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Article

Genotype by Trait (GT) and Genotype by Yield*Traits (GYT) Analysis of Sorghum Landraces in Tigray, Northern Ethiopia

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ABSTRACT

Genotype evaluation based on multiple traits is a new approach in plant breeding. In this study, 108 sorghum landraces along with two standard checks were planted at three locations of Tigray in the 2018 and 2019 growing seasons. The objectives of this study were to investigate the trait profiles of sorghum landraces, and to identify superior sorghum landraces using GYT and GT analysis methods. The correlation computed for the genotypes showed positive and highly significant ($P < 0.01$) correlation of grain yield with traits Pnt, Pwd, Pwt and TGWT, and negative and non-significant correlation with DH, DF and DM. The trait profile of the landraces were also displayed using both GT and GYT biplots. The GYT biplots was instrumental to rank genotypes based on their overall superiority of yield trait combinations using ATC graph of the biplot and GYT superiority index, which is not applicable using the GT biplot. Accordingly, LR106 > LR25 > LR102 > LR12 > LR78 > LR103 > LR1 > LR74 > LR15 were best ranked landraces. Thus, the GYT analysis approach is informative for effective genotype evaluation and selection. We revealed that analysis of sorghum landraces based on multiple traits is crucial to develop superior varieties, and the details of this study are significant for thoughtful sorghum breeding programs.

KEYWORDS: trait profile; multi-trait combinations; trait association; superior landraces

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INTRODUCTION

Sorghum [*Sorghum bicolor* (L.) Moench; 2n = 2x = 20] belongs to the Poaceae family and Andropogoneae tribe [1]. It is the fifth most important cereal crop worldwide after maize, rice, wheat, and barley [2]. In Ethiopia, the crop is cultivated by about 6 million smallholder farmers dominantly in arid and semi-arid areas which cover about 75% of the land size of the country [3]. Sorghum holds the third position in terms of production (5.1

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million tons) and area coverage (1.8 million hectares) next to teff and maize with an average yield of 2.8 t/ha [4], which is very low as compared to its potential, and production in other countries such as Egypt (5.4 t/ha), China (4.8 t/ha), the USA (4.6 t/ha) and Argentina (4.4 tons per hectare) [5].

The low yield per hectare is mainly associated with the effects of genotype by environmental interactions [6–8]. The genotype by environment interaction is expected to be very high in arid and semi-arid areas because of the unpredictability of environmental conditions which makes the identification and selection of superior varieties difficult. Due to this, the mismatch between the varieties released and the target environments remains the major challenge of plant breeding [9]. And, varieties released but not adopted by farmers, and varieties grown by farmers but not released through the formal variety-releasing systems are common phenomena in such areas [10]. The very low adoption rate (1%–2%) of improved varieties of sorghum [11] alongside more than 95% of the farmers' grow locally adapted landraces in Ethiopia [12] could be also an indication of the effect of genotype by environment interaction on sorghum in Ethiopia, especially in the northern parts where low soil fertility and moisture stress prevails.

Therefore, addressing the genotype by environment interactions effects (GEI) and determining the trait profile and usefulness of the various traits of the crop is essential for the effective utilization of available genetic diversity and, to identify stable and superior genotypes either for direct release and/or use as source germplasm for further breeding activities. The GGE (genotypic main effect plus genotype by environment interaction) biplots are effective tools to determine the patterns of genotype by environment interactions thereby visualizing the relationship between genotypes and environments [13]. Based on the GGE biplot approaches, genotype by trait (GT) biplots have been used to explore the relationship of traits graphically [14,15].

Recently [16] introduced the genotype by yield*trait (hereafter, GYT) analysis as a new novel method to select genotypes based on multiple traits. Like the GT, the GYT is also based on the GGE biplot approach in which yield is a key trait, and the traits other than yield are judged based on their value to combine with yield. The GYT biplot analysis is instrumental to demonstrate the strengths and weaknesses of the genotypes graphically [17]. Besides, this approach also provides a superiority index (SI) which allows for evaluating genotypes concerning multi-traits. The SI ranks genotypes by the mean of all traits [16]. Since the development of GYT biplot method in recent years, it has been applied to evaluate genotypes of various crops such as wheat [18–20], Barley [21,22], Oat [16], Sesame [23]. However, there are no research publications conducted to evaluate sorghum genotypes using GYT methods. The objectives of this study were to investigate the trait profiles of sorghum landraces and identify superior sorghum landraces using GYT and GT approaches and compare the methods.

MATERIAL AND METHODS

Description of the Experimental Sites

The experiment was conducted at three districts (Tahtay Adyabo, Tselemti, and Mereb Leke) of Tigray in the 2018 and 2019 growing seasons (Figure 1). 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 is lowlands, 39% medium, and the rest eight percent is classified as highlands, and the altitude ranged from 500 meters above sea level in the northeast to almost 4000 in the southwest [24]. Agriculture is the backbone of the economy of the region in which 65% of the land is under cultivation and more than 95% of the farmers are smallholder farmers. Cereal crops provide the major means of livelihood for the people. Of which, sorghum is the first crop in terms of area coverage (239,044 hectares) and production (7.2 million quintals) [4].

