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GENOTYPIC VARIATION, INHERITANCE AND GENETIC ADVANCE IN BREAD WHEAT (*Triticum aestivum* L.) GENOTYPES IN ETHIOPIA

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ABSTRACT

Forty-nine bread wheat (*Triticum aestivum* L.) genotypes were studied under rainfed conditions at three agroecologically varied locations in South-Western Ethiopia namely, Chena, Masha and Shey Bench, during 2017and 2018 with the objective to estimate their genetic variability, heritability and genetic advance using 7 x 7 simple lattice design. Data were collected for 12 agronomic characters. The analyses of variance revealed highly significant differences ($p \leq 0.01$) among wheat genotypes for all the traits studied at these locations, except for the number of effective tillers plant^{-1} at Chena and biomass yield at Masha wherein genotypes had significant differences only at $p \leq 0.05$ level and the number of spikelets spike^{-1} at Shey Bench wherein genotypes showed non-significant difference. The phenotypic coefficients of variation were relatively greater than those of genotypic coefficients of variation for most of the characters studied; however, the magnitudes of differences were relatively high for the number of tillers, number of kernels spike^{-1}, biomass yield and grain yield. High heritability coupled with moderate genetic advance (as % mean) were observed for days to heading, days to maturity, spike length and grain filling period at all these locations. Therefore, any improvement in these characters would result in a substantial increment in grain yield in South-Western Ethiopia which, otherwise, is rich in natural resources but poor in their efficient utilization.

Keywords: Bread wheat, GCV, genetic advance, heritability, PCV, variability

INTRODUCTION

Bread wheat, a self-pollinating annual plant, is the largest cereal crop extensively grown as staple food sources in the world (Mollasadeghi and Shahryari, 2011) which accounts for 20% of nutritional sources of the people (Khabiri *et al.,* 2012). It provides nearly 55% of carbohydrates, 20% of daily protein and 21% calories for about 40% of global population (Khan and Naqvi, 2012). An estimated 1.2 billion poor people depend on wheat, a crop that is particularly vulnerable to climate change (USDA, 2017). To meet this demand, it was estimated that global wheat grain production must annually increase by 2% till 2050 (Rosegrant and Agcoili, 2010). However, the current trend shows lower rates of wheat yield increases (0.9% year^{-1}) which may result in no change to the per capita wheat harvest by 2050. World wheat production in 2019 was 762.2 million metric tons with average yield of 3.5 t ha^{-1} accounting for nearly 30% of global cereal production (Global Trade, 2020).

Ethiopia is the 2nd largest wheat producer in sub-Saharan Africa and the crop is cultivated on 1.7 million ha land with annual production of 4.54 million tons and productivity of only 2.67 t ha^{-1} (CSA, 2017) as compared to the world average yield of 3.34 t ha^{-1} (FAO, 2017 a,b). Wheat production self-sufficiency is only 75% and the remaining 25% of wheat is imported and also obtained through food aid. However, cereal consumption has been increasing by 20% in recent years, making it the second most consumed cereal in Ethiopia after corn (USDA, 2017). Although the productivity of wheat has increased during the last few years in Ethiopia, it is still very low as compared to other wheat producing countries. The low yield productivity is attributed to many factors, such as unavailability of quality seed of varieties that are high yielding as well as adapted to wide range of agro-ecologies of the country. Hence, the first step in the development of varieties is assessing the genetic variability of available genotypes for the characters of agronomic interest (Rahman *et al.*, 2016).

The knowledge of genetic variability and the extent of variations among genotypes in a population is essential not only for the selection of better genotypes but also to help in designing crop improvement through combination breeding. In addition, genetic improvement to develop varieties with high yield potential and tolerance to abiotic and biotic stresses, with acceptable end-use quality, is the viable and environmentally-friendly option to sustainable increase in wheat yield. Despite Bench Shako, Kaffa and Sheka zones being the potential wheat-producing areas in South-Western Ethiopia, the potential of these areas for wheat crop is unexploited due to the lack of improved varieties and detailed information on the extent of adaptability and production status of the improved bread wheat varieties in the area (CSA, 2012). The present study was, therefore, aimed to quantify variability and estimate heritability and genetic advance among genotypes of bread wheat for yield and yield-contributing characters.

