

Research

Genetic diversity, correlation and genotype \times yield \times trait (GYT) analysis of grain yield and nutritional quality traits in sorghum (*Sorghum bicolor* [L.] Moench) genotypes in Tigray, northern Ethiopia

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Abstract

Selecting sorghum genotypes with higher grain yield and nutritional quality is essential to tackle food insecurity and malnutrition in arid and semi-arid areas. Therefore, this study aimed to determine the genetic diversity, trait association and genotype by yield by trait (GYT) analysis and to select superior sorghum genotypes. One hundred and ten sorghum genotypes were evaluated at three locations in Tigray during the 2018 and 2019 growing seasons using alpha lattice design. Traits such as grain yield, protein content, ash content, starch content, zinc content, iron content, calcium content and magnesium content were profiled. Results showed that wide range and highly significant ($p < 0.001$) genotype mean performance in each environment as well as combined environments. Several highly performing genotypes were distinguished for each trait studied that could be exploited as breeding parents or direct use. This study further detected highly significant variation ($p < 0.001$) among the test genotypes for all the traits studied in individual environments and across environments suggesting the presence of sufficient genetic diversity for selection. The high broad-sense heritability ($H^2 > 0.9$) in all individual environments and moderate to high ($H^2 > 0.041 < 0.82$) in pooled environments recorded in the present study assured the possibility of effective selection among the genotypes. Besides, strong positive and negative associations were detected between some of the traits in individual and across environments. The significant positive association between traits indicates that both the traits can be improved concurrently through direct selection. Using the GYT analysis, we suggest ten promising sorghum genotypes for direct use or breeding programs in arid and semi-arid areas in general and in Tigray in particular.

Keywords Alpha lattice · Broad-sense heritability · Genotype variance · Mean performance · Superior genotypes

1 Core idea

- Wide range and higher mean performances of sorghum genotypes were attained in individual and combined environments in Tigray

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- Considerable genetic variations are available among sorghum genotypes in Tigray
- All the traits studied had higher heritability in individual environments and medium to high heritability in combined environments
- Significant positive and negative correlations were detected between some of the traits in each individual and combined environments
- Several superior genotypes of sorghum were selected for all traits studied that could be exploited as breeding parents for sorghum improvement
- Ten promising sorghum genotypes were selected using the GYT approach for direct use or breeding programs

2 Introduction

Sorghum (*Sorghum bicolor* [L.] Moench $2n = 2x = 20$), a C4 photosynthetic crop, is among the five top cereal crops that feed the world [1]. In Africa, sorghum is the fourth most widely cultivated cereal crop after maize, rice, and wheat and second in area coverage next to maize [1]. Sorghum possesses a wide array of ecological adaptations ranging from the dry lowland areas of the semi-arid tropics to high rainfall and humid regions, as well as in the more temperate regions of the world [2]. It is a staple food for more than half a billion people in Sub-Saharan Africa and Asia [3]. Sorghum is the second cheapest source of energy next to finger millet [4] and its grains are good sources of various minerals, vitamins, carbohydrates and proteins essential for human well-being [5–7]. Besides, sorghum is gluten-free [8], which makes it an excellent food crop for people who have gluten intolerance. Due to its high nutritional value, the market interest in sorghum grains is markedly growing worldwide [9].

Sorghum is the most diversified crop having 28 domesticated species categorized into five basic races *i.e. bicolor, guinea, caudatum, dura and kafir* and ten hybrid races [10]. All races of sorghum are grown across the diverse agroecological zones and farming systems of Ethiopia [11, 12]. Sorghum is the first fully assembled C4 crop using traditional Sanger sequencing [12] and is considered as ‘gold standard’ reference due to its high percentage assembly [13]. The broad genetic base harbored mainly in sorghum landraces is essential for providing the gene pool necessary for the development and deployment of farmers’ preferred varieties. Hence, collection and assembly followed by thoughtful quantification of the genetic diversity of such a collection are essential for efficient crop improvement and conservation programs.

Ethiopia is the world’s fourth largest sorghum producer after the United States, Nigeria and Mexico with a total annual production of 4.45 million metric tons [14]. In Ethiopia, sorghum stands fourth in terms of production after maize, wheat and teff, and third in terms of area coverage next to teff and maize [15]. The crop serves as the main stable food for the vast population of the country. It is mainly cultivated in rain-fed and low-input environments, where acute shortage of food and malnutrition prevails. Ethiopian farmers grow diverse forms of sorghum varieties with over 95% of the area allocated for sorghum production covered by landraces [16]. Landraces are heterogeneous and adapted to diverse growing conditions and are potential sources of desirable traits for crop improvement [17, 18]. Given its center of origin and diversity [19, 20], and tremendous variation in agro-ecologies, Ethiopia is endowed with extremely rich genetic diversity of sorghum landraces [2, 16, 21, 22], which serves as sources of various important traits. For instance, drought tolerance [16, 23, 24], nutritional quality traits [21, 25, 26], resistance to grain mold [27] and resistant to ergot and green bug [28]. Ethiopia is also among the top nations that have made significant contributions to the sorghum germplasm collections in the world [29]. Moreover, there is still unexplored high genetic variability in Ethiopian sorghum landraces [2, 24].

Selecting genotypes with improved yield and nutritional quality, especially with respect to mineral content would have a significant contribution to intervening the high prevalence of food shortage and malnutrition, especially in arid and semi-arid areas where sorghum is the stable food [30, 31]. Nonetheless, selecting in one trait may result in the reduced level of the other one or more target traits [32], which hinders the progress of crop improvement. To address the challenges of unfavorable association of key traits, Yan and Frégeau-Reid (2018) introduced the genotype by trait by yield (GYT) analysis approach. The GYT approach is a new novel tool to identify superior genotypes based on multiple traits such that grain yield is the main trait that determines the usefulness of the genotypes while the other target traits are valued based on their merit in combining with grain yield [33]. The average tester coordinator (ATC) graph of the GYT biplot meaningfully rank the genotypes based on multiple yield by trait combinations and at

the same time shows the strengths and weaknesses of the genotypes [33]. GYT analysis has been widely applied to identify superior genotypes in various crops such as oat [34], wheat [35], cotton [36] and sorghum [37].

Although numerous publications are available regarding the high genetic diversity of sorghum in Ethiopia, most of the studies are concentrated on yield and other agronomic traits with less emphasis on the genetic variability for nutritional quality traits. Genetic variation of local landraces of sorghum in Tigray Region of Ethiopia has not been studied adequately using agronomic and nutritional quality traits. Moreover, there is no research conducted so far to evaluate sorghum genotypes based on the genotype by yield by trait (GYT) approach using grain yield and nutritional quality traits. The objectives of the study were to assess genetic diversity and association in grain yield, starch, protein, ash, zinc (Zn); iron (Fe), calcium (Ca) and magnesium (Mg) contents, and to identify superior genotypes for grain yield and nutritional quality.

