Research Article

Genetic variation, genetic advance, heritability and correlation analysis of phenotypic traits in tetraploid wheat (*Triticum turgidum* spp.) landraces and some improved cultivars of Ethiopia

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Abstract

Tetraploid wheat species from Ethiopia hold ample genetic variation, which could provide a source for improvement of wheat. A total of 196 Ethiopian tetraploid wheat (*Triticum turgidum* spp.) accessions, including 174 landraces and 22 improved cultivars, were evaluated at Sinana and Debrezeit to assess morphological variation, genetic advance, heritability and correlation based on 11 phenotypic traits. Except for spike length, highly significant variation ($P < 0.001$) among genotypes for all traits was observed. The observed mean and range values of the phenotypic traits revealed high variability in the accessions. Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) values were high for grain yield, biomass yield and harvest index. Seed yield showed highly significant ($P < 0.001$) negative correlation with days to booting and days to maturity and positive correlation with all traits. The estimates of heritability (H^2) for grain yield and the number of spikelets per spike respectively ranged from 41.78 to 84.62%. The genetic advance as a percentage of mean was low for the number of seeds per spikelet, days to booting and days to maturity; intermediate for plant height, thousand kernel weight and spike length and high for the number of spikelets per spike, the number of effective tillers per plant, grain yield, biomass yield and harvest index, respectively. The number of spikelets per spike gave a high value of genetic advance and heritability implying high genetic gain from its selection.

Introduction

Wheat is a commodity with a high market value that generates income for farmers in Ethiopia, the largest wheat producer in sub-Saharan Africa. Two types of wheat are predominantly grown in Ethiopia: tetraploid wheat, indigenous to the country, and hexaploid wheat, a recent introduction to the country (Getachew and Worede, 1991; Alamerew *et al.*, 2004). The majority of tetraploid wheat species grown by farmers are mixtures of landraces varying in botanical and morphological features. For millennia, farmers have preferred to grow mixtures of tetraploid wheat landraces to add variety to their diet and to reduce the risks of losses due to new disease or pest outbreaks or due to unusual environmental conditions (Pecetti and Damania, 1996) because of useful alleles they possess as compared to hexaploid wheat. Ethiopia is a centre of diversity for the cultivated tetraploid wheat ($2n = 4x = 28$) (Vavilov, 1929; Abate, 2018; Brasesco *et al.*, 2019). Despite this potential, Ethiopia remains a net importer of wheat due to the huge gap between production and consumption (Abate, 2018; Brasesco *et al.*, 2019) emanating from very low national yield (Haile *et al.*, 2013a, 2013b) and increased demand for wheat (Zegeye *et al.*, 2020). The mean productivity of wheat in Ethiopia is 3 tons per hectare (t/ha) (CSA 2021) which is below the attainable yield for the crop which can be up to 5 t/ha (Alemu *et al.*, 2019; Zegeye *et al.*, 2020; Nigus *et al.*, 2022). Hence, low productivity continues to be the major challenge facing wheat production in Ethiopia (Alemu *et al.*, 2019). Accordingly, continuous enhancement of wheat yield is crucially needed. This necessitates the development of wheat varieties that are high yielding with the required quality and are stable under biotic and abiotic stresses. This requires a continuous supply of new germplasm as a source of desirable genes and gene variants (Asmamaw *et al.*, 2019) for which tetraploid wheat landraces are a valuable source.

Tetraploid wheat has been under cultivation in Ethiopia for thousands of years and has acquired a diverse set of characteristics and enormous genetic variability. However, the diversity present in tetraploid wheat through domestication has not been fully evaluated (Negisho *et al.*, 2021). Landraces are dynamic population(s) of cultivated species that have historic origin with distinct identity and locally adapted in association with traditional farming systems

(Ceccarelli, 2016). Landraces possess wide genetic diversity and are underutilised primary sources of desirable genes for economically important traits (Teklu and Hammer, 2008; Haile et al., 2013b; Muleta et al., 2017). Tetraploid wheat holds diverse alleles for disease resistance that can reverse the existing genetic diversity erosion in established, elite cultivars Muleta et al. (2017). The development of new varieties is critical to enhancing the yield of wheat, and use of landrace populations is a viable strategy to improve yield and yield stability as well as resistance to biotic and abiotic stresses (Abbasabad et al., 2016).

Crop improvement substantially depends on the extent of genetic variability existing within the species and their crop wild relatives. The genetic variation that exists among plant populations is a basic requirement for their efficient improvement and also serves as an evidence to prove whether the population of such plants can withstand unpredictable changes in the environment (Nandwani, 2019). Crop breeding programmes depend on the availability of large germplasm collections, which are invaluable source of parental strains for hybridization and subsequent development of improved varieties (Asins and Carbonell, 1989). More than 7000 tetraploid wheat landraces were maintained at the Biodiversity Institute of Ethiopia (https://ebi.gov.et/). However, only limited portions of the collections were characterized (Negisho et al., 2021) using morphological markers (Getachew and Worede, 1991; Belay et al., 1993; Bechere et al., 1996; Belay et al., 1997; Kebebew et al., 2001; Alamerew et al., 2004; Eticha et al., 2005; Faris et al., 2006; Teklu and Hammer, 2008; Tsegaye et al., 2012; Mengistu et al., 2015; Asmamaw et al., 2020). Therefore, more information is needed about phenotypic and genetic variation present in Ethiopian

tetraploid wheat landraces through morphological characterization to reveal the potential input of the landraces for breeding (Teklu and Hammer, 2008).

Genetic variability among tetraploid wheat genotypes can be estimated based on quantitative traits (Azene et al., 2020). Furthermore, knowledge of the naturally occurring diversity in tetraploid wheat landraces helps to identify diverse groups of genotypes to be incorporated in the breeding programme (Azene et al., 2020). To inform breeding, it is important to estimate heritability and genetic advance (Pandey and Tiwari, 1983). Heritability denotes the proportion of phenotypic variance that is due to genetic reasons (Singh, 1990). Genetic advance provides a prior quantitative estimate of the magnitude of the progress that can be achieved through selection (Panse and Sukhatme, 1957). In this study, we assessed the genetic variation, heritability, genetic advance and correlation of phenotypic traits in 196 tetraploid wheat germplasm to inform future breeding programmes.

