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Genetic Variability, Heritability And Genetic Advance Of Quality Traits Of Bread Wheat (*Triticum Aestivum L.*) Genotypes In South Eastern Ethiopia

Research Article

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Abstract

Information on the extent of genetic variation among characters is important to design breeding strategies and to develop varieties for the targeted area of production. Therefore, this research was conducted at Sinana Agriculture Research Centre testing site and at Robe on farm, south eastern Ethiopia, with the objectives of evaluating advanced bread wheat genotypes for quality traits. The experiment was conducted in 2018 cropping season using 21 promising lines and 4 released varieties in triple lattice design. Data were collected for 13 grain quality characters. Pooled analysis of data showed that there was significant ($P<0.01$) differences among genotypes hectolitre weight, wet gluten content, dry gluten content, gluten index, average kernel thickness, SDS sedimentation test, protein content and moisture content. For genotype x environment interaction, for wet gluten content, dry gluten content, gluten index, average kernel thickness, SDS sedimentation test, protein content and moisture content revealed significant ($P<0.01$) differences among genotypes. In pooled analysis, genotypic coefficient variation (GCV) and (PCV) was relatively higher for SDS sedimentation followed by wet gluten content. In all studied traits, the phenotypic coefficient of variation values were higher than genotypic coefficient of variation values across locations, indicating the higher influence of environmental factors than genetic factors for the phenotypic expression. In pooled analysis heritability in broad sense and genetic advance as percent of mean (GAM) ranged from 38.6% (dry gluten content) to 97% (SDS sedimentation test) and 2.6% (hectolitre weight) to 34.5% (SDS sedimentation). High heritability coupled with genetic advance was observed for SDS sedimentation in combined analysis. This implies the potential of improving wheat for end product use quality through direct selection. Generally, it has been observed the presence of variability among the genotypes studied and the possibility of increasing grain quality traits to improve quality in the study area.

Keywords: Genetic Variation, Genotypes, Quality Traits And Heritability.

Introduction

Wheat (*Triticum spp*) is one of the most important and widely grown food crops with more than 25,000 different cultivars [39]. Its cultivation was started with wild einkorn (diploid) and emmer (tetraploid) wheat around 10,000 years ago during Neolithic Revolution, the first series of agricultural revolutions. Due to its wide adaptability to diverse climatic conditions and its multiple end-uses along with dynamic nature of genomes and polyploidy character, it has become a crop of financial and nutritional importance especially after the emergence of hexaploid wheat [32]. Ethiopia is the second largest wheat producer next to South Africa in sub-Saharan Africa with more than 1.637,647 ha and productivity close to 2.11 t/ha and wheat stands fourth in area coverage (FAO, 2016). 81% of the total land cultivated to grain crops is covered by cereals out of which wheat accounts for 13.14% of the area (CSA, 2011). Wheat the second most consumed cereal in Ethiopia next to maize, accounting for approximately 11% of the national calorie intake in the country (200 kcal/day in urban areas and 310 kcal/day in rural areas). It has versatile uses in making various human foods such as bread, biscuits, cakes and sandwich [18]. It is also one of the major cereal crops grown in the Bale highlands of Ethiopia and this region is regarded as the largest wheat producer in Sub-Saharan Africa (Efrem et al., 2000).

Grain yield and quality of crop variety is the end result of interac-

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tion between variety and environment in which it is grown [22]. Grain size and hardness, protein content and its composition as well as starch content and its ability to gelatinize are important variables that determine wheat quality [34]. Wheat quality depends upon the genetic factor but environmental condition such as growth location and agronomic practices prevailing during different wheat growth stages greatly alter wheat quality attributes. Generally, wheat quality refers to its suitability for a particular end use based on physical, chemical and nutritional properties of the grain.

Genetic variability, which is due to genetic differences among individuals of a population, is the core of plant breeding because proper management of diversity can produce permanent gain in the performance of plant and can buffer against seasonal fluctuations [4]. Estimation of the magnitude of variation with in genotype for important plant attributes will enable breeders to exploit genetic diversity more efficiently. This is due to the critical role of genetic variability in determining the amount of progress to be made by selection. Hence, estimation of the extent and pattern of genetic variability existing in the available genotypes is essential to breeders [23]. High heritability is also needed to have better opportunity to select directly for the characters of interest. This is mainly because of the opportunity associated with high heritability in correct identification and measurement of the genotypes based on phenotypic values and in avoiding errors in genotypic classification [4].

In Ethiopia, the wheat improvement research since its inception prior to 1930's [19] has focused mainly on improving grain yield and disease resistance, except very recent where by quality is becoming essential breeding objective. Particularly nowadays, with the emerging agro industries using wheat as a raw material, good processing quality of wheat grain has become important breeding objective [15]. Information on physical and chemical quality parameters is necessary to assess the suitability of wheat varieties for different industrial uses. Generating information on variability and heritability of quality traits of advanced breeding lines is important to identify desirable quality traits for release. However, such activities are lacking in advanced bread wheat lines currently under yield trial in South Eastern Ethiopia. Rather, the trend is to check for quality traits at the end of the breeding scheme. However, such kind of attempt will not be rewarding as some promising genotypes might be discarded before reaching final stage of breeding (variety verification trial).