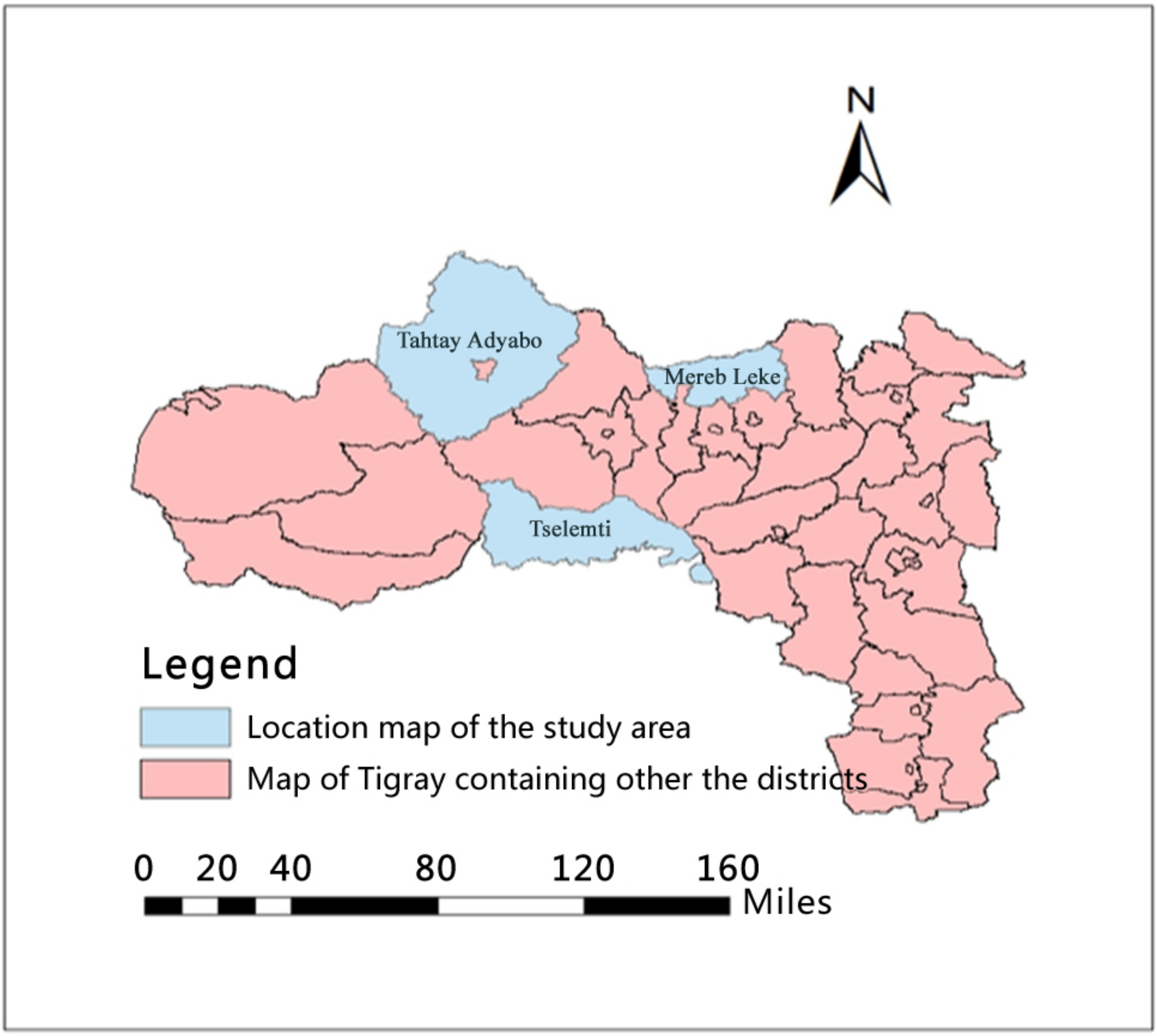

Figure 1. Location map of the study area in Tigray.

Table 1. Descriptions 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

m.a.s.l, meters above sea level; mm, millimeters.

Materials and Experimental Design

The study consisted of 108 sorghum landraces collected from Tigray northern Ethiopia along with two standard checks Melkam and Dekeba (Supplementary Table S1). The checks are early maturing varieties released for the drought areas of the country including Tigray. The experiments were arranged in alpha lattice design [25] having two replications with single rows of 5 meters length per landrace. The distance between rows and between plants within rows was 0.75 meters and 0.25 meters, respectively. The land was tilled twice using a traditional oxen-drawn plow and seedbeds were prepared using human power. UREA (100 kg/ha) and DAP (100 kg/ha) was applied as per the recommendations for the area.

Table 2. Data collected on quantitative traits of sorghum landraces.

SN	Data collected	Description of traits
1	Days to heading (DH)	Number of days from emergence to when 50% of plants have bear heading in a plot
2	Days to flowering (DF)	Number of days from emergence to when 50% of plants have started flowering in a plot
3	Days to maturity (DM)	The date when 90 percent of the plants are physiologically mature counting in days taken from planting up to physiological maturity
4	Thousand seed weight (TGWT)	Weight of 1000 seed (g) counts at 12% moisture content
5	Grain yield (GY)	Total grain weight per plot (kg) after threshing then converted into tons per hectare
6	Panicle length (Pnl)	Panicle length measurement (cm) from the base of the panicle to the tip from five randomly selected plants per plot at maturity
7	Panicle width (Pwd)	Panicle width measurement in the widest diameter of the panicle on five randomly selected plants per plot at maturity
8	Panicle weight (Pwt)	The weight panicle of five randomly selected plants per plot at maturity

Taking the growing environment in to concern, in which grain yield is highly affected by yield and maturity-related traits, and the failure of previous research and extension service to deliver improved sorghum varieties to the area, we include the above traits (Table 2) as our breeding objectives to broaden the information about the trait profile and usefulness of the landraces, thereby, improve our selection efficiency by identifying superior genotypes to be used for further breeding programs.

Genotypes × Trait (GT) and Genotype × Yield × Trait (GYT) Biplot Analysis

The GT biplots were constructed as described by [13,14] which is the same way as the GGE biplot except that environments is replaced by traits. It was generated from the GT table (Supplementary Table S2) containing the mean performance of each trait of the genotypes. For clarity, we used only the numbers of the genotype with the prefix +. For example, LR1 was modified to +1; LR80 was replaced with +80; LR100 was replaced with +100, and so on for both GT and GYT biplot constructions.