Materials and methods

Planting materials

A total of 196 tetraploid wheat (Triticum turgidum spp.) genotypes, representing 174 landraces and 22 varieties, collected from different parts of the country were used in this study (Supplementary Table S1). The landraces accessions used were originated from the different Ethiopian wheat producing regions: Shewa, Jima, Bale, Tigray, Wello, Gonder, Gojam, Agaw Awi (Fig. 1). The released varieties and 40 of the landraces were obtained from
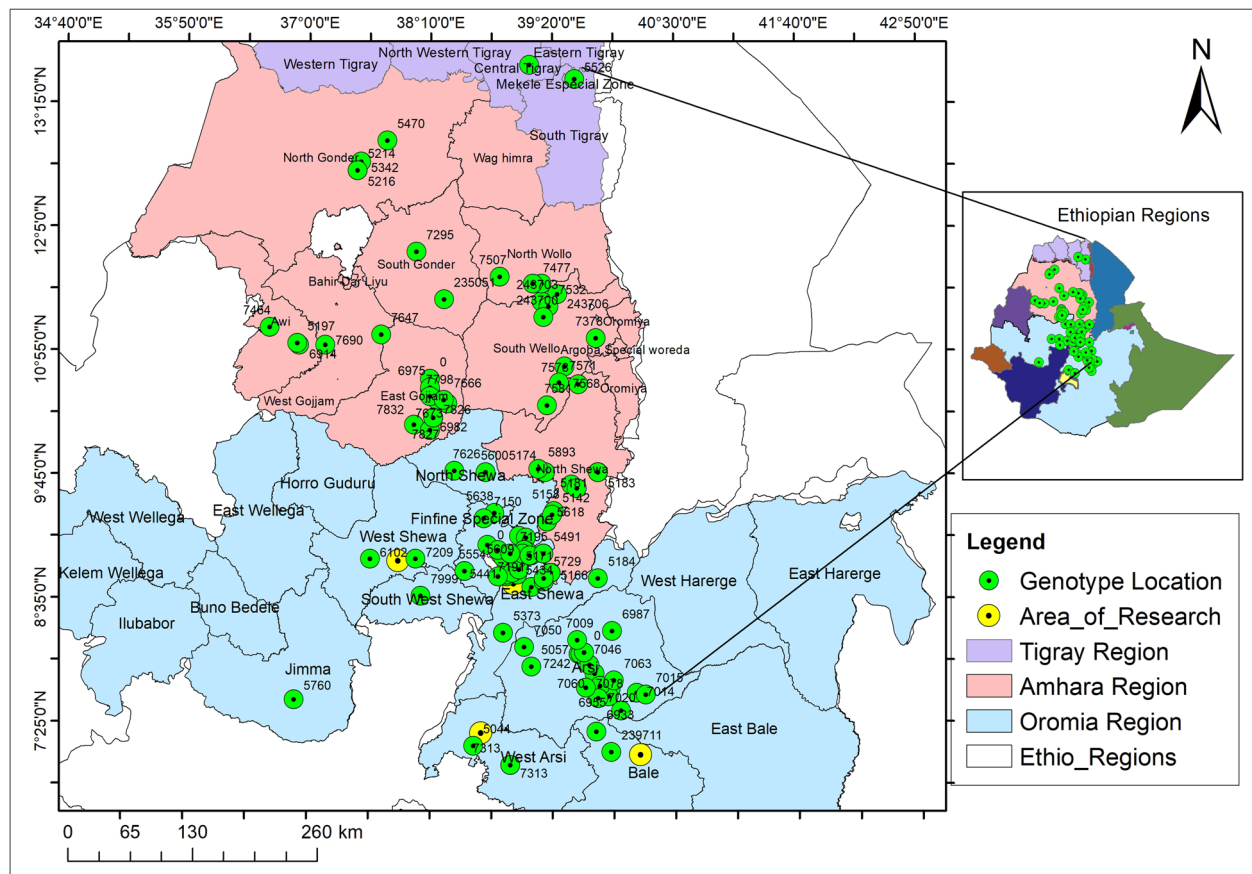

Figure 1. Geographical map of Ethiopia, indicating areas of the collection of the tetraploid wheat landraces and field trial sites of the research.

Debrezeit Agricultural Research Centre (www.eiar.gov.et). The remaining 134 landraces were obtained from Sinana Agricultural Research Centre (http://www.iqqo.org). The landraces were collected by the Biodiversity Institute of Ethiopia (IBE).

Methods

Each genotype was grown in plots of two rows of 1 metre long and 20 cm inter-row spacing with two replicates per accession in a simple lattice design at Debrezeit and Sinana during 2020. Debrezeit Agricultural Research Centre is located at an altitude of approximately 1900 m above sea level, with latitude of 80 44′ N and longitude of 380 85′ E. Sinana, located at an altitude of 2400 metre above sea level, has a range of mean annual rainfall of 563–1018 mm with minimum and maximum temperature of 7.9 °C and 24.3 °C, respectively. All agronomic recommendations were used as recommended: 100 kg urea and 150 kg DAP per hectare and three times hand weeding was applied. Ten plants were randomly selected and tagged for phenotypic data collection. The data were collected for 11 quantitative morphological traits using the descriptors for wheat (IBPGR, 1985). Days to booting, days to maturity, seed yield and biomass yield were recorded on a plot basis.

Plant height

Height of plant at maturity, measured in cm from ground to top of spike.

Spike length

The length of spike from the base of spike to the tip of spike measured in cm.

Days to booting

Counted as days from sowing to 50% of plants in booting stage.

Days to maturity

Counted as days from sowing to 50% of plants at physiological maturity.

Number of spikelet per spike

The average number of spikelet per spike from five typical spikes randomly selected from a growing accession.

Number of seeds per spikelet

The average number of seeds from a spikelet – obtained from the central portion of the five randomly selected typical spikes.

