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Genetic Variation and Association of Grain Quality Traits in Tetraploid Wheat (*Triticum turgidum* spp,) Landraces and Some Improved Cultivars of Ethiopia

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Research Article

Keywords: Ethiopia, tetraploid wheat, grain quality traits, variability analysis, correlation analysis

Posted Date: August 30th, 2022

DOI: https://doi.org/10.21203/rs.3.rs-2003386/v1

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Abstract

A total of 196 tetraploid wheat (*Triticum turgidum* spp) germplasm, representing 174 landraces and 22 improved cultivars, of Ethiopia were evaluated assess to the variation and correlation of traits using 8 grain quality traits, There was a highly significant ($p < 0.001$) variation among the genotypes for all traits. Except for vitreousness percentage, all the traits were highly significantly ($p < 0.001$) affected by the environment. Range values revealed that there was high variability among the genotypes in their thousand kernel weight, Zeleny index, and vitreousness percentage; medium variability in gluten content and low variability in seed yield, and protein content. The mean values of thousand kernel weight, seed yield, gluten content, protein content, Zeleny index, and vitreousness percentage respectively was 34.24 ± 0.28,3.25 ± 0.06, 26.49 ± 0.21,13.3 ± 0.06, 41.57 ± 0.57, and 68.44 ± .1.12. The values of PCV and GCV were high for seed yield, Zeleny index, vitreousness percentage; intermediate for gluten content and thousand kernel weight and low for protein content. Estimate of broad sense heritability (H^2) ranged from 33.57% for seed yield to 66.36% for Zeleny index. The observed genetic advance and GAM were high for seed yield and Zeleny index; intermediate for thousand kernel weight, gluten content, and vitreousness percentage, and low for protein content. Seed yield showed a highly significant positive correlation with thousand kernel weight and vitreousness percentage and a positive correlation with protein content and gluten content (0.1). The present result concluded that there was high variation among the genotypes in their grain quality. The implication for breeding was discussed.

Introduction

Ethiopia, the largest wheat producer in sub-Saharan Africa, is a centre of diversity for the cultivated tetraploid wheat (Haile Jemanesh et al. 2013; VAVILOV, 1929; Brasesco et al., 2019; Abate, 2018), which has acquired a diverse set of characteristics and enormous genetic variability (Oliveira et al. 2012). The genetic variability held in tetraploid wheat is vital to meet the diversified goal of breeding (Asmamaw, Keneni, and Tesfaye 2020), including the grain quality of wheat.

Wheat grain, an excellent staple food, has numerous beneficial compounds of nutritional and health value. Wheat is unique among cereal grains due to the special bread that is only made from its flour (Kollers et al. 2013). The insoluble storage protein of wheat, collectively called 'gluten', gives wheat its functional properties (Tipples, 1994). Most of the world's food supply comes from cereals. As a result, the nutritional quality of cereals is a vital part of the world's diet (Elias and Manthey 2005).

There is an increasing need for high-quality foods, particularly wheat-based products (P. Bhalla and Singh 2017). With the increase in grain production, research is giving special attention to improving wheat’s technological qualities such as the strength of flour, gluten quantity and quality, protein content, and others (Keler, Martynova, and Ovchinnikova 2020). Most of the world's food supply comes from cereals, making the nutritional quality of cereals a vital part of the world's diet (Elias and Manthey 2005).

Wheat grain is an excellent staple food with numerous nutritional and health-beneficial compounds due to the special bread that is only made from its flour (Kong et al. 2013), which makes wheat unique among cereal grains. The insoluble storage proteins of wheat collectively called 'gluten,' give wheat its functional properties (K. H. Tipples 1994). Depending on the unique properties of the protein it contains, wheat grain has many foods and non-food benefits(Shewry 2009) making the grain quality of wheat the second crop yield (Keler, Martynova and Ovchinnikova, 2020).