The GYT analysis was done following the steps described by [16] First, GT two-way table (Supplementary Table S2) was converted to GYT two-way tables (Supplementary Table S3). For the number of days to heading (DH), days to flowering (DF) and days to maturity (DM), the GYT table was created by GY/DH, GY/DF and GY/DM, respectively. For the traits such as panicle weight (Pwt), panicle length (Pnl), panicle width (Pwd) and thousand seed weight (TGWT), the GYT table was created as GY*Pwt, GY* Pnl, GY*Pwd and GYT*GWT, respectively (Supplementary Table S3). Then, the GYT table was standardized to mean zero and unity variance. The standardization was done to minimize bias that could arise from the difference in the units associated with the measured traits. This was done as:

$$\mathrm{P}ij = \frac{\mathrm{T}ij - \mathrm{T}j}{\mathrm{S}j}$$

Where: Pij is the standardized value of genotype i for a trait or yield-trait combination j in the standardized table, Tij is the original value of genotype i for yield-trait combination j in the GYT table, Tj is the mean across genotypes for yield-trait combination j, and Sj is the standard deviation for yield-trait combination j.

The standardized GYT tables for each trait were used to generate the biplots using GGEBiplotGUI package in R software version 4.0.2. 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.

RESULTS

Phenotype Correlations of the Traits

The correlation computed for the genotypes across all locations evaluated over two years showed a positive and highly significant ($P < 0.01$) correlation of grain yield with traits Pnl, Pwd, Pawt and TGWT and grain yield did not correlate with DH, DF (Table 3).

Table 3. Coefficient of phenotypic correlations among the traits of sorghum evaluated across three locations and over two years.

Traits	GY	DH	DF	DM	Pnl	Pwd	Pwt
DH	−0.03ns						
DF	−0.04ns	0.99**					
DM	−0.02ns	0.84**	0.83**				
Pnl	0.57**	0.02ns	0.01ns	0.04ns			
Pwd	0.39**	0.29**	0.27**	0.33**	0.32**		
Pwt	0.80**	0.08ns	0.06ns	0.14ns	0.44**	0.52**	
TGWT	0.72**	0.32**	0.30**	0.31**	0.42**	0.59**	0.83**

**Significant at $P < 0.01$; *Significant at $P < 0.05$; ns, non-significant.

Genotype by Trait (GT) Biplot

The GT biplot (Figure 2) generated from the GT data explores 77.6% of the total variations among the traits. According to [13,14] the angle of cosine between the vectors indicates the Pearson correlation between the traits. The cosine angles <90° (acute angle), 90° (right angle), and >90° (abutse angle) of the vectors indicate positive correlations, no correlations and negative correlations between the traits, respectively. Accordingly, Figure 2 shows a positive correlation of GY with Pnt, Pwd, Pwt and TGWT and, a negative correlation with DH, DF and DM.

The angle between the vectors of the genotype i and trait j shows the value of the genotype for that trait [13]. Thus, from Figure 2, it is possible to determine the trait profile of the landraces (the weakness and strength of the genotypes). Accordingly, LR106, LR12, LR102, LR23, LR75 and, LR14 revealed higher GY, Pnl, and Pwt. Genotypes such as LR25, LR74 exhibited better TGWT and Pwd. Genotypes such as LR56, LR58 and LR59 exhibited more to DH, DF, and DM indicating that the landraces are late maturing varieties.

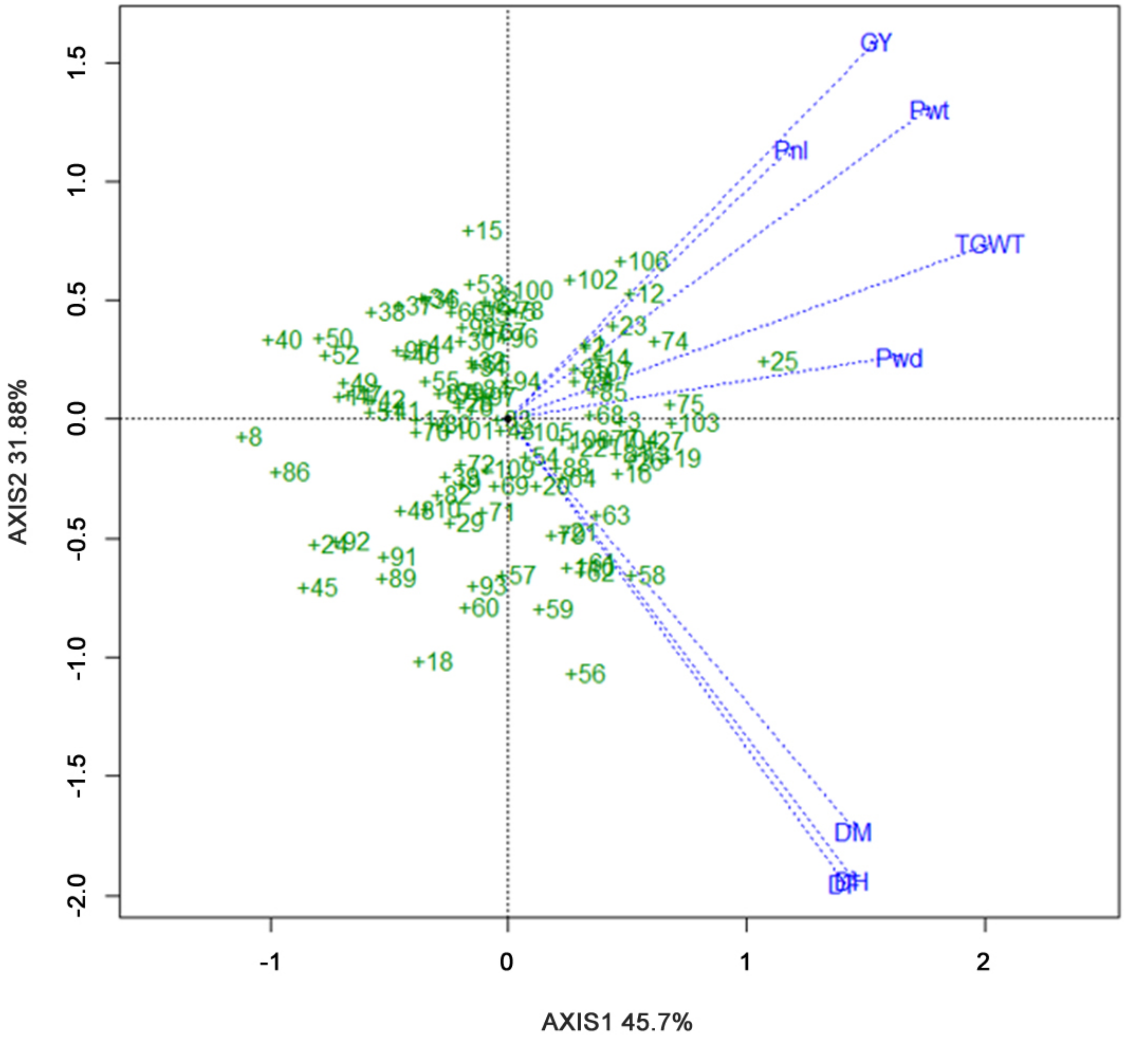

Figure 2. GT biplot of trait relationship of 108 sorghum landraces and two standard checks evaluated at three locations of Tigray in 2018 and 2019. The numbers indicated the codes given for the landraces.