3 Materials and methods

3.1 Planting materials and study locations

The study used 108 sorghum landraces collected from Tigray, northern Ethiopia along with two improved varieties (Melkam and Dekeba) obtained from Tigray Agricultural Research Institute (TARI). The field trials were conducted at three locations (Tahtay Adyabo, Tselemti, and Mereb Leke) of Tigray in the 2018 and 2019 main growing seasons. Tigray is located in the northern part of Ethiopia between 12°15'N-14°15'N latitude and 36°28'E-39°59'E longitude (Table 1). About 53% of Tigray region is lowlands, 39% mid-altitude and the rest 8% percent is classified as highlands, and the altitude ranges from 500 m above sea level in the northeast to almost 4000 in the southwest [38]. The agro-ecological description of the study sites is provided in Table 1.

3.2 Field evaluation

The descriptions of the genetic materials used in the study are presented in Supplementary Table S1. The experimental layout used was an alpha lattice design with two replications at each experimental site. On each plot, the seeds were sown in a single 5 m long row. The spacing between rows and between plants within a row were 0.75 and 0.25 m, respectively. The land was tilled twice-using traditional oxen-drawn plows, and seedbed preparation, planting and harvesting were done manually. All other agronomic practices were applied as per the recommendations for the area. After harvesting at physiological maturity, panicles were sun-dried for 15 days. Thereafter, panicles from each plot were threshed, winnowed, and seeds packed.

3.3 Data collection

Data on grain yield was collected from each plot and converted to tone per hectare ($t\ ha^{-1}$). A composite seed sample of one kg from each accession was tagged and packed in cloth bags. Thereafter, the samples were taken to Mekelle University, Ethiopia, for grain nutritional quality analysis, using Near Infra-Red Spectrophotometers (DA 7250 Perkin) method. The NIRS machine was calibrated and standardized for grain analysis of sorghum by the technicians at

Table 1 Agro-ecological description of the experimental sites

Experimental site	Altitude m.a.s.l	Longitude	Latitude	Temperature (°C)		Rainfall mm/annum	
				2018	2019	2018	2019
Tahtay Adyabo	1025	37°45'E	14°24'N	20–35	20–37	677	1069
Mereb Leke	1395	38°47'E	14°23'N	14–34	15–34	510	1051
Tselemti	1450	38°10'E	13°41'N	19–32	20–33	1301	1685

Temperature and rainfall data were obtained from the Meteorological Agency of Ethiopia, Tigray office, Mekelle

Mekelle University. The grain samples were bulked from the two replications and each bulked samples were measured twice. This method is a time- and cost-effective method to analyze grain quality [39]. The traits such as protein, ash and starch content of the sorghum seeds were expressed in terms of percentages, whereas Fe, Zn, Ca and Mg concentrations were expressed in terms of parts per million (ppm).

3.4 Data analysis

The data collected on grain yield and nutritional traits of one hundred and eight sorghum landraces along with the two improved varieties were analyzed using linear mixed models in META-R software [40]. Each location and year were treated as an independent environment. The mean performance, association among the traits, variances and heritability in individual environment (Tahtay Adyabo 2018, Mereb-Leke 2018, Tselemti 2018, Tahtay Adyabo 2019; Mereb-Leke 2019, and Tselemti 2019, hereafter referred as En1, En2, En3, En4, En5 and En6, respectively), and combined across the testing environments were computed using the models implemented in linear mixed effect model in R (lmer) package from package lme4 of R. The models used for this study are described below [41].

The model for the analysis of variance in individual environments is given as

$$Y_{ijkl} = \mu + rep_i + block_k(rep_j) + gen_j + \varepsilon_{ijk}$$

where Y_{ijk} = the trait of interest, μ = the mean effect, rep_i = the effect of the i th replicate, $block_j(rep_i)$ = the effect of the j th incomplete block within the i th replicate, gen^k = the effect of the k th genotype, ijk = the error associated with the i th replication, j th incomplete block and the k th genotype.

For the combined analysis, new terms are added to the model for the individual environment as:

$$Y_{ijkl} = \mu + env_i + rep_j + rep_j(env_i) + block_k(env_i \times rep_j) + gen_j + env_j \times gen_j + \varepsilon_{ijkl}$$

where env_i and $env_j \times gen_j$ = the effects of the i th environment and the environment by genotype interaction, respectively.

Broad-sense heritability (H^2) in individual and across environments were estimated using the formula:

$$H^2 = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_e^2/nr}$$

and

$$H^2 = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_{ge}^2/nEnvs + \sigma_e^2/(nEnvs \times nr)}$$

where σ_g^2 , σ_e^2 , σ_{ge}^2 , nr and $nEnvs$ = the genotype variance, error variance, genotype by environment interaction variance, number of replication and number of environments, respectively.

The least of significance differences (LSD) at 5% of significance was calculated as:

$$LSD = t(0.05, dfErr) \times ASED,$$

where t = the cumulative Student's t distribution, 0.05 = the selected α level (5%), $dfErr$ = the degrees of freedom for error in the linear mixed model, and $ASED$ = the average standard error of the differences of the means.

The coefficient of variation was calculated using the formula:

$$CV(\%) = \left(\frac{\sqrt{MSE}}{Grandmean} \right) \times 100,$$

where MSE = the mean squared error.

3.5 Genotype by yield by trait (GYT) analysis

GYT analysis was done following the steps described by Yan and Frégeau-Reid (2018). First, the Genotype by Trait (GT) two-way table was converted to GYT two-way table (Supplementary Table S2). This was done by multiplying grain yield

by each trait (grain yield *starch, grain yield*protein, grain yield*ash content, grain yield*zinc, grain yield*iron, grain yield*calcium and grain yield*magnesium, hereafter, referred to as gy*sta, gy*pro, gy*ash, gy*Zn, gy *Fe, gy*Ca and gy*Mg, respectively). Then after, the GYT table was standardized to mean zero and unity variance to minimize biases due to differences using the formula:

$$P_{ij} = \frac{T_{ij} - T_j}{S_j}$$

where: P_{ij} = the standardized value of genotype i for a trait or yield-trait combination j in the standardized table, T_{ij} = the original value of genotype i for yield-trait combination j in the GYT table, T_j = the mean across genotypes for yield-trait combination j , and S_j = the standard deviation for yield-trait combination j .