In the past, grain quality was not a decisive criterion of variety selection; thus, the breeding programs gave emphasis only to the improvement of grain yield and disease resistance (Drikvand et al. 2018; Tadesse, Bishaw, and Assefa 2018). Nowadays, however, the grain quality of wheat is becoming central to food processing and nutritional value and is a decisive factor for consumer acceptance and commercial value of wheat cultivars (X. Wang et al. 2017) due to the current increase in the requirement for high-quality food, especially for wheat-based products (Bhalla and Singh, 2017). Things have changed due to changing food habits, increasing urbanization and trends toward raising middle-class society (Wang et al., 2017) that make grain quality of wheat central to human well-being (Kong et al. 2013). Thus, in addition to enhancing yield, improving grain quality of wheat is also vital. As a result, apart from grain yield and disease resistance, quality is becoming a solid criterion of wheat variety selection (M. Johnson 2017) and improving wheat grain quality. Hence, critically looking for better quality varieties suiting for preparing different end products is becoming a criterion for developing new varieties (Peña et al. 2002).

Wheat quality characteristics are essential contributors to wheat yield and quality (Drikvand et al., 2018; Tadesse, Bishaw, and Assefa 2018) and determine the quality and the type of wheat in the market (Johnson et al., 2019; Sardana, 2000; Tipples et al., 1994). The quality of end-products is related to the wheat grain quality, which, in turn, is determined by the genotype, the environment, and crop management; for example, high-quality pasta begins with good quality grain. The most important variables determining wheat grain quality include protein content, gluten content, and vitreousness (Troccoli et al., 2000;Tipples et al., 1994; Keler et al., 2020; Blckman & Payne, 1987; Sardana, 2000; Elias & Manthey, 2005; Wang et al., 2003; Chichti et al., 2018; Drikvand et al., 2018; Dobraszczyk et al., 2002). These important wheat quality characteristics are very much influenced by the effects of the genotype, the environment, and the genotype-by-the environment interactions (Tipples, 1994).

To meet the current increase in the requirement for high quality wheat-based food products (P. L. Bhalla, Sharma, and Singh 2017), assessing the diversity of the existing landraces for their grain quality traits is crucial. Ethiopia is a centre of diversity for tetraploid wheat landraces (Haile, Hammer, Badebo, Nachit, et al. 2013; VAVILOV, 1929). These land races are untapped primary sources of desirable genes useful for economically important traits such as grain quality. They are endowed with ample genetic resources vital to meet the diversified goal of breeding (Haile Jemanesh et al. 2013; Muleta et al. 2017). Despite the existing potential, Ethiopia is importing wheat from abroad due to huge gap between production and consumption (Abate 2018;Brasesco et al. 2019) to fill gap for industry (Haile Jemanesh et al. 2013).This necessitates the development of wheat varieties that are high yielding with the required grain quality traits through the continuous assessment of the landraces. This requires a continuous supply of new germplasm as a source of desirable genes (Asmamaw, Keneni, and Tesfaye 2020) for which tetraploid wheat are the potential source. The study of Haile Jemanesh et al. (2013) and that of Teklu and Hammer (2008) focused mainly on phenotypic diversity. However, phenotypic diversity alone cannot clearly indicate the existing genetic diversity in the landraces. (Alemu et al. 2020) made genome wide association mapping for grain shape and colour traits in Ethiopian durum wheat (*Triticum turgidum* ssp. durum). Grain shape and colour strongly influence yield and quality of durum wheat (Alemu et al. 2020). The existing landraces collected and maintained by Ethiopian Biodiversity Institute were not fully studied to effectively exploit the existing germplasm for different economically important traits. Therefore, assessing these landraces for their seed colour, vitreousness, grain protein content, Zaleny indes, seed yield, thousand kernel weight and gluten content is of great value in developing cultivars with the required end use quality. Therefore, this study was initiated to assess the extent and pattern of genetic diversity of tetraploid wheat landraces of Ethiopia on the basis of grain quality traits.

Material And Methods

Planting material

A total of 196 tetraploid wheat (*Triticum turgidum* spp) genotypes, representing 22 released varieties and 174 landraces, were used in this study (Supplementary table s1). The landraces were collected from different parts of the country (Fig. 1) by the Biodiversity Institute of Ethiopia (IBE). The released varieties and 40 landraces were obtained from Debrezeit Agricultural Research Centre; however, 134 landraces were obtained from Sinana Agricultural Research Centre.