The "which won where/what" of the genotypes based on traits is displayed in Figure 3. The perpendicular lines divide the biplot into eight polygon sectors containing the vertex landraces (LR25, LR106, LR18, LR45, LR8, LR40, and LR15) which are displayed furthest away from the biplot origin. Vertex genotypes are winner genotypes for the trait placed within the corresponding sectors [13]. Genotypes and traits displayed in the same sector of the polygon indicate the genotypes have higher than the average value for a trait [13]. Thus, LR56, LR58, LR19, G59 had higher values for traits such as DM, DH, and DF while LR106, LR25, LR103, LR12, LR23, LR75, and LR74 had higher values for traits including GY, Pnl, Pwd, Pwt and TGWT. Out of the eight sectors, only two had traits in their sectors which implied that the landraces in the other polygons were less desirable for the traits investigated.

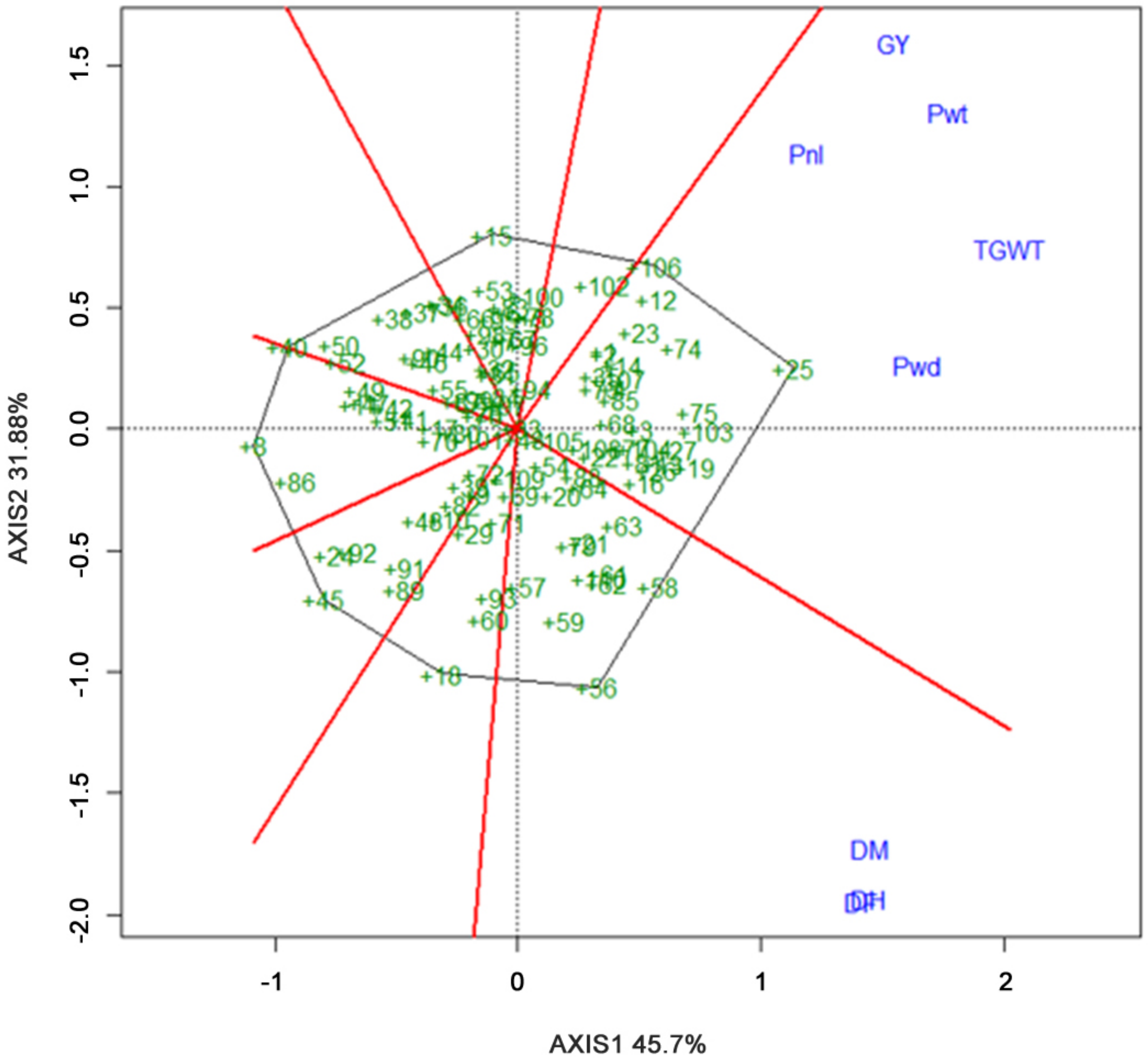

Figure 3. GT biplot showing which won where/what view of 108 sorghum landraces and two standard checks evaluated at three locations of Tigray in 2018 and 2019.

Genotype by Yield*Trait (GYT) Biplot

The GYT biplot generated from the standardized GYT data displays about 96.4% (PC1 93.4% and PC2 3.0%) of the total variations explained among the traits (Figure 4). All the GYT biplots were interpreted following the explanations made by [16].