Material and Methods

Description of experimental sites and experimental materials

The experiment was conducted during the cropping season of 2018/19 at two locations, Sinana Agricultural Research Center (SARC) on station and at Robe area on farmer's field. SARC station is located 070 07' N latitude and 400 10' E longitude and at an altitude of 2400 meters above sea level. The soil texture type of the area is clay loam having black color and the soil pH ranges between 6.3-6.8 (SARC, 2013). The amount of rainfall from August to December 2018, during crop growing seasons, was 401.5 mm. The monthly mean maximum and minimum temperatures were 24.5^{0}C and 14.4^{0}C, respectively. The Robe area experiment was conducted on farmer's field is located 7006'44"N and 40001'33"E with altitude 2464 m. a. s. l. The amount of rainfall from August to December 2018 during crop growing seasons, was 350.3 mm. The monthly mean maximum and minimum temperatures were 21.60C and 8.5 0C, respectively.

The experimental materials comprised of 21 bread wheat genotypes and 4 released varieties obtained from SARC. The genotypes were retained from the 2015 bread wheat regional variety trials at SARC. The details of the genotypes are summarized in Table 1.

Experimental Design and Trial Management

The experiment was laid out in 5x5 triple lattice design. The plot size was 6 rows of 2.5 m length with 0.2 m spacing between rows (with a gross plot size of 3m2), and the spacing between plots and blocks was 0.4 m and 1m, respectively. Planting was done by hand drilling. Seed rate was 150 kg/ha (45 g/plot) and Urea and DAP fertilizers were applied at the rate of 50 kg/ha and 100 kg/ha, respectively. The field was weeded twice by hand (at 25 and 45 days after planting). For data collection, the middle four rows were used (2 m2 area). All cultural practices were applied uniformly to all experimental units.

Data Collected: Random homogeneous grain samples in replicates each genotype were used for laboratory analysis.

Thousand kernel weight (g): The weight of randomly sampled 1000 kernels.

Hectolitre weight (kg/hl): Weight of one-liter volume random sample of grain for each experimental plot.

Average kernel length (AKL): Was determined using a digital caliper by aligning 10 sets of 25 seeds end to end (brush to germ) putting crease down according to [38].

Average kernel width (KW): Was measured on the respective sets of 25 seeds by placing the seed crease down, side by side so that each contacted adjacent seed was taken at their widest points using digital caliper.

Average kernel thickness (AKT): Was measured in the same manner on respective sets of 25 seeds by placing them with the edge of the kernels.

Protein content (%) and moisture content (%): Were determined using Mininfra SmarT Grain Analyzer [29].

Wet and dry gluten content: Wet Gluten was prepared from whole meal by the Glutomatic 2200 gluten wash chamber. Gluten Index Centrifuge 2015 was used to force the wet gluten through a specially designed sieve cassette. The wet gluten is further dried in the Glutork 2020 for dry gluten content (ICC, 2000).

Gluten index (%) = (Gluten remaining on the sieve (g)/Total gluten (g)) X 100

Wet Gluten content (WGC) = Total wet gluten (g) X 10
Dry Gluten content (DGC) = Dry gluten weight (g) X 10

Sodium Dodecyl Sulfate (SDS) sedimentation test: The SDS sedimentation volume was measured according to AACC Method No.56-70 [1].

Vitreoussneous: Kernel vitreousity was estimated by using transmitted light according to ICC standard number 129 (ICC, 2000).

Grain hardness (%): was determined by particle size index (PSI) method as described in the AACC method 55-31 [1].

Data Analysis: The SAS GLM (General Linear Model) procedure SAS Institute Inc (2002) was employed for the analysis of variance. Duncan's Multiple Range Test (DMRT) at 5% probability level was used for mean comparisons, whenever genotypes differences were significant. Comparison of the relative efficiency of lattice design to Randomized Complete Block Design (RCBD) was done after data were analyzed for both designs and it showed that less efficient than RCBD. Therefore, for the flexibility of lattice design [12] the data were analyzed as per RCBD.

Phenotypic and genotypic variability: The phenotypic and genotypic variances and coefficient of variations were estimated according to the methods suggested by [9].

Heritability (H2) in broad sense for all traits was computed using the formula adopted from [3] and Falconer (1990).

Genetic advance (GA) and genetic advance as percent of mean (GA %): for each trait was computed using the formula adopted from [20, 3].