Methods

Grain quality traits data collection and analysis

Each genotype was grown in two rows of 1 meter long and 20 cm inter-row spacing in a simple lattice design with two replications at Sinana and Debrezeit Agricultural Research Centre. All agronomic recommendations were used as recommended. Seed samples from 196 genotypes were assessed for their grain quality traits at Sinana grain quality laboratory on a plot basis. The grain quality traits studied were seed colour, seed yield, thousand kernel weight, Zeleny index, protein content, moisture content, gluten content, and vitreousness percentage; of these, the later four traits were determined using MINIFRA SmarT grain analyser (M*ininfra SmarT Grain Analyzer Operating Manual, 2013, Version 1.3. Infracont Kft.*Www.Infracont.Hu., *2013)*. Vitreousness was estimated from the seed sample using illuminated purity work board model S-115 by using transmitted light according to ICC standard number 129 (ICC, 2000).

Seed colour: visual observation of seed colour: 1(white), 2(red), and 3(purple).

Thousand kernel weight (g): the weight of thousand grains of wheat genotypes.

Homogeneity of the error MS from individual analysis of variance at Sinana and Debrezeit was checked following the formula of (Gomez and Gomez 1984); described as: F = Larger error MS/smaller error MS. The error variances were homogeneous for all the triats studied. The combined ANOVA was performed by the model: Y = Replication + genotypes + Location + Genotypes x Location + Replication: bock. The variability of each quantitative grain quality trait was estimated using simple statistical measures such as mean, range, phenotypic and genotypic variances, and coefficient of variation. The phenotypic, genotypic, environmental, and genotype by environment interaction coefficient of variations, broad sense heritability (H^2), and genetic advance were the parameters assessed using excel program. The phenotypic and genotypic variation and coefficient of variations were calculated using the formula suggested by Singh and Chaudhary (1985) and Allard (1960).given below:

Genotypic variance ($\delta^2 g$)

$\delta^2 g = (MSg - MS_{gl})/rl$ where MSg stands for mean square of genotype, MS_{gl} represents mean square due to genotype by environment interaction, l is number of locations and r stands for number of replications.

Environmental variance ($\delta^2 e$)

($\delta^2 e$) = MSe where MSe stands for combined error mean square.

Genotype by environment interaction variance (δ^2_{gl})

(δ^2_{gl}) **= (**MS_{gl}-MS_e)/r

where MS_{gl} represents mean square due to genotype by environment interaction, and MSe represents combined error mean square.

Phenotypic variance (δ^2_p) = $\delta^2_g + (\delta^2_{gl}/l) + (\delta^2_e/rl)$

Estimates of coefficient of variation will be obtained as follows.

Phenotypic coefficient of variation (PCV)

$$PCV = \frac{\sqrt{\sigma^2_p} x100}{\mu}$$

where PCV = phenotypic coefficient of variation, δ^2_p = phenotypic variance and μ = population mean for the trait considered.

Genotypic coefficient of variation (GCV)

$$GCV = \frac{\sqrt{\sigma^2_g} x100}{\mu}$$

where GCV = genotypic coefficient of variation, δ2g = genotypic variance and μ = population mean for the trait considered.

Environmental coefficient of variations (ECV)

$$ECV = \frac{\sqrt{\sigma^2_e} x100}{\mu}$$

where ECV = environmental coefficient of variation, δ2e = error variance and μ = population mean for the trait considered.

Genotype by environment interaction coefficient of variation (GECV):

$$GECV = \frac{\sqrt{\sigma^2_{gl}} x100}{\mu}$$

*w*here δ^2_{gl} = genotypic by environment interaction variance and $\boldsymbol{\mu}$= population mean for the trait considered.

PCV and GCV values below 10%, 10%-20% and above 20% were considered to be low, intermediate and high respectively (Burton and DeVane 1953).

Broad sense heritability (H^2) and genetic advance

Broad sense heritability, for the two locations combined, was estimated based on the formula given by Allard (1960) as follows: $H^2 = (\delta^2g/\delta^2p) \times 100$; where $\delta^2p = \delta^2g + (\delta^2gl/l) + (\delta^2e/rl)$, δ^2e = error variance, δ^2g = genetic variance, δ^2p =phenotypic variance, l = the number of locations and r = the number of replications and was categorized as low (below 40%), medium (40%-80%), and high or very high (above 80%) (Mesele, Mohammed, and Dessalegn 2015).