The yield-trait combinations (GYT) displayed in Figure 4 demonstrate that there are positive correlations among all the traits. This is because the traits include grain yield in their component. The acute angle between the vectors of the landraces *i* and *j* also shows the value of the landrace. Accordingly, LR25 showed higher GY*TGWT, LR106 and LR23 showed higher GY*Pnl, LR73 and LR12 showed higher GY*Pwd, and LR103 and LR74 showed higher GY*Pwt.

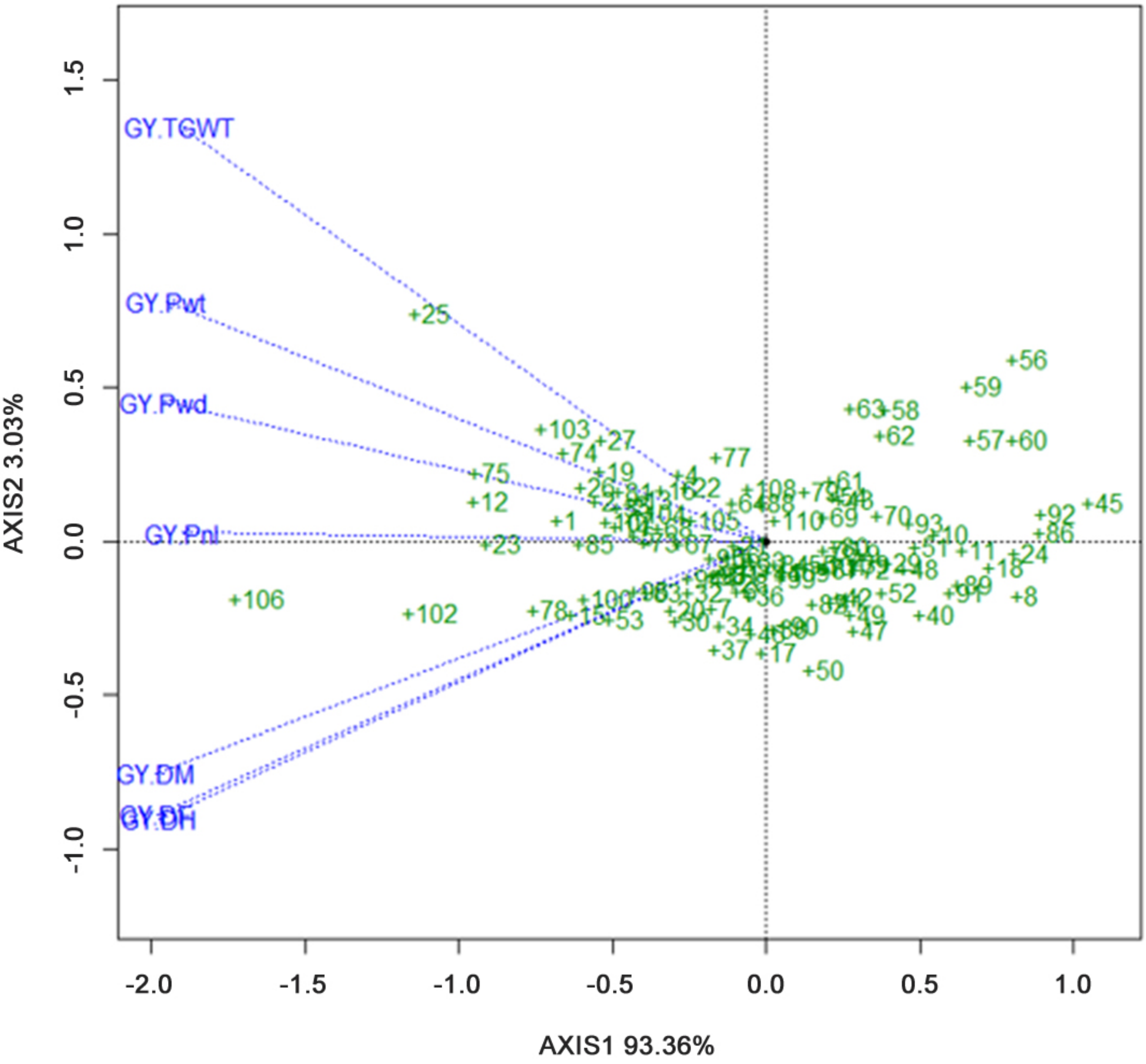

Figure 4. GYT biplot showing the relationship among the yield-trait combination of 108 sorghum landraces and two standard checks evaluated at three locations of Tigray in the 2018 and 2019 growing seasons.

Based on the “which won where/what” analysis (Figure 5), we address the following key points. The perpendicular lines divided the polygon into five sectors, the vertex landraces in each sector are indicated by the polygon peaks, and landraces that are desirable for a GYT are found in its sector as a group. Thus, landraces such as LR106, LR102, LR12, LR75, LR23, LR78 and LR26 are closely correlated with GY*Pwt GY*Pnl, GY*Pwd, GY*DM, GY*DF, and GY*DH. LR25 and LR27 are closely correlated with GY*TGWT. Landraces such as LR50, LR8, LR45 and LR56 did not correlate with any GYT combinations. Out of the five polygons, only two had traits in their sector.

