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Estimates of genetic variability and correlation of traits among ten accessions of wheat (Triticum aestivum L.) evaluated under open field condition

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In Nigeria and the rest of the world, wheat receives exceptional attention because of the critical role it plays in satisfying human and livestock nutritional needs. However, the productivity of the crop in the wheat-producing belt of Nigeria has been limited by adverse environmental conditions which may be tied to climate change. This paper was conducted to show the genetic variableness and inter-character association within the wheat crops in the Southwestern Nigeria environment of Akungba-Akoko. These accessions were grown in the field in a randomized complete block design (RCBD) and replicated 3 times. Result analysis shows higher differences ($P \leq 0.05$) among accessions for all traits measured. Plant height ranged from the lowest (4.29cm) in ACC1 to the highest (5.37 cm) in ACC6. Grain yield/plot was highest (10.35 g) in ACC4, while it was lowest (1.20g) in ACC9. Grains/spike, tillers/plant, and spike length showing higher heritability (>60%) coupled with higher genetic advance as percent of the mean (GAM) (>20%) suggested that direct selection can be made based on these traits for the improvement programme of wheat. Grains/spike exhibiting positive correlation with grain yield/plot (0.72) indicated that its selection will positively improve yield of wheat in this environment.

Keywords: Heritability, grains, GAM, productivity, photoperiod

1. Introduction

Wheat is considered the world's most extensively adapted crop (Ulukan, 2008), providing near 20 percent of calories of the world's population (Arjona et al., 2020). It is the largest cereal crop and it grows as staple food source around the globe. Wheat being the essential element of everyday diet plans has sufficient degree to be controlled for making different food sources by enhancing with supplements/ nutrients/ phospholipids and so on to contain different conditions like hypertension, diabetes, bone problem and skin irregularities (Mecha et al., 2017). Globally, wheat is an important cereal crop (Ren et al., 2021), which receives the most attention of specialists in plant breeding and production. However, its production is severely limited by environmental conditions (Christian et al., 2021; Elahi et al., 2020). In Nigeria, domestic wheat productivity has consistently been very low, largely because the wheat producing belt of Nigeria lies in the northern region of the country (Mala and Aminu, 2017), because the sensitivity of major wheat varieties to photoperiod (Lin et al., 2021) has favoured the north over the southern Nigeria until the emergence of the novel day length insensitive varieties. However, the region is also critically affected by drought and prevailing high temperatures which are a few of the limiting factors recognized as the bane of wheat production (Okechukwu et al., 2016). Unfortunately, information on wheat production and its genetic variability in the southern region of Nigeria is lacking even though the longer cropping season and higher rainfall is more favourable to crop production. There is therefore the need to exploit southern agro-ecologies within Nigeria for performance evaluation of wheat in order to mitigate the imminent decline of genetic diversity of the crop.

Aggregates of crop species are controlled primarily by the hereditary constituents connecting with the climate. Decrease in the hereditary changeability makes crops progressively defenseless against infection outbreaks and unfriendly climatic change (Ajayi et al., 2017). Subsequently the more assorted the plants are, the more prominent the possibility of taking advantage of the variety to create useful recombinants and wide variety in segregating generations during hereditary improvement. For a fruitful reproducing programmeme, the presence of hereditary changeability assumes a fundamental part (Sandhu et al., 2015). Exact data on the nature and level of hereditary inconstancy and difference present in wheat would subsequently be significant in choosing guardians for advancing unrivaled assortments in crop improvement programmemes.

Considering the way that genotype by climate communication (GEI) influences the aggregates of crop species across a scope of conditions, it is essential to segment the noticed phenotypic changeability into heritable and non-heritable parts in view of pertinent boundaries, like phenotypic and genotypic coefficient of variety, heritability and hereditary development. These boundaries are truth be told vital in further developing qualities (Ajayi et al., 2017). A few specialists have determined genotypic, phenotypic parts of fluctuation and heritability for various characteristics. These characteristics incorporate plant tallness, grain yield, seed weight, thousand grain weight, number of spikelets and days to half heading (Ndirigwe et al., 2020; Olumekun et al., 2020; Sulaiman et al., 2020).

Since there is need for a strategy to comprehend the genetics and advancement of gatherings of attributes all the while, raisers utilize phenotypic and genotypic contrasts joined with connections among qualities. Relationship appraises how much one attribute influences another quality (Ajayi et al., 2014). Relationship is of incredible importance and could be actually used in forming a viable choice plan (Ajayi et al., 2017). Connection examination has been conveyed in sweet potato (Agaba et al., 2016), in bread wheat (Khames et al., 2016) and in different lines of wheat under limited water system (Singh et al., 2017).