Results and Discussion

Test of homogeneity of error variance showed that the error mean squares were homogeneous for hectolitre weight, wet gluten content, dry gluten content, gluten index, average kernel thickness, SDS sedimentation test, protein content and moisture content. Combined data analysis was done only for the above mentioned characters. Therefore, analysis of variance across locations showed that there was significant ($P<0.01$) differences among bread wheat genotypes for all combined traits. Genotype x environment interaction showed that there were significant ($P<0.01$) differences among genotypes for wet gluten content, dry gluten content, gluten index, average kernel thickness, SDS sedimentation test, protein content and moisture content. This indicated that genotypes responded differently to varying environment for these traits.

Genotype performance for quality parameters: Mean performance values of the studied genotypes for different quality parameters are given in Table 2. The present study revealed sig-

Table 1. Description of bread wheat genotypes used in the experiment.

S.N	Genotype	Pedigree
1	ETBW 7866	CHUANMAI32//2*INQALAB 91*2/KUKUNA
2	ETBW 7524	PBW343*2/KUKUNA//AKURI
3	ETBW 7402	QUAIU/5/FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ
4	ETBW 7559	ROLF07*2/5/FCT/3/GOV/AZ//MUS/4/DOVE/BUC
5	ETBW 7661	TUKURU//BAV92/RAYON/3/FRNCLN
6	ETBW 7409	ROLF07*2/5/REH/HARE//2*BCN/3/CROC_1/AE.SQUARROSA (213)//PGO/4/HUITES
7	ETBW 7528	BABAX/LR42//BABAX*2/3/KUKUNA/4/TINKIO #1
8	ETBW 7527	JUCHI/HUIRIVIS #1
9	ETBW 6114	SOKOLL//SUNCO/2*PASTOR
10	ETBW 7698	FRNCLN/4/WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1
11	ETBW 7638	ATTILA/3*BCN*2//BAV92/3/KIRITATI/WBLL1/4/DANPHE
12	ETBW 7797	SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/PFAU/MILAN
13	ETBW 6873	WBLL*2/KUKUNA/5/PSN/BOW//SERI/3/MILAN/4/ATTILA/6/WBLLI*KKTS
14	ETBW 7729	MUNAL/3/KIRITATI//PRL/2*PASTOR/4/MU
15	ETBW 8005	SERI.1B//KAUZ/HEVO/3/AMAD/4/FLAG-2
16	ETBW 7998	SERI.1B//KAUZ/HEVO/3/AMAD/4/FLAG-2
17	ETBW 8003	SERI.1B//KAUZ/HEVO/3/AMAD/4/FLAG-2
18	ETBW 7715	MILAN/S87230//BAV92/3/AKURI#1/4/MILAN/S87230//BAV92
19	ETBW 7595	SKAUZ/BAV92//2*WBLL1*2/KKTS
20	ETBW 7435	WAXWING*2/4/BOW/NKT//CBRD/3/CBRD
21	ETBW 7718	MUNAL/3/KIRITATI//PRL/2*PASTOR/4/MUNAL
22	Dambel (2015)	AGUILAL/3/PYN/BAU//MILAN
23	Sanete (2014)	14F/HAR1685
24	Sofumer (2000)	LIRA/TAN
25	Madawalabu (2000)	TL/3/FN/NAR59*2/4/BOL'S'

nificant variation among genotypes for hectolitre weight, which ranged from 79.8 kg/hL (ETBW7866) to 85 kg/hL (ETBW7661 and ETBW7528). This result agrees with result of Birhanu et al. (2016) who reported an average hectolitre weight of 80.06 kg/hL with a range of 76.1 kg/hL to 84.1 kg/hL. Kernel thickness ranged from 2.7 mm (ETBW7866) to 3 mm (ETBW7528, ETBW7638 and Madawalabu). (21) also found comparable result with the present study, in which ranged from 2.6 mm to 2.9 mm. In the current study, the grain moisture content varied from 8.8% (ETBW7524 and ETBW7698) to 9.5% (ETBW7998). According to Shure [43] the wheat grains with moisture content below 12% can be stored for an extended period as flour with low moisture content is more stable during storage.

Highly significant variation was observed among genotypes for grain protein content, which ranged from 12.6 (ETBW7595) to 14.5% (ETBW7729). The differences in protein content among different wheat cultivars could be related to genetic difference [46]. Ermias [15] also reported a range of 11.5-15.4% for this trait, which within the range of result in the present study. According to [21], the protein content should be between 11 and 13% to produce bread with better quality in Iranian wheat cultivars he studied [5] reported variation in protein content from 9.7% to 13.5% among Pakistani wheat varieties, while [26] found a range of 9.71% to 15.42% in protein content of different bread wheat varieties.