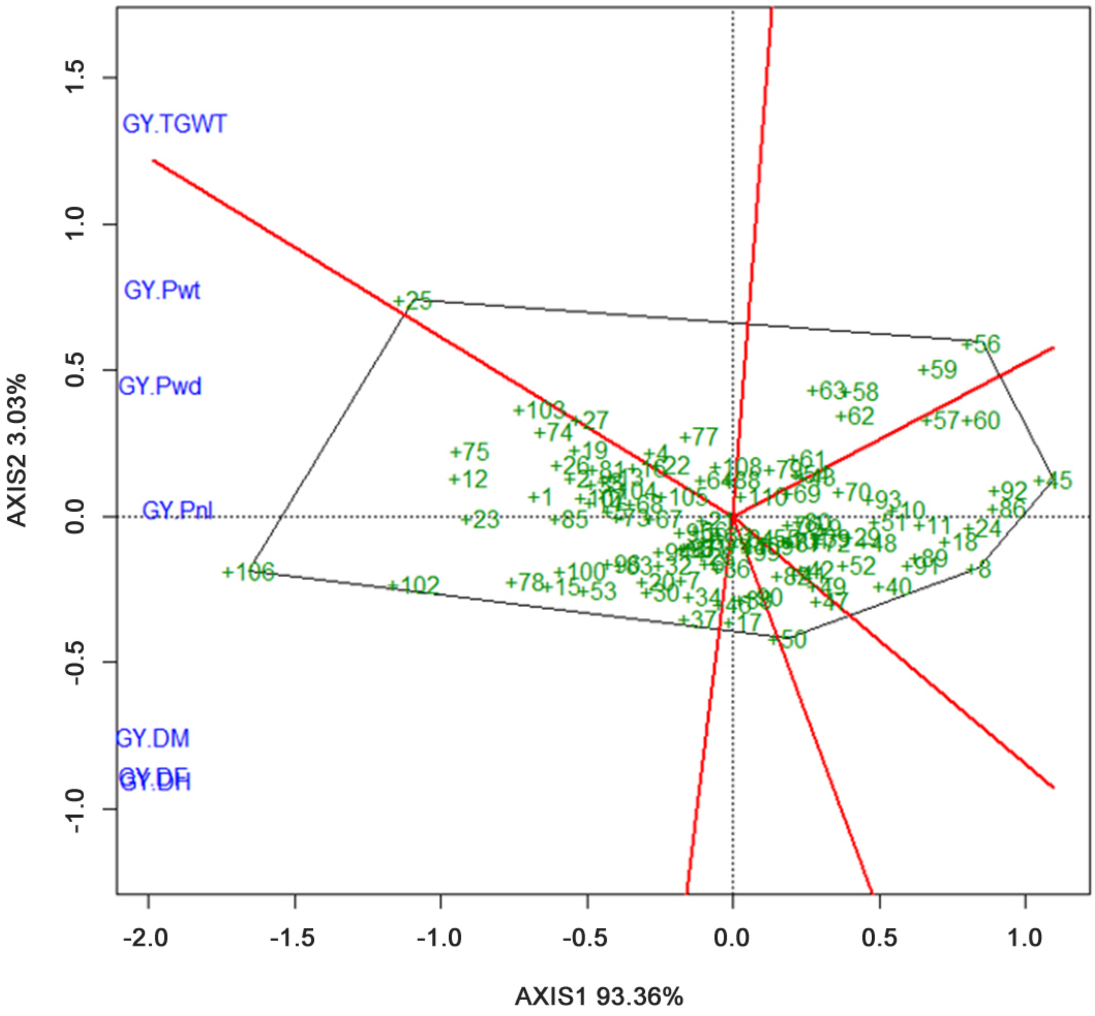

Figure 5. Which-won-where/what view of the GYT biplot of 108 sorghum landraces and two standard checks evaluated at three locations of Tigray in 2018 and 2019.

Figure 6 shows the ATC view of the GYT biplot generated from the standardized yield trait combination data. The small circle in the biplot indicates the average yield trait combinations and the line passes through the biplot origin and average yield trait combination is called the average tester axis (ATA) which is used to rank genotypes based on their overall superiority. Genotypes located close to ATA tend to have balanced trait profiles whereas those located far from the ATA in either direction have apparent strengths and/or weaknesses. From Figure 6, the best ranked landraces include LR106 > LR25 > LR102 > LR12 > LR78 > LR103 > LR1 > LR74 > LR15 whereas; landraces such as LR45, LR92, LR86, LR56, and LR24 were identified as the poorer genotypes. These results were confirmed by the superiority index generated from the yield-trait combinations (Table 3). LR106, LR102, LR are good in panicle length. Landraces such as LR25, LR75, LR103, and LR12 are good in TGWT, Pwt, Pwd but poor in DH, DF and DM.