To extend the collection of information in help of wheat rearing, especially in South-western Nigeria, this paper hence set off to decide the hereditary changeability and connection of attributes among increases of wheat under field conditions.

2. Materials and Methods

Ten accessions of wheat (Table 1) were grown between September and December, 2018 to analyse the genetic variableness and correlation of traits for yield and its components. These accessions were obtained from the Lake Chad Research Institute, Maiduguri, Nigeria and have been previously screened for drought tolerance as described in Olumekun et al. (2020). The study was carried out at the Experimental Field of the Department of Plant Science and Biotechnology, Adekunle Ajasin University, Akungba-Akoko (Latitude 7.2° N, Longitude 5.44' E, Altitude 423 M above sea level), Ondo State, Nigeria. The experiment was laid out in a randomized complete block design (RCBD) and replicated three times. Accessions were planted in each replicate (at 3 seeds per hill) in plots of 1 m x 0.9 m each at spacing of 20 cm by 30 cm intra and inter row with a total of 15 stands in each plot.

Table 1. List of accessions of wheat used for estimates of genetic variability under open field condition

S/N	**Accession ID**	**CODE**
1	Entry 28	ACC1
2	Entry 31	ACC2
3	Entry 7	ACC3
4	Entry 8	ACC4
5	Entry 6	ACC5
6	Entry 23	ACC6
7	Entry 15	ACC7
8	Entry 29	ACC8
9	Entry 4	ACC9
10	Entry 10	ACC10

2.1. Data collection

Data collection was based on 5 randomly selected plants from each plot. Average of the 5 selected stands was determined per plot per replicate, after which the mean values of the three replicates of each accession was calculated. The quantitative traits observed included stem height and the number of tillers which were recorded at five weeks after planting. Stem height was measured with a plastic meter rule from the base of each selected plant to the base of the topmost leaf, while tillers were counted. Days of initial spike formation was determined from the day of planting to day of spike initiation. Number of spikelets per spike was obtained by counting all developed spikelets per spike from each hill per plot. Number of days to physiological maturity was determined by recording the number of days when 50% of plants within a plot matured and turned brown. Grain yield per plot was determined by weighing the number of grains per plot. Spike length was determined by measuring randomly selected spikes with a ruler in centimeters and 1000-grain weight obtained by weighing 1000-grains on a sensitive weighing balance.

2.2. Data analysis

Information were exposed to examination of fluctuation (ANOVA) utilizing the generelized linear model (GLM) technique of SPSS adaptation 20. Means were isolated utilizing Duncan Multiple Range Test (DMRT) at $P \leq 0.05$. Genetic parameters were estimated and categorized according to the procedures cited in Ajayi *et al*. (2014).

3. Results

Analysis of results revealed significant differences among accessions for all traits measured ($P \leq 0.05$) (Table 2). Spike length had the highest coefficient of variation, CV, (9.42%), followed by stem height (7.56%) while the trait with the lowest CV (0.31%) was number of days to physiological maturity.

Table 2. Mean square values of quantitative traits of Ten (10) accessions of wheat evaluated under open field conditions

Source of variation	**DF**	**PH (cm)**	**NT**	**NDH**	**NSPS**	**SL (cm)**	**NPM**	**NGS**	**1000-GW (g)**	**GYP (g)**
Accession	9	0.35^{*}	7.06^{*}	107.76^{*}	14.17^{*}	2.52^{*}	59.34^{*}	64.31^{*}	18.88^{*}	26.29^{*}
Replication	2	0.18^{*}	0.29^{*}	3.15^{ns}	0.20^{*}	0.12^{ns}	0.54^{*}	0.30^{*}	0.30^{*}	0.24^{*}
Error	18	0.14	0.15	6.43	0.20	0.38	0.13	0.22	0.19	0.11
CV (%)		7.56	5.45	3.45	1.95	9.42	0.31	3.73	1.21	5.35

*: Significant at $P \leq 0.05$; ns: Not significant; DF: Degree of freedom; CV: Coefficient of variation.

PH: Plant height; NT: Number of tillers per plant; NDH: Number of days to 50% heading; NSPS: Number of spikelets per spike; SL: Spike length; NPM: Number of days to physiological maturity; NGS: Number of grains per spike; 1000-GW: 1000-Grain weight; GYP: Grain yield per plot.