Highly significant variability was observed among genotypes for wet gluten content value, which ranged from 20.3% (ETBW7559) to 42.5% (ETBW7527) with the average mean value of 32.4%. Correspondingly, highly significant genetic variability with the range value of 19.7% to 43.4% was reported by [11] for this trait. [43] reported variation in wet gluten content from 13.5% to 41.4% among 23 bread wheat cultivars grown under Arsi condition. On other hand, Jirsa et al. (2005) found 18.4% to 46.9% for bread wheat varieties studied at Prague. [33] also reported wet gluten in the range 12.77 to 44.06% in Uttar Paradesh wheat varieties, while [30] found a range of 25.0 to 33.5% for durum wheat cultivars tested at Sinana. Generally, the present finding for wet gluten content is within the range reported in most of these previous studies. The genotypes with the highest wet gluten content can be preferred by bread bakers since high wet gluten content

Table 2. Over all mean performance of bread wheat genotypes studied across locations.

Genotypes	HLW	WGC	DGC	GI	KT	MC	PC	SDS
ETBW 7866	79.8^{i}	29.7^{h}	10.3^{n}	88.3^{a}	2.7^{j}	8.9^{g-i}	13.8^{b-e}	81.7^{bc}
ETBW 7524	80.6^{f-i}	34.3^{c}	13.9^{c-e}	67.8^{gh}	2.9^{e-g}	8.8^{hi}	13.8^{b-e}	64.5^{i-k}
ETBW 7402	84.3^{a-c}	26.6^{i}	9.2^{o}	75.8^{d-g}	2.9^{d-f}	9.3^{a-c}	12.7^{fg}	65.3^{h-j}
ETBW 7559	82.1^{d-f}	20.3^{k}	8.9^{o}	87.7^{a}	2.9^{b-e}	9.1^{b-f}	13.6^{b-e}	77.7^{cd}
ETBW 7661	85^{ab}	30.2^{h}	12.6^{f-i}	78.5^{b-f}	2.9^{a-d}	9.1^{c-g}	13^{e-g}	64.4^{i-k}
ETBW 7406	79.9^{hi}	31.5^{fg}	11.9 $^{i-k}$	69.9^{f-h}	2.9^{e-g}	9.2^{b-f}	13.2^{d-g}	73.3^{ef}
ETBW 7528	85.0^{a}	41.4^{a}	13.5^{d-f}	70.3^{e-h}	3.0^{a}	8.9^{hi}	13.4 $^{c-g}$	63.4^{jk}
ETBW 7527	82.9^{b-e}	42.5^{a}	15.3^{ab}	80.3^{a-d}	2.9^{f-h}	9.1^{d-g}	13.4^{c-g}	74.7^{de}
ETBW 6114	83.2^{a-e}	32.8^{de}	13.2 $^{e-h}$	86.8^{b}	2.8^{hi}	9.2^{b-e}	13.7^{b-e}	67.6^{g-i}
ETBW 7698	82.6^{c-f}	34.6^{c}	13.3^{e-g}	86.5^{ab}	2.9 $^{a-d}$	8.8^{i}	14.2 $^{a-c}$	71^{eg}
ETBW 7638	81.3 $^{e-i}$	38.8^{b}	14.6 $^{a-c}$	78.4^{b-f}	3.0^{a-c}	9.1^{b-f}	14.9^{a}	87^{a}
ETBW 7797	84.4^{a-c}	34.8^{c}	12.4 $^{g-j}$	76.8^{c-f}	2.8^{ij}	9.1^{e-h}	14.1^{a-d}	51.8^{m}
ETBW 6873	82.9^{a-e}	33.0^{de}	12.3 $^{i-j}$	78.8^{b-e}	2.8^{f-h}	9.3^{a-}d	13.5^{c-g}	69.2^{h}
ETBW 7729	82.3^{c-f}	31.9^{ef}	14.4 $^{b-d}$	78.5^{b-f}	2.8^{h-j}	9.0^{e-h}	14.5^{ab}	81.5^{b}c
ETBW 8005	81.9^{d-g}	32.2^{ef}	12.4 $^{g-j}$	76.0^{e-g}	2.9^{de}	9.1^{b-f}	13.5^{c}-f	60.5^{kl}
ETBW 7998	83.1^{a-e}	33.8^{cd}	11.5 $^{j-l}$	75.7^{d-g}	2.9^{de}	9.5^{a}	14.1^{a-c}	61.8^{j-l}
ETBW 8003	82.4^{c-f}	38.1^{b}	14.9 $^{a-c}$	76.5^{c-g}	2.9^{d-f}	9.3^{ab}	12.9^{e-g}	58.6^{l}
ETBW 7715	82.6^{c-f}	34.8^{c}	14.4^{bc}	87.0^{ab}	2.9^{a-d}	9.1^{d-h}	13.9^{b-d}	77.7^{cd}
ETBW 7595	83.2^{a-e}	30.4^{gh}	13.2^{e-h}	78.6^{b-e}	3.0^{ab}	9.0^{e-h}	12.6^{g}	65.2^{h-j}
ETBW 7435	83.3a-e	29.4^{h}	10.5^{m-n}	76.9^{c-f}	2.9^{c-e}	9.1^{b-f}	12.9^{e-g}	63.2^{jk}
ETBW 7718	82.9^{a-e}	24.7^{j}	11.1^{k-n}	85.9^{ab}	2.9^{e-g}	9.1^{e-h}	14.2^{a-c}	83.5^{ab}
Dembel	83.9^{a-d}	38.7^{b}	15.5^{a}	67.9^{gh}	2.9^{d-f}	8.9^{f-h}	13.4^{c-g}	62.7^{j-l}
Sanete	79.9^{g-i}	33.7^{cd}	11.3^{k-m}	65.3^{h}	2.8^{hi}	9.2^{b-e}	13.5^{c-g}	35.5^{n}
Sofumer	83.7^{a-d}	26.3^{i}	11.3^{k-m}	76.6^{c-f}	2.8 $^{g-i}$	9.1^{b-f}	12.7^{fg}	49.9^{m}
Mada walabu	82.0^{d-f}	25.8^{ij}	10.7^{l-n}	84.7^{ab}	3.0 $^{a-c}$	9.3 $^{a-c}$	12.9^{e-g}	62^{j-l}
Means	82.6	32.4	12.5	9.1	78.2	2.9	13.5	66.9
CV	2.3	3.3	6.5	2.2	9.7	2.3	5.8	5.6