The standardized GYT tables for each trait were used to generate biplots using GGEBiplot GUI package in R-software version 4.0.1 [42]. The biplots were based on singular value decomposition of trait-standardized data (scaled by standard deviation, centered by tester-centered G + E and trait-focused symmetrical singular value partition). For clarity purposes, we use only the numbers of the genotype with the prefix +. For example, LR1, was replaced to + 1; LR80 was replaced to + 80; LR100 was replaced to + 100 and so on for GYT biplot constructions.

The following equation was used to construct the GYT biplot:

$$P_{ij} = (\alpha \lambda_1^\alpha \zeta_{i1}) * (\lambda_1^{1-\alpha} \Gamma_{1j} / d) + (d \lambda_2^\alpha \zeta_{i2}) * (\lambda_2^{2-\alpha} \Gamma_{2j} / d) + \varepsilon_{ij}$$

where ζ_{i1} and ζ_{i2} = eigenvalues for PC1 and PC2, respectively, for genotype i ; Γ_{1j} and Γ_{2j} = eigenvalues for PC1 and PC2, respectively for yield-trait combination (or trait) j , and ε_{ij} = residual from fitting the PC1 and PC2 for genotype i on yield-trait combination j ; λ_1^α and λ_2^α = singular values for PC1 and PC2, respectively, and α = singular value partitioning factor. When $\alpha = 1$ (i.e., SVP = 1), the biplot is said to be genotype-focused and is suitable for comparing genotypes. When $\alpha = 0$ (i.e., SVP = 2), the biplot is said to be environment-focused and is suitable for visualizing correlations among environments. The scalar d is chosen such that the length of the longest vector among genotypes equals to that among environments; this is important for generating a functional biplot [43].

4 Results

4.1 Mean performances of the genotypes

The average mean performance of the genotypes for all the traits across the six environments (three locations and two years) is presented in Table 2. The result showed that highly significant variation ($p < 0.001$) among genotypes in all traits studied. Mean grain yield was 2.7 t ha⁻¹, with a range of 1.4–4.1 t ha⁻¹. The highest yielding genotypes were LR106, LR102, LR25, LR75 and LR23. The average starch, protein, ash, zinc, iron, calcium and magnesium contents were 65.1%, 10.3%, 1.9%, 35.3 ppm, 36.8 ppm, 243 ppm, and 1096.8 ppm, respectively. The highest starch, protein, ash, zinc, iron, calcium and magnesium contents were depicted by LR14 (69.4%), LR65 (11.2%), LR10 (2.3%), LR23 (43.7 ppm), LR38 (47.8 ppm),

Table 2 Combined mean values, standard deviation and five best performing sorghum genotypes evaluated across six test environments in Tigray in 2018 and 2019

Traits	Mean	Range	SD	Top five genotypes for each trait
GY (t ha ⁻¹)	2.7***	1.4–4.1	0.6	LR106 > LR102 > LR25 > LR75 > LR23
Starch (%)	65.1***	59.1–69.4	2.3	LR14 > LR27 > LR25 > LR16 > LR > LR4
Protein (%)	10.3***	9.5–11.2	0.3	LR 65 > LR 57 > LR 107 > LR 95 > LR 98
Ash (%)	1.9***	1.5–2.3	0.2	LR10 > LR 84 > LR 12 > LR 81 > LR 110
Zn (ppm)	35.3***	29.7–43.7	2.4	LR 23 > LR 45 > LR 12 > LR 27 > LR 98
Fe (ppm)	36.8***	26.5–47.8	4.9	LR 38 > LR 12 > LR 87 > LR 10 > LR 69
Ca (ppm)	243.4***	210.2–289	16.7	LR 16 > LR 26 > LR 15 > LR 39 > LR 74
Mg (ppm)	1096.8***	932–1345.6	71.5	LR 4 > LR 41 > LR 27 > LR 99 > LR 86

Where LR = landraces, SD = standard deviation, *** = significant at $p < 0.001$, Zn, Fe, Ca, Mg, = zinc, iron, calcium and magnesium, respectively, ppm = parts per million

LR16 (289 ppm) and LR4 (1345.6 ppm), respectively. The minimum values for each of the traits were 1.4 t ha⁻¹, 59.1%, 9.5%, 1.5%, 29.7 ppm, 26.5 ppm, 210.2 ppm and 932 ppm for grain yield, starch, protein, ash, zinc iron, calcium and magnesium, respectively (Table 2).

4.2 Variances and broad-sense heritability

Table 3 demonstrates genotypic variance and heritability for grain yield and nutritional quality traits of the sorghum genotypes in each testing environment. All traits showed significant genotypic variances in all environments. All measured traits showed the highest genotypic variances in En1 except for grain yield, which showed the highest genotype variance in En4. On the contrary, the lowest genotypic variance due to starch, ash, zinc and magnesium content was observed in En3, while the lowest genotype variance due to grain yield, protein and calcium was recorded in En4, En2 and En6, respectively (Table 3).

Combined analyses of variances presented in Table 4 showed highly significant variances ($p < 0.001$) due to genotypes (σ^2g) and genotype by environment interaction ($\sigma^2g \times e$) effects for all studied traits. Similarly, highly significant environmental variances (σ^2e) were observed for all traits, except for calcium, which was significant ($p < 0.05$). The variance due to genotype by environment interaction effect was higher than σ^2g and σ^2e for all the traits studied except for grain yield in which the variance due to genotype was relatively higher than the $\sigma^2g \times e$ and σ^2e .

In the present study, all traits were highly heritable ($H^2 > 0.9$) as per the established scale [44] in all individual environments (Table 3). However, a partitioned genotype by environment interaction component reduced the broad-sense heritability across environments (pooled analysis), which ranged from $H^2 = 0.41$ (protein content) to $H^2 = 0.82$ (grain yield) (Table 4).