3.1. Mean values of quantitative traits of ten accessions of wheat studied under open field condition

The mean performance for quantitative traits of the wheat accessions are presented in Table 3. The highest mean value of stem height was recorded in ACC6 (5.37 cm) while the accession with the lowest mean value was ACC1 (4.29 cm). Number of tillers per plant ranged between 4.60 in ACC to 10.20 in ACC4. Number of days to 50% heading was lowest (62.13 days) in ACC4, while ACC10 headed late around 77.93 days after planting. ACC3 attained physiological maturity first around 111.60 days, while the last to physiologically mature was ACC6 around 123.60 days. Accession ACC6 had the longest spike (8.43 cm), followed by ACC4 (7.61cm) while the lowest value for spike length (5.46cm) was obtained in ACC10. ACC4 and ACC5 had the highest value for number of spikelet's per spike (24.07), while the lowest (18.13) was obtained in ACC1. Number of grains per spike ranged between 7.27 in ACC9 and 20.33 in ACC4. 1000-grain weight was lowest (31.67g) in ACC9 while the highest (40.00g) was obtained in ACC8. Grain yield per plot ranged from the lowest (1.20 g) in ACC9 to the highest (10.35 g) in ACC4.

Table 3. Mean values of quantitative traits of Ten (10) accessions of wheat evaluated under open field conditions

ACC	PH (cm)	NT	NDH	NSPS	SL (cm)	NPM	NGS	1000-GW (g)	GYP (g)
ACC 1	4.29±0.06^{a}	4.60±0.12^{a}	71.87±1.95^{cd}	18.13±0.07^{a}	5.75±0.39^{ab}	122.40±0.31^{f}	9.60±0.12^{c}	33.33±0.33^{b}	8.92±0.12^{g}
ACC 2	4.47±0.15^{ab}	7.13±0.27^{d}	67.60±2.12^{bc}	24.20±0.31^{c}	6.49±0.80^{ab}	112.67±0.18^{b}	8.53±0.24^{b}	36.67±0.33^{d}	4.10±0.10^{c}
ACC 3	4.85±0.15^{abc}	6.27±0.18^{c}	75.67±0.64^{de}	21.47±0.32^{b}	5.92±0.13^{ab}	111.60±0.23^{a}	19.93±0.44^{f}	35.00±0.00^{c}	8.87±0.04^{g}
ACC 4	5.03±0.33^{bc}	10.20±0.12^{f}	62.13±1.14^{a}	25.07±0.29^{d}	7.61±0.19^{cd}	123.47±0.29^{g}	20.33±0.29^{f}	38.33±0.33^{e}	10.35±0.21^{h}
ACC 5	4.77±0.08^{abc}	7.60±0.35^{d}	66.33±2.03^{ab}	25.07±0.29^{d}	6.56±0.36^{abc}	117.20±0.31^{de}	11.00±0.46^{d}	36.67±0.33^{d}	5.40±0.22^{d}
ACC 6	5.37±0.40^{c}	8.36±0.32^{e}	79.27±0.96^{e}	23.93±0.27^{c}	8.43±0.19^{d}	123.60±0.12^{g}	14.20±0.12^{e}	38.33±0.33^{e}	7.33±0.13^{f}
ACC 7	5.19±0.12^{bc}	7.33±0.13^{d}	68.20±0.95^{bc}	22.20±0.20^{b}	6.53±0.21^{abc}	115.40±0.12^{c}	8.40±0.40^{b}	35.00±0.00^{c}	5.85±0.25^{d}
ACC 8	5.13±0.08^{bc}	7.40±0.12^{d}	77.07±0.13^{e}	24.53±0.35^{cd}	6.76±0.21^{bc}	117.60±0.31^{e}	13.67±0.07^{e}	40.00±0.00^{f}	6.65±0.46^{e}
ACC	4.59±0.35	7.13±0.37	77.87±1.8	24.47±0.1	5.75±0.23	122.40±0.12	7.27±0.07	31.67±0.33^{a}	1.20±0.00^{a}

9	^{ab}	^{d}	6^{e}	3^{cd}	^{ab}	^{f}	^{a}		
ACC 10	4.93±0.07^{abc}	5.47±0.18^{b}	77.93±0.96^{e}	22.20±0.23^{b}	5.46±0.17^{a}	116.60±0.31^{d}	11.27±0.07^{d}	35.00±0.00^{c}	2.25±0.03^{b}

Means with the same superscripts in the same column are not significantly different from one another at $P \leq 0.05$ using DMRT. ACC: Accessions; PH: Plant height; NT: Number of tillers per plant; NDH: Number of days to 50% heading; NSPS: Number of spikelet per spike; SL: Spike length; NPM: Number of days to physiological maturity; NGS: Number of grains per spike; 1000-GW: 1000-Grain weight; GYP: Grain yield per plot