MATERIALS AND METHODS

Experimental materials

The experimental materials comprised of forty-nine bread wheat genotypes released from different agricultural research centers of the country. The genotypes ‘Ogolcho’, ‘Hoggana’, ‘Hulluka’, ‘Shorima’, ‘Kekeba’, ‘Danda'a’, ‘Dagelu’, ‘Pavon-76’, ‘Jefferson’, ‘King Bird’, ‘K6290-Bulk’, ‘K6290-Bulk’, ‘Mitike Kubsa Galama’, ‘Tusi’, ‘Katar’, ‘Hawi’, ‘Sirbo’, ‘Doddota’, ‘Bobicho’, ‘Meraro’, ‘Millinium’, ‘Honqolo’, ‘Wane’, ‘Bollo’, ‘Hidase’, ‘Biqa’ and ‘KBG-01’ were procured from Kulumsa Centre; ‘Mekelle-1’, ‘Mekelle-2’, ‘Mekelle-3’ and ‘Mekelle-4’ from Mekelle Centre; ‘Ga'ambo’ from Werer Centre; ‘Gassay’ and ‘Tay’ from Adet Centre; ‘Alidoro’, ‘Enkoy Dashen’, ‘Et-13 A2’, ‘Kulkulu’ and ‘Batu’ from Holleta Centre; ‘Sofumar Mada-Wolabu’, ‘Mandoye’, ‘Sanate’ and ‘Dinkinesh’ from Sinana Centre; ‘Dereselgne’ from Deberzeit Centre and ‘Menze’ from Dabre Berhan Centre. These genotypes were released during 1994-2012.

Description of the study area

The experiments were conducted in Chena, Masha and Shey Bench woredas (districts) of Bench Bonga, Sheka and Shako zones, respectively. Shey Bench is situated at the latitudes 5° 30′ - 7° 00′ N, longitudes 34° 00′- 36° 00′ E at the altitude of 1400 - 2485 m above sea level (masl). It receives average annual rainfall 1547 - 2000 mm while average temperature ranges between 22 and 29°C. Chena site is situated at the latitudes 6° 24′ - 7° 70′ N, longitudes 35° 69′ - 36° 78′ E at the altitude of 500-3350 masl. It receives average annual rainfall 1600 - 2200 mm while average temperature ranges between 18 and 21°C. Masha experimental site is situated at the latitudes 70° 24′ - 70° 52′ N, longitudes 35° 13′-35° 35′ E at the altitudes of 1900 - 2750 masl. It receives average annual rainfall 1800 - 2200 mm while average temperature ranges between 12 and 29°C.

Experimental design and management

The experiment was laid out in a 7 x 7 simple lattice design. Each genotype was planted in a plot consisting of six rows of 2.5 m length and 1.2 m width with spacing of 20 cm between the rows. The distances between plots, blocks and replications were 0.5, 0.5 and 1.5 m, respectively. A seed rate of 150 kg ha^{-1} and fertilizer rate of 100 kg ha^{-1} containing NPS were uniformly applied in all the treatments. Weeding and other agronomic practices were followed as per the recommendations for the respective sites.

Data collection

Ten randomly selected plants from the four central rows of each plot were used for data collection. Data on days to 50% heading, days to physiological maturity, plant height, productive tillers $plant^{-1}$, number of kernels $spike^{-1}$, number of spikelets $spike^{-1}$, spike length, grain yield, biomass yield (Donald and Hamblin, 1976) and harvest index (Donald and Hamblin, 1976) were collected.

Statistical analysis

The mean values of the genotypes were subjected to analysis of variance based on triple lattice design. Analysis of variance was done using Proc lattice and Proc GLM procedures of SAS 9.3 after testing the ANOVA assumptions (SAS, 2011). Mean separations were estimated using least significant difference (LSD) test at 5 and 1% levels of significance.