Number of effective tiller per plant

The number of tillers bearing spike from the five randomly selected plants.

Biomass yield per plot

Dry weight of the above ground wheat per plots taken at harvest.

Grain yield per plot

The grain weight of all plants grown per plot taken from each genotype, moisture content adjusted to 12.5%.

Thousand kernel weight

Thousand grains were counted from each genotypes harvested from a plot and their weight in gram was recorded.

Harvest index

The ratio of dried grain weight per plot divided by above ground biomass at 12.5% moisture content.

Phenotypic data analysis: Analysis of variance (ANOVA) for each location was carried out using the PBIB test in R by considering genotypes and block as fixed and random factors, respectively. In each location, the observed phenotypic response of the ith genotype in the jth replication and lth sub-block was computed using the following model:

$$Y_{ijl} = \mu + g_i + y_j + bl(j) + \varepsilon_{ij}$$

where y_{ijl} = the observed phenotype, μ = the grand mean, g_i = fixed effect of the ith genotype, y_j = effect of the jth replication, $bl_{(j)}$ = random effect of the lth block nested within the jth replication and ε_{ijl} = random error term.

The combined ANOVA across the locations was executed by considering genotype as a fixed effect and the block, and location as random effects according to the following model:

$$Y_{ijkl} = \mu + g_l + r_{ijk} + l_i + b_{ijkl} + (gl)_{il} + \varepsilon_{ijkl}$$

where Y_{ijkl} = observed response of genotype l and replication j of block k of location i; μ = grand mean; g_l = fixed effect of genotype l; r_{ijk} = effect of replication j in location i; l_i = random effect of location i that is $\sim NID(0, \delta_e^2)$; b_{ijkl} + random effect of block k nested within replication j in location i that is $\sim NID(0, \delta_b^2)$; $(gl)_{il}$ = random effect of the interaction between genotype l and location i that is $\sim NID(0, \delta_{gl}^2) + \varepsilon_{ijkl}$ = random residual effect that is $\sim NID(0, \delta_\epsilon^2)$.

Homogeneity of the error mean square (MS) was tested from individual ANOVA at Sinana and Debrezeit was checked following the F-max technique of Hartley (1950) described as: maximum F statistics (F_{max}) = Larger error mean square (MSE)/ smaller error mean square (MSE). The error variance is declared as homogenous if the larger MSE is not three times greater than the smaller MSE (Gomez and Gomez, 1984). After deciding that the error variances were homogeneous for specific triat, the combined ANOVA was performed. The statistical significance between genotypes is decided based on P-value that corresponds to the F statistics. If P-value is less than the specified alpha (α) level, the null hypothesis is rejected and the difference between the genotypes concluded significant; however, if the P-value is not less than the specified alpha (α) level, the null hypothesis is accepted and we conclude that the genotypes showed statistically no significant difference (https://statisticalpoint.com/anova-f-value-p-value).

The variability of each quantitative trait was estimated by simple statistical measures such as mean, range, phenotypic and genotypic variances and coefficient of variation. Phenotypic, genotypic, environmental and genotype by environment

interaction coefficient of variation, broad sense heritability (H^2), and genetic advance were the parameters assessed. 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 the mean square of genotype, MS_{gl} represents the mean square due to genotype by environment interaction, l is the number of locations and r stands for number of replications.

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

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

$$\delta^2_{gl} = (MS_{gl} - MS_e)/r$$

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

Phenotypic variance (δ^2_p)

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

Estimates of coefficient of variation will be obtained as follows.

Phenotypic coefficient of variation (PCV)

$$PCV = \frac{\sqrt{\sigma^2 p}}{\mu} \times 100$$

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

Genotypic coefficient of variation (GCV)

$$GCV = \frac{\sqrt{\sigma^2 g}}{\mu} \times 100$$

where GCV = genotypic coefficient of variation, $\delta^2 g$ = genotypic variance and μ = population mean for the trait considered.

Environmental coefficient of variations (ECV)

$$ECV = \frac{\sqrt{\sigma^2 e}}{\mu} \times 100$$

Coefficient of variation due to genotype by environment interaction was computed by the formula

$$GECV = \frac{\sqrt{\sigma^2 gl}}{\mu} \times 100$$

where, δ^2_{gl} = genotypic by environment interaction variance and μ = population mean for the trait considered.

Table 1. Mean square of combined ANOVA of quantitative traits

Source of variation	df	SdPSp	SpPSp	SpL	TPP	PH	TKW	SY	Mo	BY	HI	DB	DM
Replication	1	0.44*	115.3***	19.78***	660.5***	9804***	627***	5.21*	5.78***	411***	1898***	64	766***
Genotypes	195	1.05***	6.34***	5.81***	6.18	275.55***	106.94***	5.82***	0.31***	66.67***	684.09***	59.35***	79.81***
Location	1	1.10**	188***	189.29***	220.3***	293536***	10,489***	188.54***	56.20***	207***	9488***	5236***	133,408***
gen:Loc	195	0.16**	3.01***	1.94*	3	99***	44***	3.39***	0.13***	36.6***	324***	34*	33***
Rep:block	26	0.17*	2.71	2.79**	5.5*	105**	40*	1.59	0.07	17.3	141	54**	47***
Pooled error	365	0.1	1.83	1.22	2.05	49.39	21.25	1.04	0.067	12.39	116.6	14.62	6.12
Mean		3	18	8.2	6	99.86	34.24	3.25	10.62	11.34	31.81	73.4	123.44
SE		0.33	1.42	1.22	1.77	8.13	4.75	1.08	0.29	3.94	10.49	5.12	4.43
CV		12.67	7.65	13.48	23.91	7.04	13.46	31.34	2.66	31.03	33.95	5.21	2
Lsd		0.45	1.88	1.54	1.99	9.77	6.41	1.42	0.39	4.9	15.02	5.32	3.44
Range		1.2–4.6	12.2–23.2	4.0–14	1.0–12.0	53.2–139.2	10.0–52.2	0.06–9.66	10.28–11.73	4.38–22.5	13.55–65.10	53–88	89–154

NB: SdpSpklet, number of seeds per spikelet; SpPSp, number of spikelet per spike; SpL, spike length (cm); TPP, number of effective tillers per plant; PH, Plant height (cm); TKW, weight of thousand kernels per plant (gm); SY, seed yield (T/ha); BY, biomass yield (T/ha); HI, harvest index; DB, days to booting; DM, days to maturity; gen, genotype; Loc, location; Rep:block, block within replication; SE, standard error; CV, coefficient of variation, and Lsd, least significant difference.