3.2. Estimates of genetic parameters and genotypic correlation of quantitative traits of ten accessions of wheat studied under open field condition

GCV and PCV respectively, lies between 3.76% and 3.77% in number of days to physiological maturity and 48.50% and 48.81% in grain yield per plot. Also, heritability in the broad sense ranged from lowest (28.19%) in stem height to the highest (99.49%) in number of grains per spike, while genetic advance as percent of mean (GAM) lied from the lowest (5.14%) in stem height to the highest (99.48%) in grain yield per plot (Table 4). Correlations revealed positive genetic associations among traits (Table 5). Stem height was significant and positively correlated with spike length (0.96); and correlated with number of tillers (0.71) and 1000-grain weight (0.75). Number of tillers was very correlated with number of spikelets per spike (0.80) and spike length (0.84). Spike length was very significant and correlated with 1000-grain weight (0.78).

	GV	**PV**	**GCV (%)**	**PCV (%)**	**H^2B (%)**	**GAM (%)**
PH (cm)	0.05	0.19	4.74	8.92	28.19	5.14
NT	2.30	2.46	21.23	21.92	93.81	42.38
NDH	33.78	40.21	8.03	8.76	91.67	16.60
NSPS	4.66	4.86	9.33	9.53	97.90	19.51
SL	0.71	1.09	12.95	16.01	80.89	26.82
NPM	19.74	19.87	3.76	3.77	99.74	7.68
NGS	21.36	21.58	37.21	37.40	99.49	76.33
1000-GW (g)	6.23	6.42	6.93	7.04	98.44	14.19
GYP (g)	8.73	8.84	48.50	48.81	98.76	99.48

Table 4. Genetic parameters of quantitative traits of ten accessions of wheat evaluated under open field condition

GV: Genotypic variance; PV: Phenotypic variance; GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation; H^2B: Heritability in broad sense; GAM: Genetic advance as percent on mean. PH: Plant height; NT: Number of tillers per plant; NDH: Number of days to 50% heading; NSPS: Number of spikelets per spike; SL: Spike length; NPM: Number of days to physiological maturity; NGS: Number of grains per spike; 1000-GW: 1000-Grain weight; GYP: Grain yield per plot.

Table 5. Genotypic correlation of quantitative traits of ten accessions of wheat evaluated under open field conditions

	PH (cm)	**NT**	**NDH**	**NSPS**	**SL (cm)**	**NPM**	**NGS**	**1000-GW (g)**	**GYP (g)**
PH (cm)	1	0.71*	0.21	0.51	0.96**	0.11	0.52	0.75*	0.23
NT		1	-0.45	0.80**	0.84**	0.32	0.44	0.60	0.28
NDH			1	-0.19	-0.21	0.06	-0.11	-0.18	-0.38
NSPS				1	0.52	0.07	0.12	0.51	-0.26
SL (cm)					1	0.45	0.44	0.78**	0.49
NPM						1	0.02	-0.00	0.17
NGS							1	0.50	0.72*
1000-GW (g)								1	0.43
GYP (g)									1

**: Significant at P ≤ 0.01; *: Significant at P ≤ 0.05. PH: Plant height; NT: Number of tillers per plant; NDH: Number of days to 50% heading; NSPS: Number of spikelets per spike; SL: Spike length; NPM: Number of days to physiological maturity; NGS: Number of grains per spike; 1000-GW: 1000-Grain weight; GYP: Grain yield per plot.

4. Discussion

Hereditary variety is the essential driver of yield improvement programs. The more variableness saw in the essential populace, the more the opportunity of progress (Ogunbayo et al. 2021). This paper featured huge contrasts among increases for all qualities among the promotions and can along these lines be taken advantage of in reproducing projects of wheat for Southwestern Nigeria. Studies have shown that adequate degree of hereditary variableness exist in wheat for different characteristics and this can be taken advantage of in reproducing programs (Okechukwu et al., 2015; Mala and Aminu, 2017). Critical replication impact for all characteristics with the exception of number of days to half heading and spike length suggested that increases acted diversely across duplicates (Elahi et al., 2020). Grain yield per plot and days to half physiological development had more noteworthy degree of variableness contrasted with different boundaries showing that powerful choice could be accomplished among such attributes for future reproducing programs. Comparable degrees of variableness have been accounted for in rice (Hannan et al., 2020; Vanisri et al., 2020; Agbowuro et al., 2021; Buelah et al., 2021; Salem et al., 2021).

