65//Pfau/Millan	Geno 18
19	Kauz ‘S’/Seri//Pfau/Milan	Geno 19
20	Shuha –7/Shuha -1//Nemura/Cettia	Geno 20
21	Jawahir -10/Sekhrah -1	Geno 21
22	Pfau/Milan//Jawahir – 9	Geno 22
23	Faris – 17//Pfau/Milan	Geno 23
24	Munia/Altar 84//Milan/3/Milan/Pastor	Geno 24
25	Bacanora T88/Ruth -2	Geno 25
26	Cham – 8/Ruth – 3	Geno 26
27	Hubara -5/3/Nesma *2/261 – 9/Firtail	Geno 27
28	Galvez/Weaver/3/Vorona/Cno79//Kauz/4/Milan//Psn/Bow	Geno 28
29	Seri.1B//Kauz/Hevo/3/Amad/4/Milan/Pastor	Geno 29
30	Mex 94.27. 1. 20/3/50Koll//Attila/3 *Bcn/4/Zafir – 3	Geno 30

Table 2: Analysis of Variance Result for the Morphological Characters Evaluated at Maiduguri in 2018/2019 Cool Season

Character	MSR (Df=2)	MSG (Df=29)	MSE (Df=58)	Min	Max	CV (%)
Days to 50% heading	4.144	39.654**	16.627	52.00	65.00	6.99
Plant height (cm)	39.800	61.729**	16.029	73.63	92.80	4.83
Spike length (cm)	0.236	1.565**	0.484	7.17	9.17	8.50
Number of spikelets per spike	0.811	4.816**	1.420	15.00	19.00	7.06
1000 seed weight (g)	40.515	22.492 ^{ns}	24.487	34.37	45.77	12.52
Grain yield (t/ha)	1.230	1.967**	0.594	3.60	7.90	14.78

Df = Degrees of Freedom, MSR = Mean Squares Replication, MSG = Mean Squares Genotypes, CV = Coefficient of Variation, * = significant at p=0.05, ** = significant at p=0.01, ns = not significant

Table 3: Means and Ranking of the Morphological Characters of the Bread Wheat Evaluated at Maiduguri in 2018/2019 Cool Season