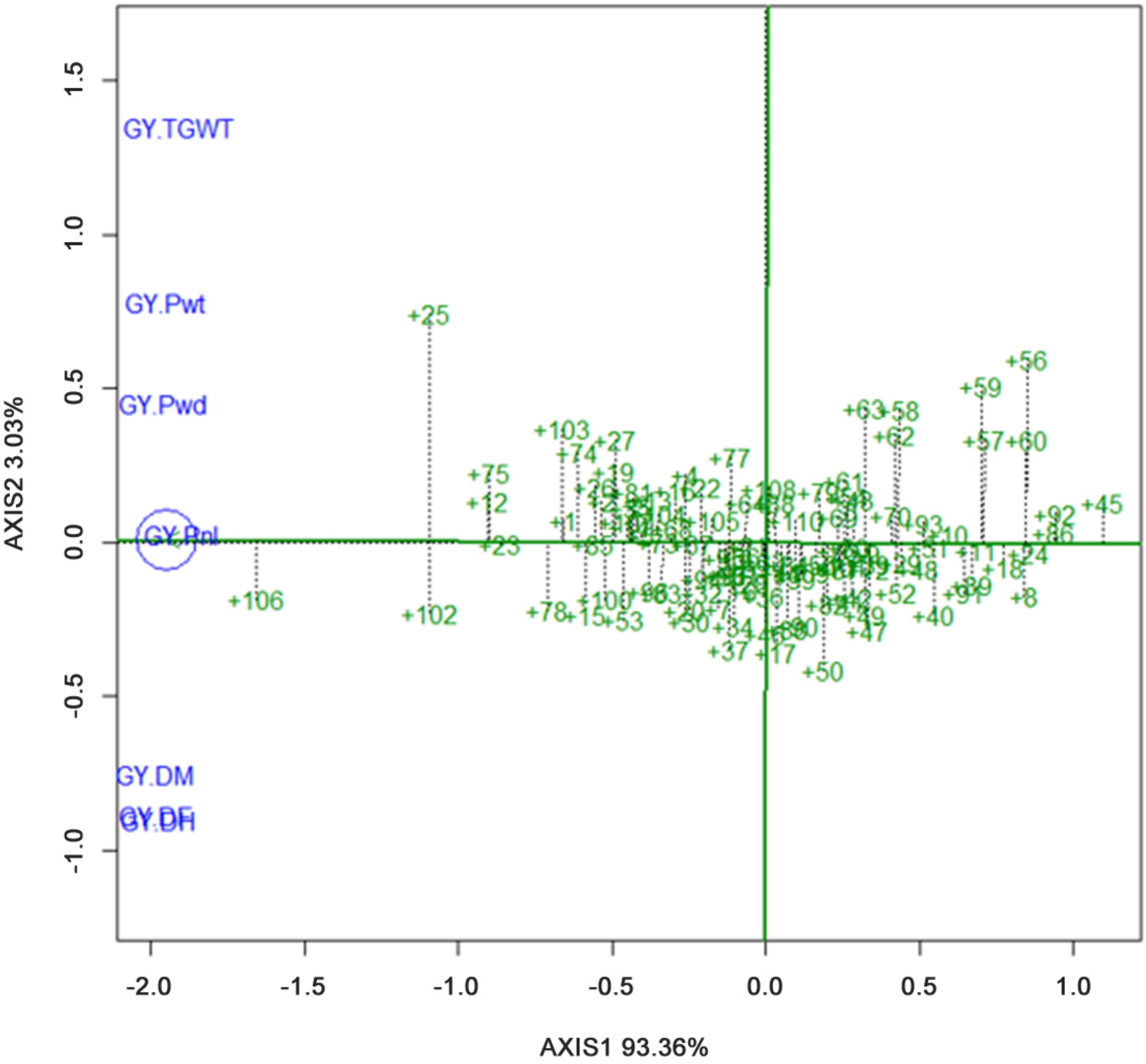

Figure 6. The Average Tester Coordination view of the genotype by yield*trait (GYT) biplot of 108 sorghum landraces and two standard checks evaluated at three locations of Tigray in 2018 and 2019.

Table 4. Top 20 and least 5 of the 108 sorghum landraces and two checks evaluated in three locations of Tigray in the 2018 and 2019.

Gen	GY/ DH	GY/ DF	GY/ DM	GY* Pwt	GY* Pnl	GY* Pwd	GY* TGWT	GY/ DH	GY/ DF	GY/ DM	GY* Pwt	GY* Pnl	GY* Pwd	GY* TGWT	mean (SI)
LR106	69.7	65.6	44.4	374.0	1148.7	416.2	173.9	3.5	3.5	3.6	3.3	2.7	3.1	3.0	3.2
LR 25	53.4	50.4	34.9	370.2	1020.8	358.5	173.9	1.5	1.5	1.7	3.2	2.0	2.1	3.0	2.2
LR102	59.8	56.0	37.6	286.8	1155.9	334.6	136.3	2.3	2.3	2.3	1.9	2.7	1.7	1.8	2.1
LR 12	54.0	51.3	34.6	278.6	1020.7	348.4	141.7	1.6	1.6	1.7	1.7	2.0	1.9	1.9	1.8
LR 75	54.2	50.9	34.2	275.8	987.6	339.2	149.9	1.6	1.6	1.6	1.7	1.8	1.8	2.2	1.7
LR 23	54.8	51.5	34.5	268.7	962.5	355.0	128.9	1.7	1.7	1.6	1.6	1.7	2.0	1.5	1.7
LR 78	55.6	52.3	34.5	234.2	800.9	309.0	129.5	1.8	1.8	1.6	1.0	0.8	1.2	1.5	1.4
LR103	49.6	46.9	31.3	302.7	830.9	315.4	130.7	1.0	1.1	1.0	2.1	1.0	1.3	1.6	1.3
LR 1	51.8	48.8	32.8	253.9	880.0	298.0	130.7	1.3	1.3	1.3	1.3	1.2	1.0	1.6	1.3
LR 74	48.0	45.2	30.1	256.9	963.8	311.9	126.1	0.9	0.9	0.8	1.4	1.7	1.3	1.4	1.2
LR 15	52.7	49.6	33.0	230.7	885.9	279.3	111.4	1.4	1.4	1.3	1.0	1.3	0.7	0.9	1.1
LR 85	49.7	46.8	31.8	221.6	894.3	304.9	120.8	1.1	1.1	1.1	0.8	1.3	1.1	1.2	1.1
LR 26	48.4	45.6	32.1	226.5	872.2	288.3	135.0	0.9	0.9	1.2	0.9	1.2	0.8	1.7	1.1
LR100	50.4	47.6	31.5	224.2	972.7	266.5	108.2	1.2	1.2	1.0	0.9	1.7	0.4	0.8	1.0
LR 2	48.9	45.8	31.3	237.8	834.0	295.6	120.9	1.0	0.9	1.0	1.1	1.0	1.0	1.3	1.0
LR 19	46.9	44.5	29.8	246.0	811.9	327.6	111.9	0.7	0.8	0.7	1.2	0.9	1.5	1.0	1.0
LR 27	46.7	44.0	30.7	232.5	752.7	316.4	130.8	0.7	0.7	0.9	1.0	0.5	1.3	1.6	1.0
LR107	47.6	44.9	29.6	222.2	900.5	291.8	109.6	0.8	0.8	0.7	0.8	1.3	0.9	0.9	0.9
LR 53	50.7	47.7	32.1	226.3	706.4	296.9	97.7	1.2	1.2	1.2	0.9	0.3	1.0	0.5	0.9
LR 14	47.6	44.6	29.3	222.8	885.1	308.0	104.4	0.8	0.8	0.6	0.8	1.2	1.2	0.7	0.9
LR 24	27.9	26.3	17.7	73.3	339.0	138.1	32.9	−1.6	−1.6	−1.7	−1.6	−1.7	−1.9	−1.6	−1.7
LR 56	24.0	22.7	15.3	95.1	273.5	159.5	63.7	−2.1	−2.1	−2.1	−1.2	−2.0	−1.5	−0.6	−1.7
LR 86	25.8	24.4	17.2	63.9	308.7	137.3	30.1	−1.9	−1.9	−1.8	−1.8	−1.8	−1.9	−1.7	−1.8
LR 92	25.3	23.8	15.9	60.8	379.2	130.2	29.8	−2.0	−2.0	−2.0	−1.8	−1.4	−2.0	−1.7	−1.8
LR 45	22.7	21.4	14.6	59.8	284.9	112.1	22.5	−2.3	−2.3	−2.3	−1.8	−1.9	−2.4	−2.0	−2.1

GY, grain yield; DM, days to maturity, DF, days to flowering; DH, days to heading, Pnl, panicle length; Pwd, panicle width; Pwt, panicle weight; TGWT, thousand-seed weight; SI, superiority index.