The impact of climate on the outflow of quantitative characteristics was uncovered by the higher PCV values contrasted with the relating GCV across attributes. Notwithstanding, such contrasts were exceptionally insignificant across characteristics demonstrating that the impact of the climate on these attributes was negligible. Comparable outcomes have been accounted for in wheat and different oats particularly for yield attributes (Tuhina-Khatun et al., 2015; Islam et al., 2020; Vanisri et al., 2020; Sorour et al., 2021). As is notable, the outflow of characteristics in crop species is impacted by added substance (heritable), predominance (non-heritable), and epistasis (non-allelic); consequently, dividing noticed variableness into GCV and PCV, which are a definitive pointers of the degree of changes for different qualities, is basic. Higher PCV and GCV in attributes, for example, number of turners per plant showed that these promotions had an expansive hereditary base for these characteristics and the chance of progress of yield through determination. Notwithstanding, moderate PCV and GCV in attributes, for example, spike length showed moderate changes among the increases for such characteristic. These have been accounted for by different specialists (Agbowuro et al., 2021; Hannan et al., 2020; Noatia et al., 2021; Donkor et al., 2021)

The fundamental capacity of the heritability in the hereditary paper of quantitative qualities is its prescient job in demonstrating the dependability of the phenotypic qualities as a manual for rearing qualities. Choice will be more viable for those attributes having higher heritability on the grounds that these qualities are represented dominatingly by added substance quality activity and could be worked on through individual plant determination (Elahi et al., 2020). Higher heritability gauges for all attributes read up with the exception of plant tallness showed a higher reaction of these qualities to choice. Comparable outcomes were likewise detailed in wheat (Dutamo et al., 2015; Singh, 2018; Rahman et al., 2020) showing higher heritability values for spike length, 1000-grain weight, and yield per plot; which exhibited the presence of added substance quality impact demonstrating the viability of determination to improve these characteristics.

The appraisals of GAM can assist with getting the sorts of hereditary activity of different polygenic attributes. Johnson et al. (1955) proposed that higher heritability gauges and higher GAM are more useful in anticipating gain under choice than heritability appraises alone. Consequently, the heritability assessments will be dependable whenever joined by a higher GAM. Higher heritability combined with higher GAM was seen in the quantity of turners per plant, spike length, number of grains per spike and grain yield per plot. Comparative outcomes were likewise announced by different laborers in wheat (Singh, 2018; Elahi et al., 2020), in different oats (Islam et al., 2020; Vanisri et al., 2020; Agbowuro et al., 2021; Buelah et al., 2021) particularly in grain yield and number of turners per plant, which showed the power of added substance quality activity. Subsequently, direct determination for such a quality would be powerful. Then again, the quantity of days to physiological development, and 1000-grain weight showed higher heritability related to low GAM proposing a transcendence of non-added substance quality activity; consequently direct determination for such characteristics would deceive the normal outcome. This was additionally affirmed by Elahi et al. (2020) who detailed higher heritability combined with a low GAM in days to development.

Positive genotypic correlation between grain yield per plot and grains number per spike suggested that direct selection for grains per spike will improve grain yield in wheat under the prevailing condition. This is supported by the findings of Feltaous *et al.* (2020), Hannan *et al.* (2020), and Vanisri *et al*. (2020). Direct selection for stem height will also positively contribute to number of tillers per plant, spike length, and one thousand grain weight. Also, number of tillers per plant had higher positive contribution to number of spike per spikelets and spike length, while spike length had a higher positive contribution to one thousand grain weight. These are similar to the findings of Moosavi *et al.* (2015), Khames *et al.* (2016), and Mecha *et al.* (2017).

5. Conclusion

This paper affirmed that the wheat showed more elevated level of changess for the characters considered, and proposed open doors exist for hereditary improvement through determination and preservation of the increases for future use. Hereditary variableness is fundamental for meet the enhanced objectives of plant rearing, like reproducing for expanded yield, more extensive transformation, beneficial characteristics, and bug and sickness opposition. It is a prerequisite for the advancement of further developed cultivars with more extensive versatility and an expansive hereditary base. The higher PCV values over GCV for every one of the characters considered means that the impact of the climate on the outflow of all characteristics and is along these lines fundamental in the assurance of yield parts and determination programs. Higher heritability combined with higher GAM recorded in characteristics, for example, number of turners, spike length, number of grains per spike and grain yield per plot exhibited that these characters are pertinent in wheat improvement programs particularly in hybridization.

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