4.3 Correlation among traits

Pearson's correlation coefficients among the traits were computed for each environment and across environments using the best linear unbiased prediction (BLUP) mean (Table 5). Some of the traits were significantly ($p < 0.001$; 0.01;

Table 3 Heritability, genotypic variance, standard error, LSD and coefficient of variation for grain yield and nutritional quality traits of sorghum genotypes evaluated in Tigray region in 2018 and 2019

Statistics	En1					En2					En3				
	H ²	σ^2g	SE	LSD	CV	H ²	σ^2g	SE	LSD	CV	H ²	σ^2g	SE	LSD	CV
Starch (%)	0.98	38.6***	0.2	0.95	0.75	0.97	28.4***	0.05	0.5	0.4	0.97	30.7***	0.1	0.5	0.36
Protein (%)	0.99	3.6***	0.0	0.29	1.52	0.97	1.6***	0.03	0.3	1.6	0.98	3.9***	0.0	0.2	0.78
Ash (%)	0.98	0.5***	0.0	0.13	3.81	0.98	0.2***	0.0	0.1	3.5	0.96	0.1***	0.0	0.2	4.86
Zn (ppm)	0.97	122.0***	0.2	0.93	1.38	0.96	56.4***	0.07	0.6	0.7	0.97	103.2***	0.1	0.7	0.99
Fe (ppm)	0.96	211.3***	1.3	2.24	3.49	0.96	179.4***	0.03	0.4	0.4	0.98	135.6***	0.2	0.8	1.18
Ca (ppm)	0.97	2412.8***	3.4	3.64	0.75	9.94	1604.1***	1.95	2.8	0.6	0.96	2015.6***	38.6	12.3	2.49
Mg(ppm)	0.91	33,640.7***	158	24.87	1.2	0.91	33,005.5***	6612	153.8	7.5	0.98	25,202.6***	17	8.2	0.37
GY t ha ⁻¹	0.91	0.52***	0.07	0.5	9.3	0.98	0.61***	0.05	0.4	9.3	0.99	0.7	0.04	0.4	6.7
	En4					En5					En6				
Starch (%)	0.96	28.2***	0.2	0.9	0.7	0.99	28.1***	0.05	0.4	0.3	0.94	25.4***	0.38	1.2	0.94
Protein (%)	0.99	2.4***	0.1	0.4	1.9	0.98	1.7***	0.03	0.3	1.6	0.98	2.4***	0.02	0.3	1.52
Ash (%)	0.92	0.3***	0.0	0.2	5.3	0.96	0.2***	0.0	0.1	3.7	0.91	0.2***	0.01	0.2	4.9
Zn (ppm)	0.94	60.9***	1.1	2.1	3.1	0.99	56.7***	0.02	0.3	0.4	0.98	77.5***	0.24	0.8	1.4
Fe (ppm)	0.95	146.7***	0.9	1.9	2.7	0.99	178.7***	0.09	0.6	0.7	0.97	81.5***	0.26	1.0	1.51
Ca (ppm)	0.96	2333.0***	15.6	7.8	1.6	0.96	1594.4***	12.4	7.0	1.5	0.95	1035.5***	2.52	3.2	0.64
Mg(ppm)	0.93	43,299.5***	47.1	13.7	0.6	0.99	36,134.0***	611.0	48.9	2.3	0.96	18,530.7***	143	23.7	1.06
GY t ha ⁻¹	0.98	0.70***	0.04	0.4	6.3	0.97	0.68***	0.03	0.3	6.4	0.96	0.52***	0.03	0.3	6.4

Where *** = significant variation at $p < 0.001$, CV = coefficient of variations, σ^2g = genotype variance, H^2 = broad sense heritability, LSD = least of significant difference, SE = standard error, Zn, Fe, Ca, Mg, = zinc, iron, calcium and magnesium, respectively, ppm = parts per million

Table 4 Heritability, variance components, standard error, least of significant differences and coefficient of variations for grain yield and nutritional quality traits in sorghum genotypes evaluated in Tigray region in 2018 and 2019

Statistic	Starch (%)	Protein (%)	Ash (%)	Zn (ppm)	Fe (ppm)	Ca (ppm)	Mg (ppm)	GY t ha ⁻¹
H ²	0.7	0.4	0.6	0.5	0.6	0.6	0.7	0.82
σ ² _g	8.1***	0.3***	0.1***	11.7***	36.7***	432.3***	7839.6***	0.25***
σ ² _{g x e}	21.8***	2.3***	0.3***	67.7***	118.8***	1400***	23,797.2***	0.25***
σ ² _e	5.9***	0.4***	0.1***	3.4***	21.9***	27.1*	917.8***	0.05***
SE	0.2	0.0	0.0	0.3	0.5	12.4	1263.9	0.15
LSD	4.4	1.1	0.4	6.7	10.0	34.4	144.5	0.70
CV (%)	0.6	1.5	4.5	1.5	1.8	1.4	3.2	14.2

Where ***=significant variation at $p < 0.001$, *=significant variation at $p < 0.05$, CV=coefficient of variations, σ²_g, σ²_{g x e}, σ²_e=genotype variance, genotype by environment interaction variance, and environment variance, respectively, H²=broad-sense heritability, LSD=least of significant difference, SE=standard error,

0.05) correlated while many of them had non-significant correlations ($p > 0.05$). Protein content had highly significant and positive association with starch (En1, $p < 0.01$), calcium (En2, $p < 0.001$ and En3, $p < 0.001$), magnesium (En3, $p < 0.001$) contents, and grain yield (En4, $p < 0.05$; En5, $p < 0.05$ and En6, $p < 0.01$). On the other hand, protein content showed a significant and negative association with ash (En1, $p < 0.001$ and En2, $p < 0.05$), iron (En1, $p < 0.01$ and En2, $p < 0.001$), and zinc (En1, $p < 0.01$; En2, $p < 0.001$ and En4, En2, $p < 0.05$). Ash content showed significant positive association with zinc (En1, En2, $p < 0.001$; En4, $p < 0.001$ and En5, $p < 0.05$) and iron concentrations (En1, $p < 0.001$; En2, $p < 0.001$; En4, $p < 0.001$ and En5, $p < 0.05$). Similar to protein content, ash content also had a significant and negative association with some traits such as calcium and zinc concentration (En3, $p < 0.01$). Zinc content exhibited a significant ($p < 0.001$) and positive correlation with iron in En1, En2, En4 and En5, and significant negative ($p < 0.05$) associations in En3 and En6. A significant negative ($p < 0.05$) association was observed between calcium and iron contents in En2 and En6, whereas a significant and positive ($p < 0.05$) association was found between calcium and grain yield in En4 and En6. Grain yield and magnesium showed a significant positive ($p < 0.05$) association in En6 only.

Correlations among the studied traits across the six test environments are presented in Table 6 and Fig. 1. Ash content showed a highly significant and positive ($p < 0.001$) correlation with zinc and iron contents. Besides, zinc and iron, starch and protein, and zinc and grain yield showed highly significant positive correlations, while calcium and iron had positive significant ($p < 0.05$) correlation with grain yield and starch, respectively (Table 6). On the other hand, protein had a highly significant ($p < 0.001$) negative association with iron concentration and significant ($p < 0.05$) association with ash and zinc contents. The rest traits had no significant association ($p > 0.05$) (Table 6).