Estimation of variance components and associations

Genotypic and phenotypic coefficients of variability were computed according to Burton and Devane (1953):

$$\text{Genotypic coefficient of variability (GCV)} = \frac{\sqrt{\sigma 2g}}{\bar{x}} \times 100$$

$$\text{Phenotypic coefficient of variability (PCV)} = \frac{\sqrt{\sigma 2p}}{\bar{x}} \times 100$$

$$\text{Environmental coefficient of variability (ECV)} = \frac{\sqrt{\sigma 2e}}{\bar{x}} \times 100$$

Where, σ^2_g = Genotypic variance, $\sigma^2 p$ = Phenotypic variance, σ^2_e = Environmental variance and $\bar{x}$ = General mean of character.

The heritability (broad-sense) was estimated based on the ratio of genotypic variance to the phenotypic variance and was expressed in percentage (Falconer and Mackay, 1996):

$$h^2_B = \frac{Vg}{Vp} \times 100$$

Where, h^2_B = Heritability, V_g = Genotypic variance, V_p = Phenotypic variance

Genetic advance (GA) in absolute unit and percent of the mean (GAM), assuming selection of superior 5% of the genotypes was estimated according to Johnson *et al.* (1955):

$$GA = K\ \sigma_p h^2$$

$$GAM = (GA/x) \times 100$$

Where, K= Intensity of selection at 5% (K = 2.06, K is selection differential), σ_p = Phenotypic standard deviation, h^2 = Heritability, and $\bar{x}$ = General mean of the character.

RESULTS AND DISCUSSION

The analysis of variance showed highly significant differences ($p \leq 0.01$) among wheat genotypes for all the traits studied at all the locations, except for the number of effective tillers at Chena, biomass yield at Masha, wherein genotypes had significant differences only at $p \leq 0.05$ level of significance and the genotypes showed a non-significant difference for the number of spikelets $spike^{-1}$

Table 1: Mean squares for the twelve characters of 49 bread wheat genotypes at three experimental sites in Ethiopia

	Locations											
	Chena				Masha				Shey Bench			
Traits	MSG	MSE	Mean	CV	MSG	MSE	Mean	CV	MSG	MSE	Mean	CV
DH	114.78**	5.25	69.35	4.36	123.83**	4.09	71.62	3.75	129.25**	6.34	67.35	9.31
DM	156.48**	4.64	132.9	5.89	159.58**	7.69	135.2	5.28	162.5**	5.86	129.4	8.84
GFP	46.06**	5.12	61.65	3.57	47.24**	5.82	63.98	2.96	53.25**	6.28	59.36	6.52
PH	112.21**	1.52	92.5	6.37	92.85**	16.24	95.4	7.76	118.85**	19.32	96.18	8.32
NT	1.79*	0.78	2.32	11.03	2.28**	0.15	1.56	10.4	2.18**	0.09	1.21	13.98
NGS	79.14**	12.09	47.65	4.8	83.89**	23.44	45.33	4.19	53.89**	21.25	39.56	7.75
NSS	6.95**	0.92	15.62	8.92	3.92**	0.91	14.15	8.31	1.45^{ns}	0.98	13.25	8.87
SL	3.82**	0.45	10.25	5.14	2.27**	0.23	8.95	4.53	2.97**	0.19	7.25	8.09
TKW	61.84**	0.43	34.63	5.64	35.69**	7.02	34.1	5.03	29.63**	8.24	28.45	7.91
BMY	2.21**	0.762	9.86	14.96	1.77*	1.26	9.29	14.3	2.57**	1.18	7.62	16.59
HI	78.15**	0.51	45.62	10.26	61.62**	35.54	43.49	11.6	49.26**	6.91	38.95	13.21
GY	2.39**	0.21	3.85	12.75	2.27**	0.25	3.75	12.1	2.18**	0.12	2.86	15.7

*, **Significant at $p \leq 0.05$ and $p \leq 0.01$ probability levels, respectively; and ns = non-significant, MSG = mean squares of genotypes, MSE = mean squares of error, CV = coefficient of variation, DH = days to heading, DM = days to maturity, GFP = grain filling period, PH = plant height, NT = number of productive tillers plant^{-1}, NGS = number of grains spike^{-1}, NSS = number of spikelets spike^{-1}, SL = spike length, TKW = Thousand-kernels weight, BMY = biomass yield, HI = harvest index, GY = grain yield (t ha^{-1}).