Expected genetic advance under selection was calculated using the formula of Allard (1960), at 5% selection intensity, as: GA = (K) (δp) (H^2); where, GA = expected genetic advance, K represents a selection differential that varies based on the selection intensity and is equal to 2.056 if one chooses 5% of the genotypes, δp stands for phenotypic standard deviation, and H^2 represents broad sense heritability. Genetic advance as percentage of a mean, which was categorized as low (< 10%), moderate (10–20%) and high (> 20%)(H. W. Johnson, Robinson, and R.E.Comstock 1955), was calculated as GA (% of mean) = $(\frac{GA}{\mu})$ x100%, where GA = genetic advance and μ = population mean for the trait.

Correlation coefficient analysis

Pearson correlation analysis of the quantitative traits was performed for quantitative traits using R software version 4.1.1(R Development Core Team 2018).

Results

Analysis of variance

Based on the combined analaysis of variance, the genotypes showed highly significant variation for all traits studied (Table 1). Except vitreousness percentage, all traits studied were highly signficantly ($p < 0.001$) affected by the environment. Seed yield, gluten content, protein content, zeleny index, and vitreousness percentage were highly signficantly ($p < 0.001$) affected by genotype by enviroment interaction. In line with the present study, Amiri et al. (2018) reported similar for thousand kernel weight, grain yield, and grain protein content in bread wheat genotypes. Moreover, Mesele, Mohammed and Dessalegn (2015) reported similar result for grain protein content. Furthermore, Taneva, Bozhanova and Petrova (2019) reported similar result for protein content, thousand kernel weight, and grain yield of durum wheat.

Table 1
Mean square of grain quality traits from combined ANOVA.

Source of variation	Df	TKW	SY	Gluten	Moisture	Protein	ZI	VITP
Replication	1	627***	5.21*	162***	5.78***	17.8***	617**	340
Genotypes	195	106.94***	5.82***	65.72***	0.31***	6.01***	377.56***	976***
Site	1	10489***	188.54***	3913***	56.20***	1257.5***	17056***	633
Geno:Site	195	44***	3.39***	32.93***	0.13***	2.9***	127***	648.4***
Rep:block	26	40*	1.59	25**	0.07	1.9**	140**	349.1*
Pooled error	365	21.25133	1.035393	10.4518	0.066852	0.79971	58.62465	185.768
	CV	14.01	33.1	13.08	2.66	7.13	19.84	20.52
	lsd	6.67	1.5	4.82	0.39	1.32	11.47	19.53

NB: Df = degrees of freedom, CV = coefficient of variation, lsd = lest significant difference, TKW = thousand kernel weight, SY = seed yield, ZI = Zeleny index, and VITP = vitreousness percentage.

Patterns of quantitative traits variation

The respective mean and range values for thousand kernel weight, seed yield, gluten content, moisture content, protein content, zeleny index, and vitreousness percentage were on average (34.24g, 23.6–44.9), (3.25t/ha, 3.25t/ha-5.98t/ha), (26.49%, 17.89%-35.26%), (10.62, 10.16–11.73), (13.3%, 11.14%-15.9%), (41.57ml, 19.48ml-63.19ml), and (68.44%, 28.48%-98.18%) were given in Table 2. In line with the present study, Taneva, Bozhanova and Petrova (2019) reported similar result for thousand kernel weight, grain yield, and protein content. Moreover, Mesele, Mohammed and Dessalegn (2015) reported similar result for grain protein content in bread wheat genotypes. Furthermore, Amiri et al. (2018) also reported similar result for thousand kernel weight and grain protein content of bread wheat under rain-fed conditions. Additionally, Modoran et al. (2010) reported similar result for Zeleny index. Kumar (2020) also reported similar result for protein content of wheat genotypes under restricted irrigation conditions.

Table 2
Mean, range, minimum, and maximum values of grain quality traits.