4.4 Genotype by yield by trait (GYT) analysis

In this study, we determine how the grain yield of sorghum is combined with other important nutritional traits using the Pearson correlations coefficient (Table 7) and GYT biplots (Fig. 2) using the combined mean data. Highly significant positive correlations ($p < 0.001$) were detected among all grain yield-nutritional trait combinations, with correlation coefficients ranging from 0.53 to 0.89. The strongest multi-trait correlation was manifested between grain yield*starch and grain yield*protein ($r = 0.89$), grain yield*starch and grain yield*calcium ($r = 0.87$) and grain yield*starch and grain yield *magnesium ($r = 0.86$). The strong positive correlation between the trait combinations is also indicated by the acute angles between the vectors of the traits on the scatter plot generated from genotype by yield by trait data (Fig. 2A). The first two PCs of the GYT biplot (Fig. 2) explained about 87.5% (PC1 = 78.34%, PC2 = 9.2%) of the total variation. The polygon of which won where/what (Fig. 2B) divided the biplot into six sectors and the yield trait combinations are located in three sectors only. The ATC view of the GYT biplot (Fig. 2C) shows the weakness and strengths of the genotypes and graphically ranks the genotypes based on their overall superiority. Furthermore, top ten promising and five bottom sorghum genotypes were distinguished using the over overall superiority index of the GYT as presented in Table 8 below.

Table 5 Correlations among grain yield and nutritional quality traits in sorghum genotypes evaluated in Tigray region in 2018 and 2019

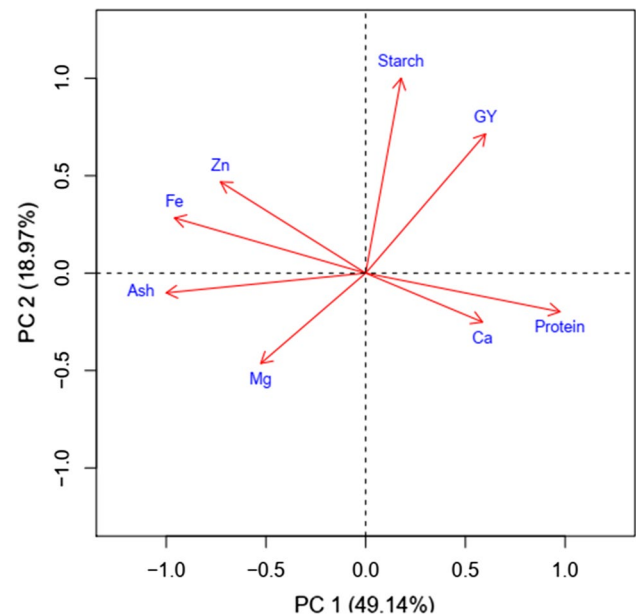
Traits	Starch (%)	Protein (%)	Ash (%)	Zn (ppm)	Fe (ppm)	Ca (ppm)	Mg (ppm)
En1							
Protein (%)	0.25**						
Ash (%)	- 0.04 ^{ns}	- 0.32***					
Zn (ppm)	- 0.10 ^{ns}	- 0.30**	0.72***				
Fe (ppm)	- 0.13 ^{ns}	- 0.28**	0.64***	0.68***			
Ca (ppm)	0.05 ^{ns}	- 0.16 ^{ns}	0.11 ^{ns}	0.13 ^{ns}	0.03 ^{ns}		
Mg (ppm)	0.11 ^{ns}	0.02 ^{ns}	0.10 ^{ns}	0.00 ^{ns}	- 0.05 ^{ns}	- 0.02 ^{ns}	
GY (t ha ⁻¹)	0.11 ^{ns}	- 0.16 ^{ns}	0.18 ^{ns}	0.11 ^{ns}	0.13 ^{ns}	0.00 ^{ns}	- 0.14 ^{ns}
En2							
Protein (%)	- 0.06 ^{ns}						
Ash (%)	0.00 ^{ns}	- 0.23*					
Zn (ppm)	0.01 ^{ns}	- 0.34***	0.17 ^{ns}				
Fe (ppm)	0.21*	- 0.48***	0.33***	0.38***			
Ca (ppm)	- 0.08 ^{ns}	0.35***	- 0.15 ^{ns}	- 0.15 ^{ns}	- 0.19*		
Mg (ppm)	0.04 ^{ns}	0.15 ^{ns}	- 0.0 ^{ns}	0.06 ^{ns}	- 0.12 ^{ns}	- 0.13 ^{ns}	
GY (t ha ⁻¹)	0.15 ^{ns}	- 0.19*	0.13 ^{ns}	0.16 ^{ns}	0.00 ^{ns}	0.08 ^{ns}	0.05 ^{ns}
En3							
Protein (%)	0.00 ^{ns}						
Ash (%)	0.05 ^{ns}	- 0.12 ^{ns}					
Zn (ppm)	- 0.05 ^{ns}	0.17 ^{ns}	- 0.25**				
Fe(ppm)	0.31***	- 0.10 ^{ns}	0.04 ^{ns}	- 0.20*			
Ca (ppm)	- 0.06 ^{ns}	0.37***	- 0.20*	0.17 ^{ns}	- 0.08 ^{ns}		
Mg (ppm)	0.07 ^{ns}	0.36***	0.05 ^{ns}	0.08 ^{ns}	- 0.07 ^{ns}	0.18 ^{ns}	
GY (t ha ⁻¹)	0.12 ^{ns}	- 0.01 ^{ns}	- 0.05 ^{ns}	0.02 ^{ns}	0.10 ^{ns}	0.08 ^{ns}	0.01 ^{ns}
En4							
Protein (%)	0.15 ^{ns}						
Ash (%)	0.12 ^{ns}	- 0.15 ^{ns}					
Zn (ppm)	0.00 ^{ns}	- 0.20*	0.48***				
Fe (ppm)	- 0.09 ^{ns}	- 0.04 ^{ns}	0.42***	0.52***			
Ca (ppm)	0.15 ^{ns}	- 0.03 ^{ns}	0.00 ^{ns}	0.06 ^{ns}	0.02 ^{ns}		
Mg (ppm)	0.10 ^{ns}	0.08 ^{ns}	0.04 ^{ns}	0.00 ^{ns}	- 0.08 ^{ns}	- 0.13 ^{ns}	
GY (t ha ⁻¹)	0.23*	0.21*	0.09 ^{ns}	0.09 ^{ns}	- 0.05 ^{ns}	0.24*	- 0.10 ^{ns}
En5							
Protein	0.16 ^{ns}						
Ash	- 0.03 ^{ns}	- 0.04 ^{ns}					
Zn (ppm)	0.16 ^{ns}	- 0.16 ^{ns}	0.27**				
Fe (ppm)	0.23*	- 0.02 ^{ns}	0.23*	0.38***			
Ca (ppm)	- 0.19*	0.11 ^{ns}	- 0.04 ^{ns}	- 0.15 ^{ns}	- 0.21*		
Mg (ppm)	0.08 ^{ns}	- 0.00 ^{ns}	- 0.04 ^{ns}	- 0.13 ^{ns}	0.05 ^{ns}	- 0.05 ^{ns}	
GY (t ha ⁻¹)	- 0.10 ^{ns}	0.24*	0.14 ^{ns}	0.17 ^{ns}	0.18 ^{ns}	- 0.03 ^{ns}	0.07 ^{ns}
En6							
Protein (%)	0.15 ^{ns}						
Ash (%)	- 0.08 ^{ns}	0.02 ^{ns}					
Zn (ppm)	- 0.05 ^{ns}	0.13 ^{ns}	- 0.14 ^{ns}				
Fe (ppm)	0.05 ^{ns}	- 0.05 ^{ns}	0.12 ^{ns}	- 0.22*			
Ca (ppm)	0.00 ^{ns}	0.20*	- 0.12 ^{ns}	0.17 ^{ns}	- 0.13 ^{ns}		
Mg (ppm)	0.01 ^{ns}	0.08 ^{ns}	- 0.02 ^{ns}	0.05 ^{ns}	- 0.10 ^{ns}	0.12 ^{ns}	
GY (t ha ⁻¹)	- 0.05 ^{ns}	0.28**	0.06 ^{ns}	0.08 ^{ns}	- 0.03 ^{ns}	0.23*	0.21*