at Shey Bench (Table 1). Significant genetic variation among genotypes for the studied characters suggests the ample scope of selection for different quantitative characters for the improvement of wheat crop. Several workers have reported significant differences among wheat genotypes for yield and yield-related traits for most of the characters studied in our experiment (Kifle *et al.*, 2016; Birhanu *et al.*, 2017). Further, the genotypes showed a considerable mean and range variations for each studied character across the locations. The mean grain yield of genotypes ranged from 2.69-4.18, 2.94-4.93 and 2.19-4.23 t ha^{-1} with a mean value of 4.01, 3.95 and 3.06 t ha^{-1} at Chena, Masha and Shey Bench, respectively (Table 2). The range and mean values suggested the existence of sufficient variability among the tested genotypes for the majority of characters providing ample scope for selecting superior and desired genotypes for further improvement of bread wheat in the study areas.

Estimates of variance components

The results of statistical analyses for the studied characters are presented in Table 2. Phenotypic coefficients of variation (PCV) ranged from 6.75% for days to maturity to 28.97% for grain yield and the genotypic coefficient of variability (GCV) ranged from 6.55 to 25.43% for the same character, respectively, at Chena. At Masha, the PCV value ranged from 6.75% for days to physiological maturity to 26.54%, for the number of productive tillers plant^{-1} and GCV ranged from 5.44% for biomass yield to 21.28% for grain yield. At Shey Bench, PCV ranged from 7.08% for days to physiological maturity to 36.67% for the number of productive tillers plant^{-1}, while GCV ranged from 3.66% for the number of spikelets spike^{-1} and 26.85% for the number of productive tillers plant^{-1}.

Among the characters studied, the lowest PCV (6.76, 6.76 and 7.09%) and GCV (6.75, 6.45 and 6.84%) were recorded for the days to maturity at Chena, Masha and Shey Bench, respectively. The respective values for plant height were 8.16, 7.74 and 8.64%; and 8.05, 6.49 and 7.33%; and for grain filling period were 8.21, 8.11 and 9.19%, and 7.34, 7.17 and 8.16%. In addition, biomass yield at Chena and Masha and the number of spikelets spike^{-1} at Masha and Shey Bench exhibited low GCV and PCV values. The results indicated that the environmental factors had more influence on the expression of these characters than the genetic factors, suggesting the limited scope for

Table 2: Estimates of ranges, mean, phenotypic and genotypic variances, phenotypic and genotypic coefficients of variations (PCV and GCV), heritability (broad-sense heritability) and genetic advance for 12 characters of 49 bread wheat genotypes tested at three locations