	Grain quality traits						
	TKW	SY	Gluten	Moisture	Protein	ZI	VITP
Mean	34.24 ± 0.28	3.25 ± 0.06	26.49 ± 0.21	10.62 ± 0.02	13.3 ± 0.06	41.57 ± 0.57	68.44 ± 1.12
Minimum	23.6	3.25	17.89	10.16	11.14	19.48	28.48
Maximum	44.9	5.98	35.26	11.73	15.90	63.19	98.18
Range	21.05	2.73	17.37	1.56	4.76	43.7	69.7

NB: TKW = thousand kernel weight, SY = seed yield, ZI = Zeleny index, and VITP = vitreousness percentage.

The minimum (23.6g) was for landraces 5609 that was obtained from North Shewa (2510 masl); on the other hand, the maximum thousand kernel weight (44.9g) was recorded from an improved cultivar Gerardo. The minimum seed yield (1.33 t/ha) and the maximum yield (5.98 t/ha) were respectively recorded from the landraces 7713 and 7626, which were respectively collected from North Shewa of Amara (2800 masl) and North Shewa of Oromia (2950 masl). The minimum gluten content (17.89%) and maximum gluten content (35.26%) were respectively recorded from landraces 242782 and 238891, which were respectively collected from East Shewa (2120 masl) and Bale (1900 masl). The maximum (15.90%) and the minimum (11.14%) protein content were respectively recorded from an improved variety cocorit/71 and the landrace MCD5-35, ETDW/15DZ004, which was collected from East Shewa (2454 m a.s.l). The maximum (63.19ml) and the minimum (19.48ml) zeleny index were respectively recorded from landraces 7683 and 5430, which were respectively collected from East Gojjam (2450 masl) and East Shewa (2450masl). The minimum (24.48%) and the maximum (98.18%) vitreousness percentage were respectively recorded from an improved variety cocorit/71 and the land race 7078, which was collected from Arsi (2440 masl).

Phenotypic and Genotypic Coefficient of Variation

The values of PCV, GCV, GECV, broad sense heritability (H^2), and genetic advance were given in Table 3. PCV and GCV below 10%, 10–20%, and above 20% were respectively regarded as low, intermediate, and high (Burton and DeVane 1953). The values of PCV and GCV were low for moisture and protein content. PCV values were high seed yield (37.18), Zeleny index (23.37) and vitreousness percentage (22.82) and intermediate for thousand kernel weight (15.1) and gluten content (15.30). GCV values were intermediate for thousand kernel weight (11.58), gluten content (10.81), Zeleny index (19.04), and vitreousness (13.22) and high for seed yield (24.03). In line with the present study, Ganno, Alemu and Ayalew (2017) reported similar result PCV and GCV values of grain protein content in bread wheat. Moreover, Taneva, Bozhanova and Petrova (2019) reported similar result on PCV and GCV values of protein content; however their result disagrees with the present study on PCV and GCV of grain yield and thousand kernel weight in durum wheat genotypes. Furthermore, Kumar, (2020) also reported similar result on PCV and GCV of thousand kernel weight; however, his result disagrees with the present study on seed yield.

Table 3
Variability, Broad Sense Heritability, and Genetic Advance.

Traits	Parameters										
	GV	*EV*	*GxEV*	PV	GCV	PCV	ECV	GECV	H^2	GA	GAM
TKW	15.73	21.25	11.38	26.73	11.58	15.1	13.46	9.85	58.85	18.27	16.59
SY	0.61	1.04	1.18	1.46	24.03	37.18	31.38	33.42	41.78	31.94	26.91
Moisture	0.05	0.07	0.032	0.08	2.11	2.66	2.44	1.22	62.5	3.42	2.85
Protein	0.78	0.8	1.05	1.51	6.64	9.24	6.73	3.36	51.66	9.81	8.44
Gluten	8.2	10.45	11.24	16.43	10.81	15.3	12.2	6.1	49.91	15.7	13.55
ZI	62.64	58.63	34.19	94.39	19.04	23.37	18.42	9.21	66.36	31.89	29.34
VITP	81.9	185.77	231.32	244	13.22	22.82	19.92	9.96	33.57	15.75	12.97

NB: TKW = thousand kernel weight (gm), SY = seed yield (t/ha). ZI = Zaleny index (ml), VITP = vitreousness percentage, GV = genetic variance, EV = environmental variance, PV = Phenotypic variance, GxEV = Genotype by Environment interaction variance, GCV = Genotypic Coefficient of Variation, PCV = Phenotypic Coefficient of Variation, ECV = Environmental Coefficient of Variation, GECV = Genotype by Environment interaction Coefficient of Variation, GA = Genetic Advance, GAM = Genetic Advance as percentage of Mean.