Broad sense heritability (H^2) and genetic advance

Heritability in broad sense, for the two locations, was estimated based on the formula given by (Allard, 1960). $H^2 = (\delta^2 g/\delta^2 p) \times 100$, where $\delta^2 p = \delta^2 g + (\delta^2 gl/l) + (\delta^2 e/rl)$ where $\delta^2 e$ = error variance, l = the number of locations and r = the number of replications. Expected genetic advance under selection was calculated with 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 the mean will be calculated as GA (% of mean) = () x100%, where GA = genetic advance and μ population mean for the trait considered.

Correlation coefficient analysis

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

Results

Combined ANOVA

A total of 196 tetraploid wheat (*T. turgidum* spp.), including 174 landraces and 22 varieties, were assessed for the genetic variation, genetic advance, heritability and correlation of their eleven phenotypic traits at Debrezeit and Sinana Agricultural Research centres during 2020. After checking for homogeneity of the error MS from individual ANOVA at Sinana and Debrezeit during 2020 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 traits studied. Table 1 illustrates the variance results from a pooled analysis of eleven phenotypic traits for 196 genotypes of tetraploid wheat genotypes at Sinana and Debrezeit during 2020.

For all traits other than the number of effective tillers per plant, the mean squares resulting from genotypes and genotype by location interaction differed significantly among genotypes ($P < 0.001$). All traits showed highly significant variation ($P < 0.001$) across locations.

Patterns of quantitative traits variation

The mean value of the phenotypic traits of the accessions along with their pedigree is given Supplementary Table S1. The respective mean and range values for the number of seeds per spikelet (3 and 2–5), the number of spikelets per spike (18 and 15–21), the number of effective tillers per plant (6 and 3–9), spike length (8.20 cm and 5.57–10.38 cm), plant height (99.86 cm and 81.45–117.86 cm), thousand kernel weight (34.24 g and 23.6–44.9 g), seed yield (3.25 t/ha and 1.33–5.98 t/ha), biomass yield (11.23 t/ha and 3.75–22.5 t/ha), days to booting (73 and 153 61–81), days to maturity (123 and 117–130) and harvest index (33.20% and 13.55–72.21%) were given in Table 2. The coefficient of variation was high for grain yield (31.34), biomass yield (31.03), harvest index (33.95) and the number of effective tillers per plant (23.91) (Table 2).

Phenotypic and genotypic coefficient of variation

The values of phenotypic coefficient of variation (PCV = the variation due to genotype and environment), genotypic coefficient of variation (GCV = the variation due genotype only), genotype by environment interaction coefficient of variation (GECV = the variation due to the interaction of genotype and environment), broad sense heritability (H^2 = how much a variation in a trait is due to genetic factors) and genetic advance (explains the degree of gain obtained in a trait under a particular selection pressure) are 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 the number of seeds per spikelet (6.98, 5.06), plant height (8.31, 6.65), moisture content (2.66, 2.11), days to booting (5.25, 3.43) and days to maturity; were intermediate for the number of spikelets per spike (17, 15.64), spike length (14.74, 12.01) and thousand kernel weight (15.1, 11.58) and were high for seed yield (37.18, 24.03), biomass yield (36, 24.18) and harvest index (41.11, 29.82). High PCV (20.79) and intermediate GCV (14.93) values were obtained for the number of effective tillers per plant.

The difference between PCV and GCV was 0.85, 1.36, 1.66, 1.82, 1.92, 2.73, 3.52, 5.86, 11.28, 11.82.13.15 for days to maturity, number of spikelet per spike, plant height, days to booting, number of seed per spikelet, spike length, thousand kernel weight, number of effective tillers per plant, harvest index, biomass yield and seed yield respectively. The observed environmental coefficient of variation were high for seed yield (31.38), biomass yield (31.04), harvest index (33.95) and the number of effective tillers per plant (23.9); were intermediate for the number of spikelet per spike (10.54), spike length (13.47) and thousand kernel weight (13.46); and were low for the number of seed per spikelet (7.52), plant height (7.04), moisture content (2.49), days to booting (4.24) and days to maturity (2).

Table 2. The mean, minimum, maximum and range values of quantitative traits at the entire genotypes level

Values	Traits										
	PH	TPP	SpSp	SDpSp	SPL	TKW	SY	HI	BY	DB	DM
Mean	99.86	6	18	3	8.2	34.24	3.25	33.2	11.23	73	123
Min	81.45	3.32	15	2	5.57	23.6	1.33	13.55	3.75	61	117
Max	117.86	8.5	21	4	10.38	44.9	5.98	63.72	22.5	81	130
Range	36.41	5.18	6	2	4.81	21.3	4.65	50.17	18.75	20	13

Remarks: SDpsp, the number of seeds per spikelet; SpPSp, the number of spikelet per spike; SPL, spike length (cm); TPP, the number of effective tillers per plant; PH, Plant height (cm); TKW, weight of thousand kernels per plant (gm). SY, seed yield (t/ha); BY, biomass yield (t/ha); HI, harvest index; DB, days to booting; DM, days to maturity; Min, minimum, and Max, maximum.