Where: HLW=hectolitre weight, WGC= wet gluten content, DGC= dry gluten content, GI= gluten index, KT=kernel thickness, MC=moisture content, PC= protein content, SDS= sodium dodecyl sulfate sedimentation test

Table 3. Range, mean, standard error and components of variation for different characters studied across locations.

Traits	Range	Mean+SE	σ^2 g	σ^2 p	GCV	PCV	GA	GAM	H^2
HLW	79.8-85	82.6±1.5	1.4	2.2	1.4	2	2.2	2.6	70.7
WGC	20.3-42.5	32.4±0.9	14	27.8	11.4	16.3	7.6	23.6	70.2
DGC	8.9-15.5	12.5±0.7	0.5	3.4	5.7	14.7	1.5	11.7	38.6
GI	65.3-88	78.2±6.2	30	44	7	8.5	11.3	14.4	82.5
KT	2.7-3.0	2.9±0.05	0.007	0.009	2.7	3.1	0.2	5.7	88.9
MC	8.8-9.5	9.1±0.2	0.02	0.04	1.5	2.2	0.3	3.2	70
PC	12.6-14.5	13.5±0.6	0.1	0.3	2.4	4.2	0.7	4.9	56.1
SDS	35.5-83.5	66.9±3.07	125.4	132.9	16.7	17.2	23.1	34.5	97.1

Where: SE=Standard error of mean, σ^2g = Genotypic variance, σ^2p =Phenotypic variance, PCV = phenotypic coefficient of variance, GCV = Genotypic coefficient of variation, H=Broad sense heritability, GA= genetic advance, GA (%) = Genetic advance as percent of mean, HLW=hectolitre weight, WGC= wet gluten content, DGC= dry gluten content, GI= gluten index, KT=kernel thickness, MC=moisture content, PC= protein content, SDS= sodium dodecyl sulfate sedimentation test.

increases water absorption, increase the protein content of bread, impart better gas retention and increase the volume of loaf [27, 11] concluded that excellent bread production process require wet gluten content more than 30%.

Significant difference among genotypes was observed for dry gluten having the range of value 8.9% (ETBW7559) to 14.5% (Dambel). The dry gluten content of the protein determines the flour quality and has significant impact on bread making quality [22]. In the same way, highly significant genetic variation was reported by [15, 42, 41] reported significant variation in dry gluten contents among Egyptian wheat cultivars, which ranged from 10.4% to 13.5% [5] reported a relatively wider range of 7.0% to 17% in Pakistani wheat cultivars, which is closely related to the results of the current study.

The mean gluten index in the current study ranged from 65.3% (Sanete) to 88.3% (ETBW7866). [13] proposed seven gluten quality classes in durum wheat. Gluten index values between 65% and 80% are considered good while values above 80% are excellent. Based on this, in the current study more than 35% of genotypes got high (>80%) gluten index values, while the rest of genotypes were categorized in good range (65% and 80%). The present result is comparable with Marufqual [27], who reported 38% to 96% values for GI. Other researchers also found highly significant differences in GI with the ranges of 59 to 96% [7] and 56 to 99% [11]. SDS sedimentation value of genotypes ranged from 35.5 ml (Sanete) to 83.5 ml (ETBW7718). According to Petrova [37], the sedimentation value of flours has been categorized into four classes: weakest (less than 15 ml), weak (between 16 ml and 24 ml), good (between 25 ml and 36 ml) and best (more than 36 ml). Ashima (6) found values ranging from 56.7 ml to 92 ml for SDS sedimentation volume.