The difference between PCV and GCV was 3.52, 13.15, 2.6, 4.49, 4.33 and 9.6 for thousand kernel weight, seed yield, protein content, gluten content, zeleny index, and vitreousness percentage, respectively. The observed difference between PCV and GCV was high for seed yield and vitreousness percentage; however, it was low for protein content, gluten content, thousand kernel weight, and zeleny index. This implies that seed yield and vitreousness percentages were substantially influenced by the growing environments; however, the environment does not play many roles in the expression of other traits.

Environmental coefficient of variation was high for seed yield (31.38); intermediate for vitreousness percentage (19.92), zeleny index (18.42), thousand kernel weight (13.46), and gluten content (12.20) and low for protein content (6.73). Genotype by environment interaction coefficient of variation was high for seed yield (33.42) and low for thousand kernel weight (9.85), vitreousness percentage (9.96), zeleny index (9.21), gluten content (6.10) and protein content (3.36).

Estimate of Broad sense heritability (H^2) and genetic advance

Broad sense heritability (H^2) values < 40%, 40–80%, and > 80% were categorized as low, medium, and high, respectively (Mesele, Wassu, and Tadesse 2015). Estimates of heritability (H^2) ranged from 33.57–66.36% for vitreousness percentage and Zeleny index, respectively (Table 3). High heritability was observed for Zeleny index (66.36%), moisture content (62.5%) and thousand kernel weight (58.85). Seed yield (41.78), vitreousness percentage (33.57), and gluten content (49.91) exhibited less than 50% heritability while others remaining traits showed greater than 50% heritability. In line with the present study, Taneva, Bozhanova and Petrova (2019) reported similar result for thousand kernel weight and protein content, however, their report disagrees with the present study for seed yield (36).

The values of both genetic advance and genetic advance as a percentage of mean were low for moisture content (3.42, 2.85) and protein content (9.81,8.44); intermediate for thousand kernel weight (18.27,16.59), gluten content

(15.70,13.55), and vitreousness percentage (15.75,16.59), and high for seed yield (31.94,26.91), and zeleny index (31.89,29.34). Zeleny index showed the highest values of genetic advance and heritability. In line with the present study, Mesele, Mohammed and Dessalegn (2015) reported similar result on the value of broad sense heritability and GAM of grain protein content. Moreover, Taneva, Bozhanova and Petrova (2019) reported similar result GAM values for protein content and thosadn kernel weight; but, their result disagrees with present study for seed yield.

Correlation

The result of Pearson correlation coefficient was given in (Table 4). Seed yield showed highly significant ($p < 0.001$) positive correlation with thousand kernel weight (0.43***) and vitreousness percentage (0.19**); positive correlation with seed colour (0.1), protein content (0.08) and gluten content (0.1) and highly significant ($p < 0.001$) negative correlation between seed yield and moisture content (-0.28***). In line with the present study, Mesele, Mohammed and Dessalegn (2015) reported that significant positive correlation of seed yield and thousand kernel weight; however, their report disagrees on seed yield and grain protein content.

Thousand kernel weight showed highly significant ($p < 0.001$) positive correlation with vitreousness percentage (0.25***) and Zeleny index (0.22**); positive correlation with gluten content (0.07) and a negative correlation with protein content (-0.06) and moisture content (-0.16). In line with this study, Amiri et al. (2018) also reported that grain yield and thousand kernel weight had a significant positive correlation.

Vitreousness percentage showed highly significant ($p < 0.001$) positive correlation zeleny index (0.71***) and gluten content (0.35***); negative correlation (-0.48***) with moisture content and a negative, but not significant, correlation with protein content (-0.02).