Genotype	Days to 50 % heading	Plant Height (cm)	Spike Length (cm)	Number of spikelets per spike	1000 – seed weight (g)	Grain yield (t/ha)
Geno 1	57.33 ^{d-1}	91.27 ^{ab}	8.83 ^{abc}	19.33 ^a	41.10 ^a	5.07 ^{c-g}
Geno 2	60.33 ^{a-g}	80.43 ^{e-j}	8.13 ^{b-g}	15.33 ^{fgh}	40.07 ^a	4.83 ^{c-h}
Geno 3	65.00 ^a	87.07 ^{a-d}	8.10 ^{b-g}	17.00 ^{c-f}	35.90 ^a	5.14 ^{c-g}
Geno 4	58.33 ^{b-i}	86.50 ^{a-f}	7.87 ^{c-g}	18.00 ^{a-d}	38.27 ^a	4.67 ^{d-g}
Geno 5	61.00 ^{a-g}	73.63 ^m	9.00 ^{abc}	17.00 ^{c-f}	42.13 ^a	4.33 ^{fgh}
Geno 6	60.00 ^{a-g}	82.97 ^{d-k}	8.33 ^{a-f}	18.00 ^{a-d}	40.27 ^a	3.60 ^h
Geno 7	64.33 ^{ab}	83.93 ^{c-h}	8.47 ^{a-f}	17.33 ^{b-e}	41.13 ^a	4.17 ^{gh}
Geno 8	63.00 ^{a-d}	83.17 ^{d-k}	7.33 ^{fgh}	17.33 ^{b-e}	36.37 ^a	4.57 ^{fgh}
Geno 9	62.67 ^{a-e}	83.60 ^{c-i}	7.57 ^{e-h}	16.00 ^{e-h}	38.57 ^a	5.07 ^{c-g}
Geno 10	56.00 ^{f-i}	82.53 ^{d-k}	7.40 ^{fgh}	15.33 ^{fgh}	38.00 ^a	5.15 ^{b-g}
Geno 11	59.67 ^{a-h}	76.67 ^{j-m}	8.40 ^{a-f}	16.33 ^{d-g}	39.37 ^a	5.40 ^{b-g}
Geno 12	53.33 ^{hi}	77.13 ^{i-m}	8.20 ^{b-g}	17.33 ^{b-e}	43.37 ^a	6.00 ^{bc}
Geno 13	57.53 ^{d-i}	80.20 ^{f-l}	8.93 ^{abc}	18.00 ^{a-d}	34.97 ^a	4.87 ^{c-g}
Geno 14	60.00 ^{a-g}	85.70 ^{b-g}	7.50 ^{e-h}	16.00 ^{e-h}	41.23 ^a	5.41 ^{b-g}
Geno 15	56.67 ^{d-i}	82.47 ^{d-k}	7.57 ^{e-h}	15.00 ^{gh}	36.87 ^a	5.33 ^{b-g}
Geno 16	56.00 ^{f-i}	80.83 ^{d-l}	9.17 ^{ab}	19.00 ^{ab}	41.67 ^a	6.00 ^{bc}
Geno 17	59.00 ^{a-h}	87.10 ^{a-d}	9.17 ^{ab}	17.33 ^{b-e}	35.23 ^a	5.13 ^{c-g}
Geno 18	57.67 ^{c-i}	83.07 ^{d-k}	7.13 ^{gh}	16.67 ^{c-g}	37.37 ^a	6.40 ^b
Geno 19	64.00 ^{a-d}	75.43 ^{lm}	8.97 ^{abc}	16.33 ^{fgh}	37.50 ^a	5.83 ^{b-e}
Geno 20	62.00 ^{a-f}	92.50 ^a	8.93 ^{abc}	17.33 ^{b-e}	39.63 ^a	4.60 ^{e-h}
Geno 21	52.00 ⁱ	79.38 ^{h-m}	8.23 ^{a-g}	16.67 ^{c-g}	38.37 ^a	5.00 ^{c-g}
Geno 22	57.67 ^{c-i}	79.63 ^{g-m}	8.60 ^{a-e}	16.67 ^{c-g}	44.17 ^a	7.91 ^a
Geno 23	60.67 ^{a-g}	86.50 ^{a-f}	8.17 ^{b-g}	18.33 ^{abc}	41.80 ^a	5.37 ^{b-g}
Geno 24	54.67 ^{ghi}	84.70 ^{c-h}	6.43 ^h	15.33 ^{fgh}	41.43 ^a	4.22 ^{gh}
Geno 25	52.33 ⁱ	89.80 ^{abc}	7.13 ^{gh}	14.33 ^h	47.77 ^a	5.20 ^{b-g}
Geno 26	60.00 ^{a-g}	84.40 ^{c-h}	8.80 ^{a-d}	18.00 ^{a-d}	36.37 ^a	5.57 ^{b-f}
Geno 27	52.00 ⁱ	86.83 ^{a-e}	8.03 ^{b-g}	17.00 ^{c-f}	42.60 ^a	6.02 ^{bc}
Geno 28	55.33 ^{ghi}	81.10 ^{d-l}	7.67 ^{d-g}	17.67 ^{a-e}	39.33 ^a	5.17 ^{b-g}
Geno 29	56.33 ^{e-i}	76.93 ^{j-m}	9.37 ^a	15.00 ^{gh}	40.50 ^a	4.53 ^{fgh}
Geno 30	56.00 ^{f-i}	83.40 ^{c-y}	8.00 ^{c-g}	18.33 ^{abc}	36.63 ^a	5.90 ^{bcd}
Mean	58.36	82.95	8.18	16.88	39.53	5.22
SEM±	2.35	2.31	0.402	0.688	NS	0.445

Means within a column followed by similar letter (s) are statistically the same at the p=0.05 level of DMRT; NS = Not Significant.

Table 4: Genetic Variance Components, Heritability and Genetic Advance of Significant Characters of the 30 Bread Wheat Genotypes Evaluated at Maiduguri in 2018/2019 Cool season

Character	δ^2_g	δ^2_{ph}	δ^2_e	$H^2_b(\%)$	GAM (%)
Days to 50% heading	7.67	24.30	16.63	31.58 Mod	5.50 Low
Plant height (cm)	15.23	31.26	16.03	48.73 Mod	6.78 Low
Spike length (cm)	0.84	1.33	0.48	63.55 High	18.40 Mod
Number of spikelets per spike	1.13	2.55	1.42	44.36 Mod	8.60 Low
1000 seeds weight (g)	*	*	*	*	*
Grain yield (t/ha)	0.46	1.05	0.59	43.54 Mod	17.62 Mod

*= did not show significant mean squares, H^2_b = Broad sense heritability, GAM = Genetic advance as percentage of mean, δ^2_g = genotypic variance, δ^2_{ph} = phenotypic variance, δ^2_e = error variance.

DISCUSSION

In general, crop breeding programme involves a large number of evaluated traits to make it possible to identify and select superior performing genotypes and enable varietal release (Fazal *et al.*, 2011; Noor *et al.*, 2019). Growth performance of different bread wheat genotypes exhibits marked variations due to a variety of internal factors and external manipulations (Hassan *et al.*, 2010; Saifullah *et al.*, 2016; Noor *et al.*, 2019). Earliness in wheat plants, as depicted by early heading and subsequent flowering and maturity, is an important indicator to show the degree of adaptation of crops to different agroecological zones. This character cannot be ignored when breeding and selecting for early maturing genotypes in marginal environments for wheat such as Nigeria. Genotypes with this attribute have the advantage to escape the terminal moisture stress when production is under rainfed condition, or the terminal heat stress when production is under irrigation, as practised in Nigeria. Variability in heading and maturity was reported by Mulugeta *et al.* (2018) similar to what was obtained in the present investigation.