Table 3. Variability, heritability and genetic advance

Parameters	SDpSp	Spkltpsp	SpL	TPP	PH	TKW	SY	Mo	BY	HI	DB	DM
GV	0.22	0.83	0.97	0.8	44.14	15.73	0.61	0.05	7.52	90.02	6.34	11.7
EV	0.1	1.83	1.22	2.05	49.39	21.25	1.04	0.07	12.39	116.6	14.62	6.12
GxEV	0.03	0.59	0.36	0.48	24.81	11.38	1.18	0.03	12.11	103.7	9.69	13.44
PV	0.26	1.58	1.46	1.55	68.89	26.73	1.46	0.08	16.67	171.02	14.84	19.95
GCV	15.64	5.06	12.01	14.93	6.65	11.58	24.03	2.11	24.18	29.83	3.43	2.77
PCV	17	6.98	14.74	20.79	8.31	15.1	37.18	2.66	36	41.11	5.25	3.62
ECV	10.54	7.52	13.47	23.9	7.04	13.46	31.38	2.49	31.04	33.95	5.21	2
GECV	5.77	4.27	7.32	11.57	4.99	9.85	33.42	1.63	30.69	32.01	4.24	2.97
H²	84.62	52.53	66.44	51.61	64.07	58.85	41.78	62.5	45.11	52.64	42.72	58.65
GA	88.71	135.76	165.06	132.11	1093.34	625.56	103.79	36.35	378.67	1415.35	338.35	538.6
GAM	29.57	7.54	20.13	22.06	10.95	18.27	31.94	3.42	33.39	44.49	4.61	4.36

NB: PH, plant height; DB, days to booting; DM, days to maturity; TKW, thousand kernel weight; TPP, tillers per plant; SYTPH, seed yield (t/ha); HI, harvest index; BY, biomass yield (t/ha); spl, spike length (cm); SDpSp, seed per spikelet; Spkltpsp, spikelet per spike; GV, genetic variance; EV, environmental variance; GxEV, genotype by environment interaction variance; PV, phenotypic variance; GCV, genotypic coefficient of variation; PCV, phenotypic coefficient of variation; ECV, environmental coefficient of variation; GECV, genotype by environment interaction coefficient of variation, H2, broad sense heritability; GA, genetic advance and GAM, genetic advance as a percentage of mean.

The value of genotype by environment interaction variation was high for seed yield (33.42), biomass yield (30.69) and harvest index (32.01); was intermediate for the number of effective tillers per plant (11.57) and was low for the number of spikelet per spike (5.77), the number of seed per spikelet (4.27), spike length (7.32), plant height (4.99), thousand kernel weight (9.85), moisture content (1.63), days to booting (4.24) and days to maturity (2.97).

Broad sense heritability (H^2) and genetic advance

H^2 values <40%, 40–80%, and > 80% were categorized as low, medium and high, respectively (Mesele *et al.*, 2015). Estimates of heritability (H^2) ranged from 41.78% to 84.62% for seed yield and the number of spikelets per spike, respectively (Table 2). High value of broad sense heritability was observed for the number of spikelet per spike (84.62) and medium value of heritability was recorded for spike length (66.44), plant height (64.07), days to booting (42.72), days to maturity (58.65), the number of seeds per spikelet (52.53), the number of effective tillers per plant (51.61), thousand kernel weight (58.85), biomass yield (45.11), seed yield (41.78) and harvest index (52.64).
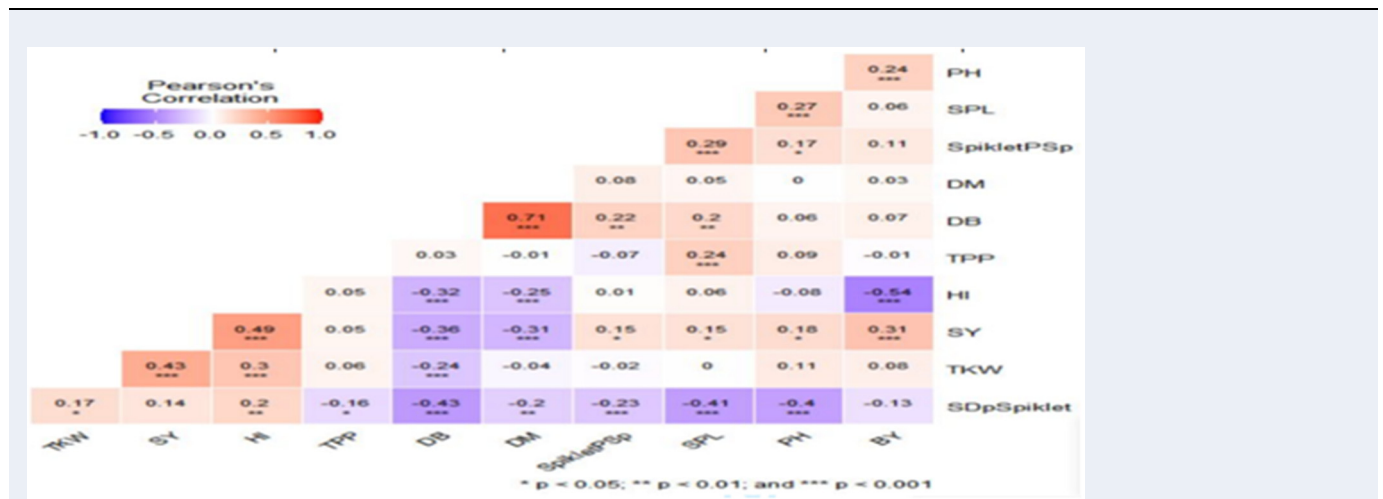
The values of genetic advance as a percentage of mean >20%, 10–20% and <10% were categorized as high, intermediate and low, respectively (Johnson *et al.*, 1955). Genetic advance as the percentage of mean was low for the number of seed per spikelet (7.54%), days to booting (4.61%), and days to maturity (4.36%); intermediate for plant height (10.95) and thousand kernel weight (18.27), and high for spike length (20.13), the number of spikelets per spike (29.57), the number of effective tillers per plant (22.06), seed yield (31.94), biomass yield (33.39) and harvest index (44.49). The observed genetic advance and broad sense heritability (H^2) were high for the number of spikelet per spike.