Zeleny index had a highly significant ($p < 0.001$) negative and positive correlation with moisture content (-0.43***) and with protein content (0.3***) and gluten content (0.61***), respectively. Protein had a highly significant positive correlation with gluten content (0.73***) and a positive correlation with moisture content (0.12). Gluten showed a negative correlation with moisture content (-0.16). In line with this study, Modoran *et al.*(2010) also reported that there was a significant positive correlation between protein content and Zeleny index of wheat.

Discussion

The present study revealed that tetraploid wheat germplasm holds signficant genetic variation for all grain qulaity traits, which could be used for the imporvement of grain quaity in the breeding programs. Moreover, high variation among the genotypes was also revealed by patterns of quantitative traits variation.

The low GCV(6.64) and PCV(9.24) values for protein content implies that there is less scope for selection because there is low variability for protein, which is slightly influenced by environment factors. There was high GCV value for seed yield (24.03) and intermediate GCV values for thousand kernel weight (11.58), gluten content (10.81), zeleny index (19.04) and vitreousness percentage (13.22); thus, this is an indication of high variability and hence, good scope for selection of these traits.

Except seed yield; which showed intermediate value, other traits showed lowest values for genotype by environment interaction coefficient of variation implying that seed yield was more influenced by environment while other traits are less influenced by environment and were due to genetic factors.

The observed difference between PCV and GCV was high for seed yield (13.15) and vitreousness percentage (9.6); however, the difference was low for protein content, gluten content, thousand kernel weight, and Zeleny index. This implies that seed yield and vitreousness percentage were substantially influenced by the growing environments.

The success of selection, in breeding programs, is largely determined by heritability and genetic advance. Pandey and Tawari (1983) documented the importance of estimating heritability, which indicates the genetic gains that is possible through selection, to predict the inheritance of quantitative traits. Genetic advance provides a prior quantitative estimate of the magnitude of the progress that can be achieved through selection (Panse and Sukhatme 1957). High heritability and high genetic advance were recorded for zeleny index indicating that the trait is under the control of additive gene effects. Seed yield had medium heritability combined with high genetic advance. The implication is that selection may be effective for zeleny index and seed yield. High heritability along with high expected genetic gain could result from the high additive gene effect and therefore targeted selection for such traits will lead to yield improvement (Panse and Sukhatme 1957). Heritability estimates with genetic advance are more useful in predicting the gain under selection than heritability alone (H. W. Johnson, Robinson, and R.E.Comstock 1955). Vitreouness percentage had low heritability coupled with medium genetic advance while protein content had low heritability combined with low genetic advance indicating the lower success in selection for these traits.

Seed yield showed highly significant ($p < .001$) positive correlation with thousand kernel weight (0.43***); significant ($p < 0.01$) positive correlation with vitreousness percentage (0.19**) and positive correlation with seed colour (0.1), protein content (0.08), and gluten content (0.1). This implies that there might be common gene(s) that control seed yield and these traits, which indicates that improving either one or all of these traits could result in high seed yield (Arega, Hussein, and Singh 2010). According to (Kearsey and Pooni 1996), the positive association of these traits with seed yield might be due to either the presence of strong coupling of genes or pleiotropic genes controlling the traits in the same direction. Kearsey and Pooni (1996) further suggested also that the presence of such genes effects lead to the improvement of yield.

Abbreviations

ANOVA
analysis of variance
GA
genetic advance.
GCA
genotypic coefficient of variation.
IBC
Institute of Biodiversity Conservation.
IBPGR
Institute of Biodiversity Plant Genetic Research.
masl
meter above sea level
PCA
phenotypic coefficient of variation.
t/ha
tonnes per hectare.

Declarations

Acknowledgements: We acknowledge Oromia Agricultural Research Institute for financial support. We also extend our appreciation to Sinana Agricultural Research centre and Debrezeit Agricultural Research centre for providing the germplasm and research area. Ethiopian Biodiversity Institute was also given thanks for collecting and maintaining tetraploid wheat landraces. We also extend our sincere appreciation to Tesfaye Tadesse and Siraj Defo for their support in quality data recording.

Funding: This study was funded by the Oromia Agricultural Research Institute.

Competing interests: The authors declare that they have no competing interests.

Authors' contributions: MF designed and implemented the experiment, analysed the data and wrote the manuscript. All authors read and approved the final manuscript.