Plant height is one of the characters that determine high yield along with the other yield-attributing characters (Saleem *et al.*, 2016). Studies of Tchalla *et al.* (2020) indicated that height in wheat plant is a significant indicator of morphological parameters of the crop phenotype and directly reflect the growth and yield status of wheat. Information regarding this trait is used to develop a selection index to increase yield while retaining an acceptable height. Taller plants are prone to lodging with subsequent yield losses. On the other hand, dwarf to semi-dwarf wheat genotypes are resilient to lodging, respond to increased nitrogen fertilization, and simplify combine harvesting in mechanized agriculture (Tamm, 2003; Begum and Dasgupta, 2019). The significant variations observed for plant heights could be the result of their genetic makeup (Jemal *et al.*, 2015). Studies by Yadav *et al.* (2015) and Saleem *et al.* (2016) on variability in plant height support the present results.

Spike length is an important character in evaluating wheat genotypes towards selection for high yield. Longer spikes may accommodate a higher number of spikelets and, consequently, a higher number of grains. Similarly, spike

length, spikelets per spike, and number of grains per spike are all yield-attributing characters. A positive performance in these attributes may lead to higher yields. Significant variations for spike length and the other yield-related characters were reported by Khan, (2013) and Gaffar, (2007), as in the present findings. High seed weight conditioned by high amount of assimilates due to efficient photosynthesis is desirable when selecting wheat genotypes for high grain yield. This character contributes to high grain yield per unit area. Significant variation for 1000 seed weight, reported by Hassan *et al.* (2010) and Karaman, (2020), differed from the present results.

Similarly, grain yield is the main character by which a genotype or cultivar is judged most commonly. It is the ultimate goal of any breeding endeavour. No cultivar is considered satisfactory unless it is able to provide a relatively high yield. However, grain yield is a complex character affected by environment and depends greatly on other yield-attributing characters. Variations in wheat grain yield, reported by Geleta *et al.* (2015), Kabir *et al.* (2017) and Dereje *et al.* (2019), corroborate our results. Many studies have shown that the overall growth performance of crop plants is linked to the level of their nitrogen-utilization efficiency (Chandana *et al.*, 2010, 2012a,b). Anjana *et al.* (2007, 2011) identified the characteristics that influence the N-use efficiency in different wheat cultivars, and studied the modulation of N-use efficiency in genotypes differing in nitrate reductase activity. It has been reported that the biochemistry of different wheat cultivars is affected by the level of nitrogen applied (Hakeem *et al.*, 2011).

Heritability estimate is a good sign for transfer of characters from generation to generation and is widely used in the establishment of a sound breeding programme, and in the formation of selection index. Genetic advance is another selection tool, furnishing information on the

magnitude of the expected genetic gain from one selection cycle (Hamdi *et al.*, 2003). Thus, heritability estimates together with genetic advance are more important to predict the resulting effect of selecting the best individuals (Manal, 2009). According to Robinson *et al.* (1955), heritability is broadly categorised as high (>60%), moderate (30% to 60%) and low (<30%). However, Johnson *et al.* (1955) categorized genetic advance as high (>20%), moderate (10% to 20%) and low (<10%). In the present study, nearly all of the evaluated characters showed moderate heritability with only spike length having a high heritability. Moderate heritability was reported for similar characters by Abinasa *et al.* (2011) and Khalid *et al.* (2011). On the other hand, high heritability was reported for spike length by Baloch *et al.* (2016) and Geleta (2020), thus corroborating the present result. The moderate genetic gain observed for spike length and grain yield agrees with the results reported by Arega *et al.* (2010) and Saleem *et al.* (2016) for these characters. Similarly, low genetic advance obtained for other characters evaluated is in agreement with reports by Kabir *et al.* (2017). The high to moderate heritability and genetic advance obtained for spike length and grain yield indicate that these traits are under the influence of additive gene effect and would invariably respond to positive selection in the early generation. The moderate heritability accompanied by low genetic advance for such characters as days to heading, plant height and spikelets per spike indicate non-additive gene effects and would cause difficulty in selection for improving these characters in the wheat genotypes evaluated. Therefore, a sensible and intelligent breeding procedure needs to be adopted.

CONCLUSION

The bread wheat genotypes evaluated for days to heading, plant height, spike length, spikelets per spike, 1000-seed weight and grain yield, showed

significant variability in all these characters with the exception of 1000-seed weight. Therefore, evaluation to select superior genotypes maybe practiced with respect to early- and high-yielding genotypes. The broad-sense heritability and genetic advance were moderate to low;

sensible and intelligent breeding programme should be designed when this set of genotypes is considered to achieve the desired improvement. These genotypes should, therefore, be tested over a number of years to be able to detect desirable and superior genotypes.

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