Correlation analysis

The result of Pearson correlation coefficient was given in Table 4. Grain yield showed a highly significant ($P < 0.001$) negative correlation with days to booting (-0.36***) and days to maturity (-0.31***) and a highly significant ($P < 0.001$) positive correlation with thousand kernel weight (0.43***), biomass yield (0.31***) and harvest index (0.49***). Grain yield, on the other hand, showed a significant positive (0.01) positive correlation with plant height (0.18*), spike length (0.15*) and the number of spikelet per spike (0.15*) and a positive correlation with the number of seeds per spikelet (0.14) and the number of effective tillers per plant (0.05).

Discussion

Genetic variation, genetic advance, heritability and correlation analysis was carried out for 196 genotypes evaluated at Sinana and Debrezeit during 2020 based on eleven phenotypic traits. The genotypes, locations and genotypes by location interaction showed significant variation for the majority of the traits evaluated (Table 1). There is significant ($P < 0.001$) variation among the genotypes for all traits other than the number of effective tillers per plant indicating the presence of genetic variation among the genotypes which in turn suggests that selection of lines can be effective in improving both yield and quality traits (Azene *et al.*, 2020). In line with this study, Azene *et al.* (2020) reported significant variation among genotypes of durum wheat in Ethiopia. The significant ($P < 0.001$) variation acorss locations and genotype by

Table 4. Pearson correlation of quantitative traits of 174 tetraploid wheat land races and 22 improved cultivars of Ethiopia

	TKW	SY	HI	TPP	DB	DM	SpikletPSp	SPL	PH	BY	
										0.24	PH
								0.27	0.06		SPL
							0.29	0.17	0.11		SpikletPSp
						0.08	0.05	0	0.03		DM
					0.71	0.22	0.2	0.06	0.07		DB
				0.03	−0.01	−0.07	0.24	0.09	−0.01		TPP
			0.05	−0.32	−0.25	0.01	0.06	−0.08	−0.54		HI
		0.49	0.05	−0.36	−0.31	0.15	0.15	0.18	0.31		SY
	0.43	0.3	0.06	−0.24	−0.04	−0.02	0	0.11	0.08		TKW
0.17	0.14	0.2	−0.16	−0.43	−0.2	−0.23	−0.41	−0.4	−0.13		SDpSpiklet

Pearson's Correlation −1.0 −0.5 0.0 0.5 1.0

* $p < 0.05$; ** $p < 0.01$; and *** $p < 0.001$

PH, plant height; DB, days to booting; DM, days to maturity; TKW, thousand kernel weight; TPP, number of effective tillers per plant; SY, Seed yield (t/ha); HI, harvest index; BY, biomass yield (t/ha); SPL, spike length (cm); SDpSpiklet, seed per spikelet; spkletPSsp, spikelet per spike.

location interaction suggest that the significant phenotypic variation among the tetraploid wheat genotypes is influenced by the environmental factors such as weather and farming practices, such as soil characteristics, field management or weather, affect how genes are expressed, which may help to explain the situation (Yao *et al.*, 2008; Persaud *et al.*, 2022). Further investigations will be required to ascertain stability of traits over several years to assess their suitability for crossing with other desirable traits in a breeding programme.

PCV and GCV below 10%, 10–20%, and above 20% were regarded as low, intermediate and high (Burton and DeVane, 1953). PCV is a measure of variation due to genetic and environmental factors and GCV is a measure of the relative variability of a trait due to genetic differences among individuals. The difference between PCV and GCV was high for seed yield, biomass yield and harvest index and low for days to maturity, number of spikelets per spike, plant height, days to booting, number of seed per spikelet, spike length, thousand kernel weight and number of effective tillers per plant implying that seed yield, biomass yield and harvest index were influenced by the environment whereas the remaining traits were mainly due to genetic factors. Arega *et al.* (2010) reported similar result on days to maturity, plant height and spike length; however, their result disagrees with the present result on the number of effective tillers per plant, the number of spikelets per spike, biomass yield, thousand kernel weight, harvest index and grain yield. Additionally, Abebe and Desta (2017) reported similar result on days to maturity, number of effective tillers per plant, biomass yield and harvest index; however, their work disagrees with the present study on spike length, grain yield and plant height. Moreover, Azene *et al.* (2020) reported similar result on PCV and GCV values of days to maturity, spikelet per spike, thousand kernel weight and spike length; however, their result disagree with the present study on the GCV and PCV values of other traits. Furthermore, Meles *et al.* (2017) reported similar results for plant height and days to maturity and thousand kernel weight; however, their result disagrees with the present result on effective tillers per plant, the number of spikelet per spike, spike length, the number of effective tillers per plant, thousand kernel weight, harvest index, grain yield and biomass yield.

The number of spikelet per spike, the number of effective tillers per plant, seed yield and harvest index gave high values of genetic advance and heritability. High heritability accompanied with high genetic advance is an indication of additive gene effects (Johnson *et al.*, 1955) and hence, high genetic gain from selection of the number of spikelets per spike would be expected. The work by Arega *et al.* (2011) on durum wheat Ethiopia agrees with the present study on GAM values of plant height (17.4), thousand kernel weight, and days to maturity while it disagrees with this study for the other traits. Moreover, Mesele *et al.* (2015) reported similar result on biomass yield, seed yield, spike length, thousand kernel weight and plant height on bread wheat of Ethiopia; however, their report disagrees with the present study on the number of effective tillers per plant, harvest index, seed per spikelet and days to maturity. Furthermore, Azene *et al.* (2020) also reported similar to the present study on days to maturity, harvest index and thousand kernel weight; however, their report disagrees with present study on plant height, spikelet per spike, spike length, biomass yield and grain yield.