Availability of data and materials**: all data were used this article.**

Ethics approval and consent to participate: not applicable.

Consent for publication: not applicable.

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Table 4

Table 4 is available in the Supplementary Files section.

Figures

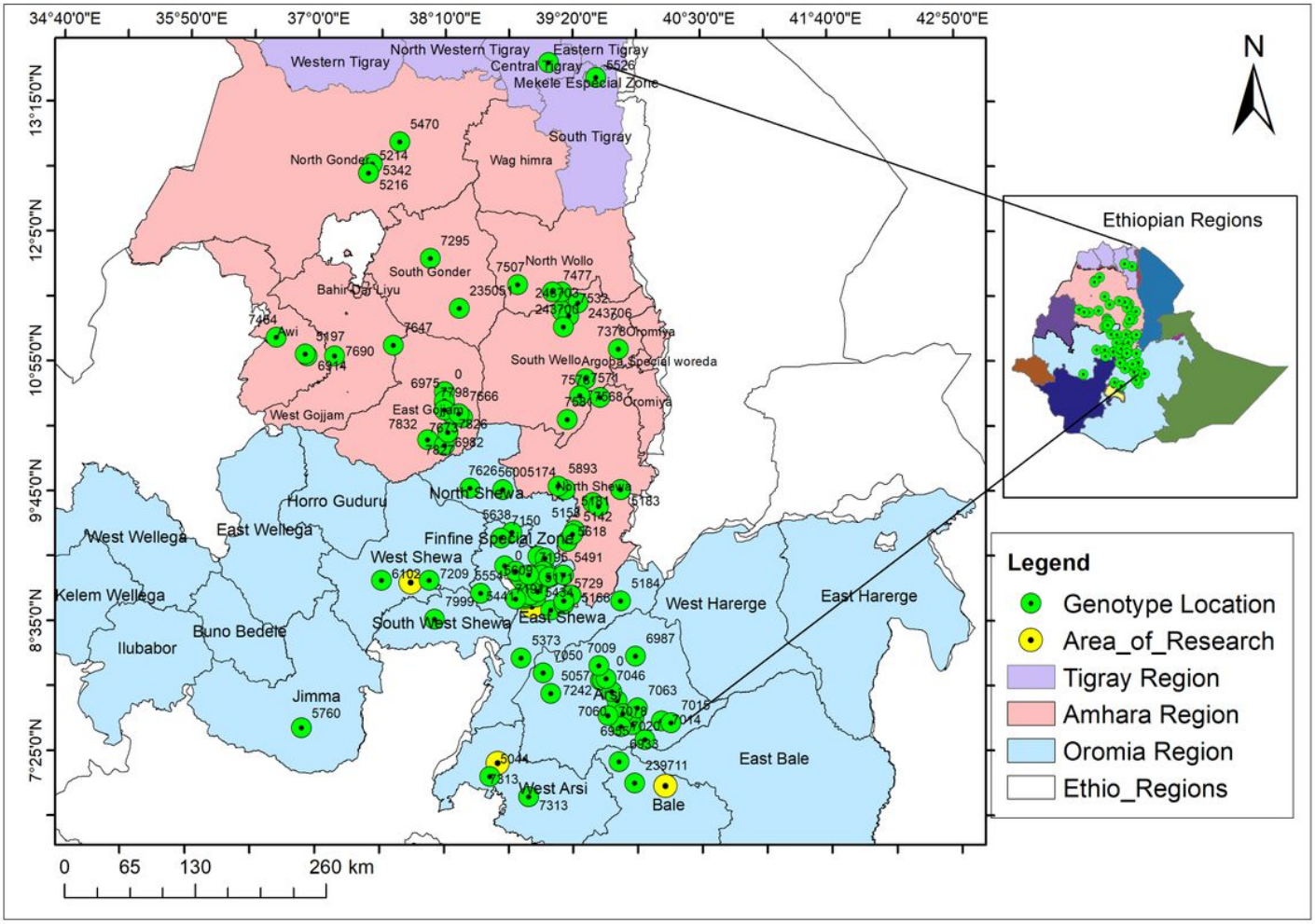


Figure 1

Geographical map of Ethiopia, indicating areas of collection of the landraces and site of research.

Supplementary Files

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