Phenotypic and genotypic coefficient of variations: Was relatively higher for SDS sedimentation (16.7%) followed by wet gluten content (11.4%). GCV estimate gives good implication for genetic potential in crop improvement through selection (20). Hence, there could be better chance for improvement of the above characters with higher GCV values across locations. While phenotypic coefficient of variability (PCV) for pooled analysis was higher for SDS sedimentation (17.2%) followed by wet gluten content (16.3%). Similarly, Yonas (2015) found the highest PCV for wet gluten while Ermias (15) reported highest PCV for SDS sedimentation. The present result is in agreement with the report of [30] who obtained moderate PCV for wet gluten and SDS sedimentation on durum wheat genotypes.

The PCV was relatively greater than GCV for all the traits. However, the magnitude of the difference was relatively high for wet gluten and dry gluten content [47] reported the greater magnitude of PCV relative to GCV for all the traits he studied. This implies that greater influence of environmental factors for phenotypic expression of these characters that makes difficult to exercise selection based on phenotypic performance of the genotypes to improve these characters.

Estimates of heritability and genetic advance

Heritability values ranged from 38.6% (dry gluten content) to 97% (SDS sedimentation test) (Table 3). Johnson et al. (1955) classified heritability estimates as low (<30%), moderate (30-60%) and high (>60%). Based on this classification, High heritability values were observed for all combined traits except protein content and dry gluten content which categorized under moderate heritability estimates value. This indicates that selection could be fairly easy and improvement is possible using selection breeding for these traits. Similarly, [31] reported high heritability for SDS sedimentation (94.01%) and Besides, [30] reported moderate heritability value for dry gluten content and grain protein content in durum wheat. In contradict to the present study [48] reported low heritability values for SDS sedimentation and wet gluten content.

In the present study, genetic advance as a percent of mean ranged from 2.6% (hectolitre weight) to 34.5% (SDS sedimentation) (Table 3). This result indicates that selecting the top 5% of the genotypes could result in an advance of 2.6 to 34.5% across locations over the respective population means. [14] classified genetic advance as percent of mean as low (<10%), moderate (10-20%) and high (>20%). Based on this classification, SDS sedimentation and wet gluten content had high genetic advance as percent of mean in the current study. Rudra et al. (2015) and [24] also reported high genetic advance as percent of mean for SDS sedimentation volume. However, [48] reported moderate genetic advance as of

percent mean for wet gluten content and low for SDS sedimentation, which disagrees with the present findings. Moderate genetic advance as percent of mean was obtained for dry gluten content and gluten index and the rest of the characters had low genetic advance as percent of mean. [30] reported moderate genetic advance as percent of mean for dry gluten content similar to the present study.

It was suggested that considering both the genetic advance and heritability of traits simultaneously is preferable than considering them separately is important for determining how much progress can be made through selection [20]. In this study, both heritability and genetic advance as percent of mean values were high for wet gluten content and SDS sedimentation at across location. The heritability of these traits is due to additive gene effects and selection may be effective in early generations for these characters [2]. These results are in agreement with the study of Bushuk [10] who reported that most quality traits in wheat had high heritability and genetic advance as percent of mean values and indicated the potential of improving wheat for end product use quality through conventional plant breeding. Similarly, [25, 36] reported that several characters contributing to good quality have high heritability and genetic advance values.

Conclusion

Information on the nature and magnitude of genetic variability present in a crop species is important for developing effective crop improvement program. In addition, estimation of the magnitude of variation within germplasm collections for important plant attributes will enable breeders to exploit genetic diversity more efficiently. Heritability of any trait is a significant genetic parameter for the selection of efficient improvement methods in bread wheat breeding. Single plant selection in the earlier generation may be effective for traits that have high heritability as compared to traits with low heritability and environment is another factor that interacts to genetic constitution and influence heritability.

References

[1]. American Association of Cereal Chemists. Approved Methods Committee. Approved methods of the American association of cereal chemists. Amer Assn of Cereal Chemists; 2000.

[2]. Ali S, Shah SM, Hassnain A, Shah Z, Munir I. Genotypic variation for yield and morphological traits in wheat. Sarhad Journal of Agriculture. 2007;23(4):943.

[3]. Allard RW. Principles of Plant Breeding. New York: John Willy and sons. Inc. 485p. 1960.

[4]. Ammar K, Kronstad WE, Morris CF. Breadmaking quality of selected durum wheat genotypes and its relationship with high molecular weight glutenin subunits allelic variation and gluten protein polymeric composition. Cereal Chemistry. 2000 Mar;77(2):230-6.

[5]. Anjum FM, Khan MR, Din A, Saeed M, Pasha I, Arshad MU. Wheat gluten: high molecular weight glutenin subunits--structure, genetics, and relation to dough elasticity. J Food Sci. 2007 Apr;72(3):R56-63. Pubmed PMID: 17995810.

[6]. Poudel A. Genetic Analysis of Bread Making Quality Stability in Wheat using a Halberd X Len Recombinant Inbred Line Population (Doctoral dissertation, Texas A & M University).