Seed yield showed positive association with thousand kernel weight, biomass yield, harvest index, plant height, spike length, the number of spikelet per spike, seeds per spikelet and effective tillers per plant. This implies that there might be common gene (s) that control seed yield and these traits, which indicates that improving either one or more of these traits could result in high seed yield (Arega *et al.*, 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. In line with present study, Arega *et al.* (2010) reported that seed yield had significant association with biomass yield, plant height, thousand kernel weight and harvest index at both phenotypic and genotypic level. This result disagrees with the work of (Baye *et al.*, 2020). Similarly, Azene *et al.* (2020) reported that there was a highly significant positive correlation of seed yield with thousand kernel weight, biomass yield and harvest index and a positive correlation with spike length. Grain yield showed a highly significant ($P < 0.001$) negative correlation with days to booting ($−0.36$***) and days to maturity ($−0.31$***). In line

with this study, Ayer *et al*. (2017) reported non-significant negative correlation of days to booting and days to maturity with seed yield, highly significant positive correlation of seed yield with spike length, highly significant negative correlation with 1000 grain weight and harvest index.

The present study result provided preliminary indications that tetraploid wheat of Ethiopia hold huge genetic variation, which could be used as potential input in the breeding programme. Most of the traits studied showed positive association with seed yield implying that improving either one or more of these traits could result in high seed yield. Further work is needed to evaluate these and additional traits under different environmental conditions to assess their suitability for contributing to future breeding programmes.

References

Abate D (2018) Review on market chain analysis of wheat in Ethiopia. *Industrial Engineering Letters* 2, 94–105.

Abbasabad EZ, Mohammadi SA, Moghaddam M and Kamali MRJ (2016) Analysis of genetic diversity, population structure and linkage disequilibrium in Iranian wheat landraces using SSR markers. *Plant Genetic Resources* 15, 1–8. https://doi.org/10.1017/S1479262115000684

Abebe AA and Desta TM (2017) Genetic variability and character association of some local wheat varieties (*Triticum species*) using agromorphological traits grown in south Gondar zone, Ethiopia. *African Journal of Biotechnology* 16, 2100–2105.

Alamerew S, Chebotar S, Huang X and Roder M (2004) Genetic diversity in Ethiopian hexaploid and tetraploid wheat germplasm assessed by microsatellite markers. *Genetic Resources and Crop Evolution* 51, 559–567.

Alemu T, Zegeye H, Kassa D, Asnake D, Solomon T and Asefa A (2019) *Wheat Product Concepts Validation and Assessment of Dissemination and Utilization Constraints*. Addis Abeba: EIAR.

Allard RW (1960) *Principles of Plant Breeding*. New York: John Wiley and Sons Inc.

Arega G, Hussein M and Singh H (2010) Genotypic variability, heritability, genetic advance and associations among characters in Ethiopian durum wheat (*Triticum durum* desf.) accessions. *East African Journal of Sciences* 4, 27–33.

Asins MJ and Carbonell EA (1989) Distribution of genetic variability in a durum wheat world collection. *Theoretical and Applied Genetics* 77, 287–294.

Asmamaw M, Keneni G and Tesfaye K (2019) Genetic diversity of Ethiopian durum wheat (*Triticum durum* desf.) landrace collections as reveled by SSR markers. *Advances in Crop Science and Technology* 7, 1–9. https://doi.org/10.4172/2329-8863.1000413

Asmamaw M, Keneni G and Tesfaye K (2020) Genetic diversity of Ethiopian durum wheat (*Triticum durum* desf) landrace collections as reveled by morphological markers. *Journal of Plant Breeding and Crop Science* 12, 258–268.

Ayer DK, Sharma A, Ojha BR, Paudel A and Dhakal K (2017) Correlation and path coefficient analysis in tuberose. *SAAR J.Agri* 15, 1–12.

Azene Y, Menzir A and Dejene T (2020) Genetic variability and association of traits in Ethiopian durum wheat (*Triticum turgidium* L. Var. Durum) landraces at Dabat research station, north Gondar. *Cogent Food and Agriculture* 6, 1–21. https://doi.org/10.1080/23311932.2020.1778604

Baye A, Berihun B, Bantayehu M and Derebe B (2020) Genotypic and phenotypic correlation and path coefficient analysis for yield and yield-related traits in advanced bread wheat (*Triticum aestivum* L.) lines. *Cogent Food and Agriculture* 6, 1–17. https://doi.org/10.1080/23311932.2020.1752603

Bechere E, Belay G, Mitiku D and Merker A (1996) Phenotypic diversity of tetraploid wheat landraces from northern and north-central regions of Ethiopia. *Hereditas* 124, 165–172.

Belay G, Tesemma T, Becker HC and Merker A (1993) Variation and inter-relationships of agronomic traits in Ethiopian tetraploid wheat landraces. *Euphytica* 71, 181–188.

Belay G, Bechere E, Mitiku D, Merker A and Tsegaye S (1997) Patterns of morphological diversity in tetraploid wheat (*Triticum turgidum* L.) Llandraces from Ethiopia. *Acta Agriculturae Scandinavica Section B: Soil and Plant Science* 47, 221–228. https://doi.org/10.1080/09064719709362464

Brasesco F, Asgedom D, Sommacal V and Casari G (2019) *Strategic Analysis and Intervention Plan for Wheat and Wheat Products in the Agro-Commodities Procurement Zone of the Pilot Integrated Agro-Industrial Park in Central-Eastern Oromia, Ethiopia*. FAO, 104 pp. https://doi.org/10.1007/978-94-015-7398-6_11

Burton GW and DeVane EH (1953) Estimating heritability in tall fescue (festzjcu Av-undinuceu) from replicated clonal material. *Agronomy Journal* 45, 478–481.

Ceccarelli S (2016) Landraces: importance and use in breeding and environmentally friendly agronomic systems. *Trends in Plant Science* 21, 31–42.

CSA (2021) The Federa Democratic Republic of Ethiopia Report on Area and Production of Major Crops I.

Eticha F, Bekele E, Belay G and Börner A (2005) Phenotypic diversity in tetraploid wheats collected from Bale and Wello regions of Ethiopia. *Plant Genetic Resources* 3, 35–43.

Faris H, Arnulf M, Getachew B and Eva J (2006) Multivariate analysis of diversity of tetraploid wheat germplasm from Ethiopia. *Genetic Resources and Crip Evolution* 53, 1089–1098. https://doi.org/10.1007/s10722-005-9776-3

Getachew TTB and Worede M (1991) Morphological diversity in tetraploid wheat landrace populations from the central highlands of Ethiopia. *Hereditas* 114, 171–176.