Traits	Range	Mean	σ^2e	σ^2g	σ^2ph	PCV (%)	GCV (%)	H^2 (%)	GA	GAM (%)
Chena site										
DH	54.5 - 81.5	69.35	5.25	54.77	60.02	11.17	10.67	91.25	14.56	21.00
DM	108 - 143	132.85	4.64	75.92	80.56	6.76	6.56	94.24	17.42	13.12
GFP	57.85 - 74.65	61.65	5.12	20.47	25.59	8.21	7.34	80.00	8.34	13.52
PH	83.5 - 120.35	92.45	1.52	55.35	56.87	8.16	8.05	97.33	15.12	16.35
NT	2.3 - 5.9	4.26	0.92	0.45	1.36	27.32	15.48	32.10	0.77	18.07
NGS	44.75 - 59.25	47.65	12.09	33.53	45.62	14.17	12.15	73.50	10.23	21.46
NSS	13 - 18	15.62	0.92	3.02	3.94	12.70	11.12	76.62	3.13	20.04
SL	7.6 - 13.56	10.25	0.45	1.69	2.14	14.26	12.66	78.92	2.38	23.18
TKW	28.02 - 48.08	34.63	0.43	30.71	31.14	16.11	16.00	98.62	11.34	32.73
BMY	6.56 - 11.58	9.86	0.76	0.72	1.49	12.36	8.63	48.72	1.22	12.41
HI	27.68 - 61.49	45.62	0.51	38.82	39.33	13.75	13.66	98.70	12.75	27.95
GY	2.69 - 4.18	4.01	0.21	1.04	1.35	28.97	25.43	77.04	1.84	45.98
Masha site										
DH	55.25 - 82.5	71.62	4.09	59.87	63.96	11.17	10.80	93.61	15.42	21.53
DM	108.7 - 144.0	135.2	7.69	75.95	83.64	6.76	6.45	90.81	17.11	12.65
GFP	58.6 - 76	63.5	5.82	20.71	26.53	8.11	7.17	78.06	8.28	13.04
PH	84.25 - 123.25	95.4	16.24	38.31	54.55	7.74	6.49	70.23	10.68	11.20
NT	2.05 - 5.65	4.56	0.65	0.82	1.47	26.54	19.80	55.63	1.39	30.42
NGS	39.5 - 60.0	45.33	23.44	30.23	53.67	16.16	12.13	56.32	8.50	18.75
NSS	13.75 - 18.75	14.15	0.91	1.51	2.42	10.98	8.67	62.32	2.00	14.10
SL	8.35 - 14.30	8.95	0.23	1.22	1.45	13.45	12.34	84.14	2.09	23.32
TKW	28.77 - 48.85	34.1	7.02	14.34	21.36	13.55	11.10	67.13	6.39	18.74
BMY	7.31 - 12.45	9.29	1.26	0.26	1.52	13.25	5.44	16.83	0.43	4.59
HI	28.43 - 62.24	43.49	3.54	29.04	32.58	13.12	12.39	89.13	10.48	24.10
GY	2.94 - 4.93	3.95	0.15	0.71	0.86	23.43	21.28	82.49	1.57	39.82
Shey Bench site										
DH	54.0 - 80.75	67.35	6.34	61.46	67.80	12.23	11.64	90.65	15.38	22.83
DM	107.5 - 135.25	129.5	5.86	78.32	84.18	7.09	6.84	93.04	17.58	13.58
GFP	57.35 - 72.9	59.36	6.28	23.49	29.77	9.19	8.16	78.90	8.87	14.94
PH	83.0 - 118.6	96.18	19.32	49.77	69.09	8.64	7.33	72.03	12.33	12.82
NT	1.8 - 3.75	3.25	0.66	0.76	1.42	36.69	26.85	53.57	1.32	40.48
NGS	37.3 - 44.25	39.56	21.25	16.32	37.57	15.49	10.21	43.44	5.48	13.86
NSS	12.5 - 16.25	13.25	0.98	0.24	1.22	8.32	3.66	19.34	0.44	3.31
SL	7.1 - 10.81	7.25	0.19	1.39	1.58	17.34	16.26	87.97	2.28	31.42
TKW	27.52 - 42.33	28.45	8.24	10.70	18.94	15.30	11.49	56.48	5.06	17.80
BMY	6.06 - 10.83	7.62	1.18	0.70	1.88	17.97	10.94	37.07	1.05	13.72
HI	27.18 - 60.74	38.95	6.91	21.18	28.09	13.61	11.81	75.40	8.23	21.13
GY	2.19 - 4.23	3.06	0.12	0.22	0.34	19.06	15.33	64.71	0.78	25.40

Where, σ^2e = error variance, σ^2g = genotypic variance, σ^2p = phenotypic variance, PCV = phenotypic coefficient of variation, GCV = genotypic coefficient of variation, H^2 = broad-sense heritability, GA = genetic advance, GAM (%) = genetic advance as percent of mean, DH = days to heading, DM = days to maturity, GFP = grain filling period, PH = plant height, NT = number of tillers plant^{-1}, NGS = number of grains spike^{-1}, NSS = number of spikelets spike^{-1}, SL = spike length, TKW = thousand-kernel weight, BMY = biomass yield, HI = harvest index, GY = grain yield (t ha^{-1}).

improvement of these characters by direct selection of high performing genotypes. This is in agreement with the reports of Kifle *et al.* (2016) and Berhanu *et al.* (2017).