Where, *** = significant at $p < 0.001$, ** significant at $p < 0.01$, * = significant at $p < 0.05$, ns = not significant ($p > 0.05$) GY = grain yield, Zn zinc, Fe = iron, Ca = calcium, Mg = magnesium, ppm = parts per million

Table 6 Pearson correlation of grain yield and nutritional quality traits in sorghum landraces evaluated across six environments in Tigray region in 2018 and 2019

	Starch (%)	Protein (%)	Ash (%)	Zn (ppm)	Fe (ppm)	Ca (ppm)	Mg (ppm)
Protein (%)	0.03 ^{ns}						
Ash (%)	0.01 ^{ns}	-0.23*					
Zn (ppm)	0.06 ^{ns}	-0.21*	0.35***				
Fe (ppm)	0.20*	-0.34***	0.49***	0.32***			
Ca(ppm)	0.00 ^{ns}	0.13 ^{ns}	-0.01 ^{ns}	0.04 ^{ns}	-0.10 ^{ns}		
Mg(ppm)	0.06 ^{ns}	-0.03 ^{ns}	0.21*	0.09 ^{ns}	0.08 ^{ns}	0.03 ^{ns}	
GY t ha ⁻¹	0.30**	0.18 ^{ns}	0.02 ^{ns}	0.26**	0.04 ^{ns}	0.22*	0.07 ^{ns}

Where, ***= significant at $p < 0.001$, ** significant at $p < 0.01$, * = significant at $p < 0.05$, ns= not significant ($p > 0.05$) GY= grain yield, Zn zinc, Fe= iron, Ca = calcium, Mg = magnesium, ppm = parts per million

Fig. 1 Scatter plot showing the association among grain yield (GY) and nutritional quality traits of sorghum genotypes evaluated in six environments of Tigray region, Zn = zinc, Fe = iron, Ca = calcium, and Mg = magnesium**Table 7** Correlation of GYT traits of sorghum genotypes analyzed six environments in Tigray

GYT traits	gy*sta	gy*pro	gy*ash	gy*Zn	gy*Fe	gy*Ca
gy*pro	0.89***					
gy*ash	0.75***	0.66***				
gy*Zn	0.83***	0.74***	0.78***			
gy*Fe	0.69***	0.53***	0.76***	0.71***		
gy*Ca	0.86***	0.84***	0.66***	0.75***	0.57***	
gy*Mg	0.87***	0.81***	0.74***	0.77***	0.63***	0.79***

Where *** = significant at $P < 0.001$, gy*sta, gy*pro, gy*ash, gy*Zn, gy *Fe, gy*Ca and gy*Mg = grain*starch, grain yield*protein, grain*ash content, grain yield*zinc, grain yield*iron, grain yield*calcium and grain yield*magnesium, respectively

5 Discussions

In the present study, we found highly significantly differences among genotypes for grain yield and nutritional traits across all environments (Table 2). As shown in Table 2, the five top performing genotypes were not the same for all traits such that different genotypes showed better performance for different traits. This suggests that the highest-performing genotypes for a particular trait could serve as a source germplasm for further breeding activities. Genotypes that contain iron and zinc better than the acceptable level, which is > 60 ppm for iron and > 32 ppm for zinc