Gomez KA and Gomez AA (1984) *Statistical Procedures for Agricultural Research*, vol. 6. New York: John Wiley and Sons.

Haile J, Hammer K, Ayele B, Nachit MM and Röder MS (2013a) Genetic diversity assessment of Ethiopian tetraploid wheat landraces and improved durum wheat varieties using microsatellites and markers linked with stem rust resistance. *Genetic Resources and Crop Evolution* 60, 513–527.

Haile J, Hammer K, Badebo A, Singh RP and Roder MS (2013b) Haplotype analysis of molecular markers linked to stem rust resistance genes in Ethiopian improved durum wheat varieties and tetraploid wheat landraces. *Genetic Resources and Crop Evolution* 60, 853–864.

Hartley HO (1950) The maximum F-ratio as a short-cut test for heterogeneity of variance. *Biometrika* 37, 308. Available at https://statisticalpoint.com/anova-f-value-p-value. How to Interpret the F-Value and P-Value in ANOVA Online Statistics library StatisticalPoint.com. IBPGR. 1985. Descriptors_Wheat.Pdf.

IBPGR (1985) Descriptors for wheat (Revised). https://hdl.handle.net/10568/73163

Johnson HW, Robinson HF and Comstock RE (1955) Estimates of genetic and environmental variability in sesame. *Agronomy* **47**, 314–318. https://doi.org/10.1017/S0014479700009510

Kearsey MJ and Pooni HS (1996) *The Genetical Analysis of Quantitative Traits*. US: Springer. https://doi.org/10.1007/978-1-4899-4441-2

Kebebew F, Tsehaye Y and McNeilly T (2001) Diversity of durum wheat (*Triticum durum* desf.) at *in situ* conservation sites in north Shewa and Bale, Ethiopia. *Journal of Agricultural Science* **136**, 383–392.

Meles B, Mohammed W and Tsehaye Y (2017) Genetic Variability, Correlation and Path Analysis of Yield and Grain Quality Traits in Bread Wheat (*Tritium aestivum* L.) Genotypes at Axum, Northern Ethiopia, 175–185. https://doi.org/10.5897/JPBCS2016.0671

Mengistu DK, Kiros AY and Pè ME (2015) Phenotypic diversity in Ethiopian durum wheat (*Triticum turgidum* Var. Durum) landraces. *Crop Journal* **3**, 190–199.

Mesele A, Wassu M and Tadesse D (2015) Estimation of heritability and genetic advance of yield and yield related traits in bread wheat (*Triticum aestivum* L.) genotypes at Ofla district, northern Ethiopia. *International Journal of Plant Breeding and Genetics* **10**, 31–37.

Muleta KT, Rouse MN, Rynearson S, Chen X, Buta BG and Pumphrey MO (2017) Characterization of molecular diversity and genome-wide mapping of loci associated with resistance to stripe rust and stem rust in Ethiopian bread wheat accessions. *BMC Plant Biology* **17**, 1–20.

Nandwani D (2019) *Genetic Diversity in Horticultural Plants*. Switzerland: Springer. https://doi.org/10.1007/978-3-319-96454-6

Negisho K, Shibru S, Id KP, Ordon F and Id GW (2021) Genetic diversity of Ethiopian durum wheat landraces. *PLoS ONE* **16**, e0247016.

Nigus M, Shimelis H, Mathew I and Abady S (2022) Wheat Production in the Highlands of Eastern Ethiopia: Opportunities, Challenges and Coping Strategies of Rust Diseases. https://doi.org/10.1080/09064710.2021.2022186

Pandey RL and Tiwari AS (1983) Heritability and genetic gain in chickpea. *International Chickpea Newsletter* **9**, 5–6.

Panse VG and Sukhatme PV (1957) Genetics of quantitative characters in relation to plant breeding. *Indian Journal of Genetics and Plant Breeding* **17**, 318–328.

Pecetti L and Damania AB (1996) Geographic variation in tetraploid wheat (*Triticum turgidum* ssp. Turgidum convar. Durum) landraces from two provinces in Ethiopia. *Genetic Resources and Crop Evolution* **43**, 395–407.

Persaud M, Persaud R, Gobind N, Khan A, Subramanian G and Corredor E (2022) Genotype by environment interactions of grain yield performance and lodging incidence in advance breeding lines of rice across environments in Guyana. *International Journal of Agricultural Policy and Research* **10**, 70–81.

R Development Core Team, R (2018) R: A Language and Environment for Statistical Computing. Edited by R Development Core Team. *R Foundation for Statistical Computing*. R Foundation for Statistical Computing. R Foundation for Statistical Computing. https://doi.org/10.1007/978-3-540-74686-7

Singh BD (1990) *Plant Breeding Principles And Methods*, 4th Edn. New Delhi: Kalyani.

Singh RK and Chaudhary BD (1985) *Biometrical Methods in Quantitative Genetic Analysis*. New Delhi: Kalyani. https://doi.org/10.2307/2530404

Teklu Y and Hammer K (2008) Diversity of Ethiopian tetraploid wheat germplasm: breeding opportunities for improving grain yield potential and quality traits. *Plant Genetic Resources: Characterisation and Utilisation* **7**, 1–8.

Tsegaye D, Dessalegn T, Dessalegn Y and Share G (2012) Analysis of genetic diversity in some durum wheat (*Triticum durum* desf) genotypes grown in Ethiopia. *African Journal of Biotechnology* **11**, 9606–9611.

Vavilov NI (1929) Origin and Geography of Cultivated Plants by N. I. Vavilov, Doris Love (z-Lib.Org).

Yao Y, Liu Q, Liu Q and Li X (2008) LAI Retrieval and uncertainty evaluations for typical Row-planted crops at different growth stages. *Remote Sensing of Environment* **112**, 94–106.

Zegeye F, Alamirew B and Tolossa D (2020) Analysis of wheat yield gap and variability in Ethiopia. *International Journal of Agricultural Economics* **5**, 89.