In general, PCV were relatively greater than those of GCV for most of the characters at all the locations; however, the magnitudes of difference were small for days to heading, days to maturity, grain filling period, spike length, thousand-kernel weight, plant height and harvest index (Table 2). This suggests that the marked influence of environmental factors for phenotype expression of genotypes was low and the chances of improvement of these traits through selection of genotypes based on phenotype would be higher. The magnitude of difference between PCV and GCV was relatively high for the number of tillers, number of kernels spike^{-1} and biomass yield. This implies greater influence of environmental factors on phenotypic expression of these characters that makes difficult or practically impossible to exercise selection based on phenotypic performance of genotypes to improve the characters. These results are in close agreement with Desalegn and Kumar (2016), Kifle *et al.* (2016) and Berhanu *et al.* (2017). The results also revealed moderate GCV and PCV indicating that there is still some possibility for the improvement of characters. Similar results depicting closer values of PCV to GCV estimates for most characters thereby showing little environmental effect on the expression of the characters (Dawit *et al.,* 2012).

Estimates of heritability (broad-sense heritability)

Heritability estimates for the 12 characters studied at three locations are shown in Table 2 which ranged from 32.17% for the number of productive tillers to 98.70% for harvest index at Chena, from 16.83% for biomass to 93.63% for days to heading at Masha and from 19.34% for the number of spikelets spike^{-1} to 93.04% for days to maturity at Shey Bench, respectively.

In general, high heritability estimates were obtained for most of the characters studied at these experimental locations. High estimates of heritability have also been reported by other researchers for most of these characters (Berhanu *et al.* 2017). On contrary, low estimates of heritability have been reported for days to heading, days to maturity and grain filling period (Kifle *et al.,* 2016). However, medium estimates of heritability were obtained for biomass yield (48.72%) at Chena and for the number of productive tillers (55.63%) and number of kernels spike^{-1} (56.32%) at Masha and for the number of productive tillers (53.57), number of kernels (43.44%) and thousand-kernel weight (56.48%) at Shey Bench. Low estimates of heritability were obtained for the number of productive tillers (32.10%) at Chena and biomass yields (16.83 and 37.07%) at Masha and Shey Bench accompanied by the number of spikelets spike^{-1} (19.34%).

Estimates of genetic advance

The present study revealed that high heritability is coupled with moderate genetic advance for days to heading, days to maturity, spikelet length and grain filling period at all the locations. This indicates that it is most likely that the heritability of these characters is due to additive gene effects, and selection might be effective for these characters (Salman *et al*., 2014; Rahman *et al*., 2016). Salman *et al.* (2014) also reported high and moderate heritability and genetic advance for days to heading, days to maturity, and thousand-seed weight. Besides, high heritability estimates together with genetic advance were observed for grain yield at Chena, for thousand-kernel weight, harvest index and grain yield at Masha and for harvest index and grain yield at Shey Bench. A number of workers have also reported similar findings for high heritability associated with high genetic advance for grain yield and harvest index (Mohammed *et al.,* 2011; Berhanu *et al.,* 2017).

A low value for both heritability and genetic advance was computed for biomass yield at Masha and the number of spikelets spike^{-1} at Shey Bench. This suggests that the low heritability of traits due to the influence of environment limits the scope of improvement by selection. The low heritability of traits may be due to the presence of non-additive type of gene action and the presence of higher environmental factors along with non-additive gene action might be the possible causes for the lower values of heritability and genetic advance (Ali *et al.,* 2007).

Conclusion: The study indicated the presence of wide genetic variation among wheat genotypes at all the three locations which can be exploited to develop high-yielding varieties. Therefore, there is higher chance of selecting genotypes for different quantitative traits and exploiting high yielding varieties within the study areas and similar agro-ecologies of the South-Western Ethiopia. The range and mean values suggested the existence of sufficient variability among the tested genotypes for the majority of characters studied which imply that there was reasonably sufficient variability. This provides ample scope for selecting superior and desired genotypes by plant breeders for further improvement of bread wheat in the study areas. High heritability (>80%) coupled with moderate genetic advance as percent of mean (10 to 20%) was observed for days to heading, days to maturity, spikelet length and grain filling period at all the locations. This indicates that presumably the heritability of these characters is due to additive gene effects, and the selection might be effective for these characters. Therefore, direct selection for these characters, and incorporation therein of selected individual genotypes in breeding program would bring improvement in the genotypes. Thus, selection for high performance of these traits could also result in increased grain yield and those traits could be taken as selection criteria in bread wheat improvement program.

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