[7]. Bilgin O, Korkut KZ. Determination of some bread quality and grain yield charactersin bread wheat (*Triticum aestivum L.*). International Journal of Agriculture and Biology (Pakistan). 2005.

[8]. Birhanu Mecha. Genetic Variability, Heritability and Genetic Advance for Yield and Yield Related Traits in Bread Wheat (*Triticum aestivum L.*) Genotypes. Global Journal of Science Frontier Research of Agriculture and Veterinary, 2016;16(7): 249-256

[9]. Burton, G.W. and Devane, G. Quantitative inheritance in grasses. Proceedings of 6th International Grassland, 1953;1: 277- 283.

[10]. Bushuk W. Flour proteins: Structure and functionality in dough and bread. Cereal foods world (USA). 1985.

[11]. Popa CN, Tamba-Berehoiu RM, Hutan AM, Popescu S. The significance of some flour quality parameters as quality predictors of bread. Scientific Bulletin. Series F. Biotechnologies. 2014;18:135-40.

[12]. Cochran WG, Cox GM. Experimental designs 2nd. ed. John Wily and Sons. Inc. New York USAPP. 1957;595.

[13]. Cubadda R, Carcea M, Pasqui LA. Suitability of the gluten index method for assessing gluten strength in durum wheat and semolina. Cereal foods world (USA). 1992.

[14]. Deshmukh SN, Basu MS, Reddy PS. Genetic variability, character association and path coefficients of quantitative traits in Virginia bunch varieties of groundnut. Indian Journal of Agricultural Sciences. 1986.

[15]. Ermias E. Assessment for quality traits, yield and yield related characters in advanced ethiopian bread wheat (*Triticum aestivum L.*) breeding lines (Doctoral dissertation, M. Sc. Thesis. Alemaya University, Ethiopia).

[16]. FAO (Food and Agriculture Organization of the United Nations). FAOSTAT: production crop data. Accessed on 15 August, 2017.

[17]. GAIN (Global agricultural information network). Assessments of commodity and trade issues by USDA staff. GAIN, Ethiopia.2014

[18]. Hailu G, Tanner DG, Mengistu H. Wheat research in Ethiopia: A Historical perspective. Addis Ababa: IAR/CIMMYT. 1991.

[19]. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans 1. Agronomy journal. 1955 Jul 1; 47(7):314-8.

[20]. Kasraei M, Nejadi J, Shafiei S. Relationships between grain physicochemical and mechanical properties of some Iranian wheat cultivars. Journal of Agricultural Science and Technology. 2015 May 10;17(3):635-47.

[21]. Kent, N.L. and A.D. Evers. Technology of cereals (4th edtn). Pergamon Press, Oxford. 1994.

[22]. Zerga K, Mekbib F, Dessalegn T. The Mean Performance of Different Bread Wheat (Triticum Aestivum. L) Genotypes in Gurage Zone, Ethiopia. Landscape Architecture and Regional Planning. 2017 Feb 16;2(1):29-35.

[23]. Yagdi KO, Sozen E. Heritability, variance components and correlations of yield and quality traits in durum wheat (Triticum durum Desf.). Pak. J. Bot. 2009 Apr 1;41(2):753-9.

[24]. Lukow OM, McVetty PB. Effect of cultivar and environment on quality characteristics of spring wheat. Cereal chem. 1991 Nov 1;68(6):597-601.

[25]. Mahmood A. Acid-PAGE gliadin composition and cluster analysis for quality traits of different wheat varieties (Doctoral dissertation, University of Agriculture, Faisalabad).

[26]. Mahkamov M. Analysis of bread making quality parameters of Tajik wheat.

[27]. Mekuria B, Emire SA. Effects of vital gluten enrichment on qualities of value added products. Journal of Food Processing & Technology. 2015 Jan 1;6(11):1.

[28]. Mininfra SmarT Grain Analyzer Operating Manual. Version 1.3. infracont Kft. 2013. Available at www.infracont.hu.

[29]. Mohammed A, Geremew B, Amsalu A. Variation and associations of quality parameters in Ethiopian durum wheat (Triticum turgidum L. var. durum) genotypes. International Journal of Plant breeding and genetics. 2012;6(1):17-31.

[30]. Abdipour M, Ebrahimi M, Izadi-Darbandi A, Mastrangelo AM, Najafian G, Arshad Y, et al. Association between grain size and shape and quality traits, and path analysis of thousand grain weight in Iranian bread wheat landraces from different geographic regions. Notulae Botanicae Horti Agrobotanici Cluj-Napoca. 2016 Jun 14;44(1):228-36.

[31]. Neem Lal Pandey. Baking quality in wheat effect of delayed Harvest, cultivars, growing conditions and nitrogen fertilization. M Sc. Thesis, Norwegian University, Norway 2013.

[32]. Paliwal SC, Singh G. Physico-chemical, milling and bread making quality of wheats of Uttar Pradesh. Journal of food science and technology (Mysore). 1986;23(4):189-93.