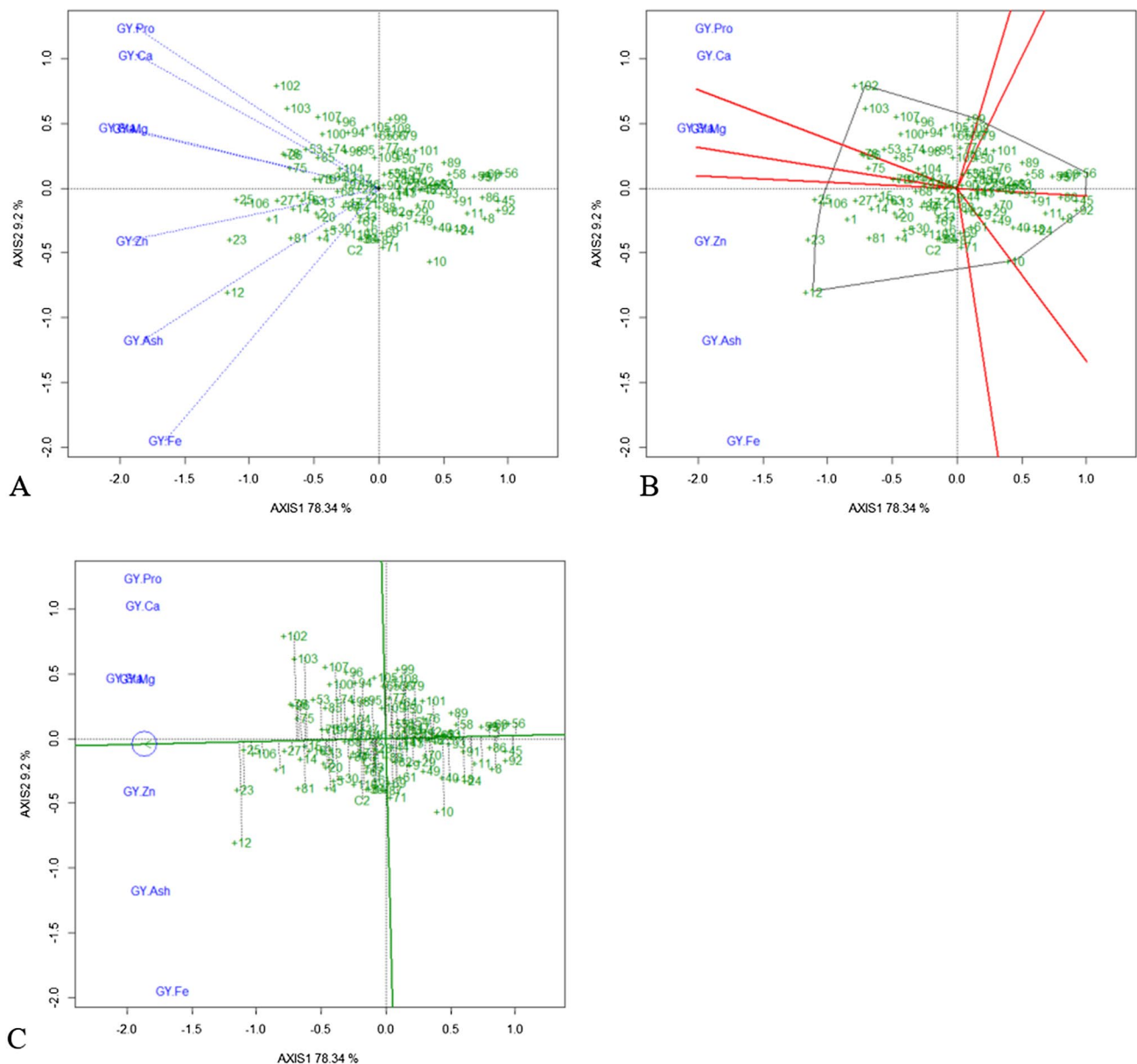


Fig. 2 GYT biplot of grain yield and nutritional traits of sorghum genotypes evaluated in six environments in Tigray. **A** = correlation between traits, **B** = 'which-won where' view of the traits, and **C** = the average tester coordinator (ATC) of the traits

[45] can be used for bio-fortification programs [31] to alleviate acute malnutrition deeply rooted in underdeveloped countries such as Ethiopia. From the present study, LR106, LR102, LR25 and LR16 can be selected for higher grain yield and starch zinc and calcium, LR23, LR45, LR38 and LR12 can be selected for higher zinc and iron content, and LR14, LR27, LR65 and LR57 can be selected for higher protein and starch contents. Nonetheless, selection in one trait may result in the reduction of the level of the other target trait [32], suggesting the need to evaluate the genotypes based on their ability to combine grain yield with other important traits such as nutritional quality traits used in this study as suggested by [33]. Interestingly, all traits studied showed a wide array of variability. The wide range showed in the value of the traits revealed that it is possible to distinguish among the genotypes for effective breeding activities. Similar to the present finding, earlier studies detected wide range of values for grain yield [2, 4], ash [46, 47], starch and protein [21, 48], iron and zinc [25, 49], calcium [25, 50] and magnesium [30, 51], in sorghum genotypes.

The tested genotypes showed highly significant variations ($p < 0.001$) for all traits studied in all individual environments. Likewise, the combined analysis showed strong significant variance ($P < 0.001$) for all traits studied due to genotype (σ^2_g), genotype by environment interaction ($\delta^2_{g \times e}$) and environments (σ^2_e) with the exception that variance due to

Table 8 Top ten promising and bottom five sorghum genotypes identified using GYT index

	Genotype	gy*sta	gy*pro	gy*ash	gy*Zn	gy*Fe	gy*Ca	gy*Mg	(Av.SI)
Top ten genotype									
1	LR12	1.69	1.30	3.14	2.64	3.14	0.80	2.05	2.11
2	LR23	1.59	1.18	1.87	3.58	2.40	1.91	1.84	2.05
3	LR25	2.37	0.76	1.75	2.48	1.60	2.28	2.34	1.94
4	LR106	1.98	2.16	1.63	2.30	1.91	1.49	1.01	1.78
5	LR1	1.58	1.92	2.26	1.52	1.54	0.52	1.42	1.54
6	LR27	1.47	0.91	0.96	1.83	1.35	1.03	1.94	1.36
7	LR102	2.20	2.33	0.35	0.38	-0.09	2.37	1.49	1.29
8	LR78	1.54	2.07	1.00	0.92	0.64	1.01	1.63	1.26
9	LR26	1.52	0.70	0.70	1.55	0.43	2.16	1.46	1.22
10	LR81	0.36	1.15	2.35	1.48	1.38	0.96	0.64	1.19
Bottom five genotypes									
1	LR57	-1.41	-1.31	-1.62	-1.64	-1.65	-1.76	-1.88	-1.61
2	LR60	-1.59	-1.40	-1.69	-1.68	-1.61	-1.31	-2.13	-1.63
3	LR92	-1.97	-2.01	-1.78	-1.31	-1.35	-2.02	-2.36	-1.83
4	LR45	-2.33	-2.20	-1.47	-1.02	-2.00	-1.98	-1.85	-1.83
5	LR56	-1.87	-1.68	-1.84	-1.69	-2.11	-1.97	-1.98	-1.88

Av.SI= average superiority index, gy*sta, gy*pro, gy*ash, gy*Zn, gy *Fe, gy*Ca and gy*Mg= grain*starch, grain yield*protein, grain*ash content, grain yield*zinc, grain yield*iron, grain yield*calcium and grain yield*magnesium, respectively

environment (σ^2_e) that had significant variation (< 0.05) for calcium content. This indicates that sorghum landraces collected from Tigray harbor high genetic variation useful for the development and deployment of nutritionally enhanced and high-yielding sorghum varieties. This agrees with previous finding [52] that reported enormous variations among sorghum landraces that are evolved in Vavilov centers of crop origin and diversity such as Ethiopia. The large genotype by environment interaction ($\sigma^2_{g \times e}$) variance relative to the genotypic variance indicates the need to select for trait stability in the target environment. The high level of genetic variation for various quantitative traits identified in the present study could be attributed to the genetic constitution of the genotypes, varied agro-ecologies and environmental conditions that could affect mineral uptake translocation and distribution. Gene flow between wild and cultivated relatives could be also a likely reason for the high genetic diversity in sorghum landraces [53]. The present results support the high genetic diversity of various sorghum traits reported earlier [4, 21, 30, 49].