DISCUSSIONS

Traits Associations and Profile

Multi-environment trials were conducted for many of the major crops worldwide. This is basically to develop a variety suitable for a wide range of environments. A variety can be considered suitable when it shows a high yield with greater stability in a target environment. However, varietal evaluation is always constrained by the environment by genotype interaction effects and undesirable associations of traits [26]. Thus, evaluations of crop varieties across locations and over years are key activities in plant breeding programs to generate information for the selection and recommendation of superior genotypes [13]. Furthermore, adequate information on the trait relationship is crucial for effective varietal decisions and recommendations [27].

Using GT biplot method, we demonstrate grain yield was positively correlated with yield-related traits such as panicle height, panicle weight, panicle width and thousand seed weight, and negatively correlated with traits such as days to heading, days to flowering and days to maturity. This implies that both positive and negative selections can be applied to deploy farmers’ preferred varieties. Similar results were also reported by [27] in their study on GT association using 17 lines and three checks in Zimbabwe. We also found the GYT biplot approaches more promising because it ranks genotypes based on their worth in combining grain yield with other target traits alongside comprehensive visualization of the weakness and strength of genotypes. Our finding conforms to the discussion made by [16].

GT vs GYT Biplot Analysis

In the study, we applied both GT and GYT biplot analysis to evaluate sorghum landraces that originated from Tigray Northern Ethiopia. The variations explained by the GT biplot were about 77.6% (Figure 2), whereas the variation explained by the GYT biplot was 93.4%. Based on the GT biplot, the correlation between the traits, and weaknesses and strength of the landraces were demonstrated. However, the GT biplot has limitations to make effective decisions on which landrace to be selected and recommended or avoided. As a result, low-yielding landraces might be selected if the other traits are superior. This is in line with the finding by [28] who stated GT biplot analysis is important to identify traits useful for indirect selections and to evaluate the weakness and strengths of individual genotypes. In addition to the proper visualization of trait profile and association of the landraces, the GYT biplot was instrumental to ranking genotypes based on their overall superiority of yield trait combination using the ATC graph of the biplot, and GYT superiority index, which is not applicable using the GT biplot approach.

Landraces that combine grain yield with longer panicle length were considered superior landraces. Accordingly, LR106, LR102, LR23, LR25, LR12 and LR75 were identified as ideal landraces. Unlike the superior landraces identified using the GT biplot, the superior landraces identified using GYT are more significant because they are evaluated based on their ability to give higher yield along with combining other important traits meaning the landraces selected are at least high-yielding. The top 20 and five bottom landraces were listed in Table 4 using the GYT superiority index, and it confirms the GYT biplot is very effective to identify superior landraces. Our finding agreed with that of [16], [17], and [21] who reported that GYT biplot is an instrumental approach to evaluate genotypes based on their worth of higher yield with a combination of other breeding traits. The authors also cited that GT biplot is not much helpful to decide on cultivar evaluations and recommendations.

Implications for Sorghum Breeding Programs

Effective utilization of the genetic variability of landraces for the selection and development of stable and superior genotypes is helpful to deploy farmers’ preferred varieties. As discussed in other literature [29,30], centers of origin are an important hotspot for generating new genetic variability essential for crop improvement and utilization programs. Likewise, the Ethiopian sorghum gene pool has been contributing to global agriculture either for direct cultivation or as a source of important traits for various breeding objectives such as sources of parental lines for hybrid development [31], resistance to the green bug [32], drought tolerance [12], resistance to mold disease [33], and high lysine content [34]. The Zera-zera landrace collected from Ethiopia has been extensively used for hybrid development [35].

In the current study, it was found that sorghum landraces outperform the standard checks evaluated based on both GT and GYT biplot approaches suggesting that the diversity of sorghum landraces in the country is not exploited to its potential in breeding programs. Therefore, the sorghum landraces that have been identified with combinations of important traits need to be included in breeding programmers. The selection of pure lines from genetically mixed landrace populations followed by subsequent performance testing and then bulking two or more superior pure lines is one of the best strategies to improve the productivity of the landrace grown by the farmers.

CONCLUSIONS

Several approaches have been applied to evaluate several numbers of genotypes across environments and over years aimed to identify superior genotypes for a specific breeding objective. The present study revealed that GYT analysis is more efficient than the GT analysis in sorghum evaluations because it enables the breeder to select based on multiple trait combinations and simultaneously explores the strengths and weaknesses of the genotypes. These could also assist to developed farmers’ preferred varieties and narrow the gap between varieties developed and target environments. Moreover, the results revealed that there is a high potential for sorghum landraces that could be utilized in sorghum breeding programs. Thus, further collection and detailed evaluation are important to exploit the potential thereby improving sorghum production and productivity in Arid and semi-arid areas of Ethiopia.

SUPPLEMENTARY MATERIALS

The following supplementary materials are available online: https://doi.org/10.20900/cbgg20230002. Supplementary Table S1: Local name, altitudes, districts and geographical zones collections and codes given for the landrace used for the study; Supplementary Table S2: Genotype by Trait of the 108 sorghum landraces and two checks evaluated in three locations of Tigray in the 2018 and 2019; Supplementary Table S3: Genotype by Yield by Trait (GYT) of the 108 sorghum landraces and two checks evaluated in three locations of Tigray in the 2018 and 2019.

DATA AVAILABILITY

The dataset of the study is available from the authors upon reasonable request.

AUTHOR CONTRIBUTIONS

Shushay Welderufael develops the draft manuscript; Fetien Abay, Amsalu Ayana and Tilahun Amede contributed in the write-up and review of the manuscript.

CONFLICTS OF INTEREST

The authors declare that there is no conflict of interest.

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