[33]. Panozzo JF, Eagles HA. Cultivar and environmental effects on quality characters in wheat. II. Protein. Australian Journal of Agricultural Research. 2000;51(5):629-36.

[34]. Pasha I. BIOCHEMICAL CHARACTERIZATION OF PAKISTANI WHEATS IN RELATION TO SRAIN HARDNESS (Doctoral dissertation, UNIVERSITY OF AGRICULTURE, FAISALABAD PAKISTAN).

[35]. Peterson, C.J., R.A. Graybosch, D.R. Shelton and P.S. Baenziger. Baking quality of hard winter wheat Response of genotypes to environment in the Great Plains. Euphytica, 1998;100: 157-162.

[36]. Petrova I. End-use quality of Bulgarian durum wheat. Bulgarian Journal of Agricultural Science. 2007;13(2):161.

[37]. Schuler SF, Bacon RK, Gbur EE. Kernel and spike character influence on

test weight of soft red winter wheat. Crop science. 1994 Sep;34(5):1309-13.
[38]. Sapone A, Bai JC, Ciacci C, Dolinsek J, Green PH, Hadjivassiliou M, et al. Spectrum of gluten-related disorders: consensus on new nomenclature and classification. BMC medicine. 2012 Dec;10(1):1-2.
[39]. SARC (Sinana Agricultural Research Centre). Annual report. 2013; 1-50.
[40]. Seleiman MF, Abdel-Aal S, Ibrahim M, Zahran G. Productivity, grain and dough quality of bread wheat grown with different water regimes. Journal of Agro Crop Science. 2011;2(1):11-7.
[41]. Senayit Wondimu. Evaluation of Some Bread Wheat (*Triticum aestivum L.*) Genotypes for quality traits, yield and yield components and association among characters. M.Sc Thesis, Haramaya University, Haramaya, Ethiopia. 2007.
[42]. Shure Soboka. Physicochemical properties in relation to bread making quality of Ethiopian improved bread wheat (*triticum aestivum l.*) Cultivars grown at Kulumsa, Arsi. M.Sc Thesis, Haramaya University, Haramaya, Ethiopia. 2013.
[43]. Khabiri E, Imani AA, Shahbazi H. Studying the grain yield and yield components in advanced rain fed wheat genotypes. Annals of Biological Research. 2012;3(12):5647-50.
[44]. Khan N, Naqvi FN. Heritability of morphological traits in bread wheat advanced lines under irrigated and non-irrigated conditions. Asian Journal of Agricultural Sciences. 2011 May 25;3(3):215-22.
[45]. Kent NL, AD Evers. Technology of cereals (4th edtn). Pergamon Press, Oxford. 1994.
[46]. Kotal BD, Arpita D, Choudhury BK. Genetic variability and association of characters in wheat (*Triticum aestivum L.*). Asian journal of crop science. 2010; 2(3):155-60.
[47]. Wieser H. Chemistry of gluten proteins. Food microbiology. 2007 Apr 1;24(2):115-9.
[48]. Yonas S. Genetic variability and association of grain yield, yield components and quality traits in durum wheat (Triticum turgidum l. var. durum) genotypes at hera liphitu, southern Ethiopia (Doctoral dissertation, Haramaya University).

Appendix Table1. Mean squares from analysis of variance for 13 Traits of 25 bread wheat genotypes evaluated at Sinana and at Robe (2016).

	Sinana			Robe			
Traits	**Msr (2)**	**MSg (24)**	**Mse(48)**	**Msr (2)**	**MSg (24)**	**Mse (48)**	**Hom.test(F=1.73)**
TKW	13.10**	21.54**	1.56	75.11**	39.36**	4.58	2.9
HLW	5.26^{ns}	3.50^{ns}	3.2	9.46^{ns}	14.45**	3.92	1.2
WGC	0.66^{ns}	140.88**	1.29	0.20^{ns}	108.51**	0.93	1.4
DGC	1.68^{ns}	19.02**	0.67	1.03^{ns}	18.58**	0.66	1
GI	81.33^{ns}	200.14**	60.14	112.59^{ns}	148.08**	55.21	1.1
GH	23.48^{ns}	10.22^{ns}	15.09	0.11	34.75**	6.35	2.4
KL	0.006^{ns}	0.14**	0.009	0.001	0.11**	0.03	3.3
KW	0.006^{ns}	0.036**	0.003	0.33	2.44**	0.16	53.3
KT	0.008^{ns}	0.03**	0.004	0.001	0.03**	0.004	1
VI	42.87**	12.86**	5.03	32.44	49.68**	15.53	3.1
MC	0.01^{ns}	0.21**	0.04	0.18*	0.07*	0.04	1
PC	33.19**	1.91**	0.72	4.73**	1.63**	0.52	1.4
SDS	28.49^{ns}	412.7**	14.09	525.16**	429.94**	14.14	1