The genetic variance (σ^2_g) component is also helpful to estimate heritability such that high σ^2_g implies minimal environmental effect on the trait and vice versa. According to the classification made by [44], the magnitude of broad-sense heritability was higher ($H^2 > 0.9$) in each environment for all the traits studied indicating that the minimal environmental effect, and thus any of the traits can be used for selection [4, 54]. The broad-sense heritability of the pooled over traits was medium ($H^2 > 30 < 60$) for protein ($H^2 = 0.4$) and zinc ($H^2 = 0.5$), and high ($H^2 > 0.6$) for the other traits studied. The medium to high broad sense heritability over environments indicates the possibility of effective selection among the genotypes for further breeding activities. The high broad sense heritability recorded in the present study also indicates these traits are controlled by the additive gene action, which could be improved through selection. As in this study, high to medium heritability in sorghum germplasm has been also reported for various agronomic and nutritional traits of sorghum by [4, 31]. As compared to the individual environment, the heritability of the pooled over analysis was reduced to the range from 0.4 (protein content) to 0.82 (grain yield). This is due to the strong effect of genotype by environment interaction ($\sigma^2_{g \times e}$) effect. This calls for the need to conduct the genotype by environment interaction analysis of the traits to identify high-yielding and stable genotypes.

In the present study, both negative and positive significant associations between some of the traits were detected in individual environments (Table 5) as well as in combined environments (Table 6; Fig. 1). However, the correlations were not in the same trend though out the individual environments. For instance, zinc content had a significant positive correlation with iron in En1, En2, En4 and En5 while significant negative associations of zinc and iron were recorded in En3

and En6. Besides, ash content had a significant positive association with zinc in En1, En4 and En5 whereas; zinc content had a significant negative association with iron concentration in En3. The variation in the association of traits in different environments might be due to variations in the nutrient content of the soil and genotype by environment interaction that may affect mineral adsorption and translocation of crops [55]. In the pooled analysis, significant positive associations were detected in traits such as ash content with zinc, iron and magnesium contents, zinc with iron and grain yield, and calcium with grain yield. On the other hand, protein showed a significant negative association with iron, with ash, iron and zinc contents (Table 6, Fig. 1).

The strong positive associations between traits might be due to common and overlapping quantitative trait loci [56] suggesting that the traits can be improved concurrently through direct selection. In line with the present study, earlier researchers noted a significant positive association between iron and zinc [21, 31], and zinc and protein contents [25, 30, 48]. Whereas negative associations were reported for grain yield with zinc and iron content [31, 57], and calcium content with iron and magnesium content [30]. Growing and selection among large segregating populations could break the negative association of grain yield with other key traits reported in the present study as well as in other earlier research [58, 59].

The GYT analysis is based on the concept that yield is the main objective and the other target traits are evaluated based on their value to combine with grain yield. In the present study, the GYT biplot (Fig. 2) explores about 87.5% of the total variation indicating the suitability of the biplot to graphically display the data for further interpretation. The positive association between the traits as revealed by the acute angle (Fig. 2A) and Pearson correlation coefficient (Table 7) is because the entire yield by trait combinations have yield as a component that is the special feature of genotype by yield by trait (GYT) [33]. The highly significant ($p < 0.001$) positive associations between the traits identified in the present study (Table 7) indicates that there is possibility of selection among the genotype based on their yield performance and nutritional quality. The finding of the present study agrees with the previous finding 33 (oat), 36 (durum wheat) 37 (cotton) and 61 (sorghum) that reported strong positive association of various traits.

The 'which-won-where' view of the GYT biplot (Fig. 2B) was useful to demonstrate the trait profile of the genotypes. The genotypes located in the same sector are closely related, and different genotypes are associated with different traits in each sector. The polygon peak contains the most effective genotypes (vertex genotypes) associated with the trait/s profile in each sector [60]. In this case, genotypes such as LR12, LR25, LR23 and LR 106 were the best genotypes in combining grain yield zinc, ash and iron contents, while LR102, LR103, LR107 were the best genotypes in combining grain yield with protein and calcium, and genotype LR75 and LR28 were best genotypes in combining grain yield with starch and magnesium.

The line perpendicular to the average tester axis (ATA) (Fig. 2C) separates genotypes with below-average means (example: LR56, LR45, LR11, LR92, LR60 and LR57) from those with above-average means (example: LR12, LR23, LR25, LR106, and LR1). Genotypes far from the ideal center are not desirable, whereas genotypes displayed near/at the ideal center are superior genotypes [61]. Therefore, landraces such as LR12, LR23, LR25, LR106, and LR1 are superior genotypes whereas, LR56, LR45, LR57, LR92, LR60 are less performed landraces. Genotypes holding higher mineral content with high-yielding backgrounds can improve the nutritional value of the crop [30]. In the present study, ten promising and five bottom landraces were identified based on the overall superiority index (Table 8) and average tester coordinator (ATC) view of the GYT biplot. These genotypes could contribute significantly to overcoming malnutrition in arid and semi-arid areas including Tigray. As in this study, [33, 35–37] also stated the ATC view of the GYT biplot is an instrumental to rank based on overall superiority and to show their overall superiority and their strengths and weaknesses. They can be also sources of parental lines for further breeding activities. Our finding confirms that the Ethiopian sorghum landraces often harbored various important traits explained by earlier researchers [2, 5, 22, 24].

6 Conclusions

Identification and selection of superior sorghum genotypes for grain yield and nutritional traits is essential to tackle the challenges of acute food shortage and malnutrition in arid and semi-arid areas like Tigray region. This study identified sorghum landraces with higher mean performance, large and useful genetic variations for grain yield and nutritional quality traits. Accordingly, various landraces were selected as breeding parents for each of the traits studied. All the traits studied were highly heritable in each environment ($H^2 > 0.9$) and moderate to highly heritable in the pooled environments implying the possibility of effective selection among the genotypes for further breeding activities. The study further found strong significant positive and negative associations between some of the traits in each environment as

well as in combined environments. Nonetheless, highly significant positive ($p < 0.001$) associations were detected in the genotype by yield by trait combinations. The significant positive association between traits suggests that the traits can be improved concurrently through direct selection. Whereas, the strong negative association between traits implies the need for growing and selection among large segregating populations to break the unfavorable association. Using average tester coordination (ATC) view of GYT biplot and overall superiority index (Mean SI) of the GYT analysis, ten promising sorghum landraces were selected for direct use or breeding programs in arid and semi-arid areas in general and in Tigray in particular.

Author contributions SW: planned, excused the field and laboratory experiments, organizes and writes the manuscript; FA, AA and TA, contributed in planning the research, supervised the field and laboratory experiments, contribute in preparing the manuscript.

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Data availability All data supporting the findings of this study will be available up on request.

Declarations

Competing interests The authors declare no competing interests.

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