

Genetic variability among Ethiopian sorghum landrace accessions for major agro-morphological traits and anthracnose resistance

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Abstract Sorghum [Sorghum bicolor (L.) Moench] is one of the major food crops serving millions of people in the semi-arid regions of the world but its production is curtailed by anthracnose, among other challenges. Breeding high yielding and anthracnose resistant sorghum cultivars is an overriding goal for water-limited environments that experience high humid conditions, including Ethiopia. The objective of this study was to assess genetic variation among Ethiopian sorghum landrace accessions based on agromorphological traits and anthracnose resistance, aiming to select promising genotypes for breeding. Three hundred and sixty six sorghum landrace accessions and three check cultivars were evaluated at the Bako Agricultural Research Center in western Ethiopia for 2 years. Data on 11 agro-morphological traits and anthracnose reaction were collected. The analysis of variance indicated that the genotype main effects were highly significant ($P \le 0.01$) for all the assessed traits. Hierarchical clustering using the phenotypic trait data grouped the accessions into five major clusters. The five clusters contained genotypes sourced from

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H. Shimelis · M. Laing · I. Mathew African Centre for Crop Improvement, University of KwaZulu-Natal, Private Bag X01, Scottsville, Pietermaritzburg 3209, South Africa different geographical origins, and two accessions that did not belong to any particular cluster. The phenotypic coefficient of variation was higher than the corresponding genotypic coefficient of variation for all traits, reflecting the confounding effect of environment and genotype interactions in the observed variation. Panicle length, anthracnose reaction and fresh biomass yield had relatively higher heritability and high expected genetic advance, suggesting that these traits could be improved by direct selection. Path coefficient analysis indicated that harvest index and fresh biomass had the strongest direct effects on grain yield. Accessions 71559, 71571, 71425, 71644, 243645, 71524, 70161, 204622, 71653 and 71551 were the best performers in grain yield, yield components and anthracnose resistance. These accessions are selected for yield and anthracnose improvement in sorghum breeding programs.

Keywords Broad-sense heritability · Genetic advance as percent of the mean · Genotypic coefficient of variability · Phenotypic coefficient of variability · *Sorghum bicolor*

Introduction

Sorghum (*Sorghum bicolor* (L.) Moench) is a widely cultivated cereal crop in the semi-arid tropical regions of Asia, Africa and Central America, serving as a staple food (Derese et al. 2018). In Ethiopia, it is the third most important crop after tef (Eragrostis tef [Zucc.] Trotter) and maize (Zea mays L.) (CSA 2017; Mengistu et al. 2018). In Ethiopia, sorghum grain is mainly used as food, whereas its stalks have multiple uses, such as animal feed, for house and fence construction, and mulching for soil and water conservation. The mean yield of sorghum grain in Ethiopia is 2.5 t ha^{-1} , whereas the potential yield of the crop can be as high as 6 t ha^{-1} (CSA 2016; FAO 2017). The low productivity of sorghum has been attributed to biotic (diseases, insect pests, and weeds), abiotic (drought and low soil fertility), and various socioeconomic constraints. Among biotic constraints, anthracnose, caused by the fungus Colletotrichum sublineolum Henn, is the most destructive disease. It has been reported to cause yield losses of up to 70% in Ethiopia, and other warm and humid sorghum-growing regions (Chala et al. 2007; Burrell et al. 2015; Patil et al. 2017). Therefore, it is imperative to develop and deploy sorghum cultivars that are tolerant to various abiotic and biotic stresses, particularly anthracnose, to improve sorghum production in Ethiopia and sub-Saharan Africa (SSA).

Genetic variability for key agro-morphological traits is crucial in sorghum breeding. Considerable genetic variation exists in sorghum for agronomic traits in SSA, including Ethiopia (Amelework et al. 2016; Mofokeng et al. 2017). The available genetic resources should be characterized using key agro-morphological traits to develop farmer-preferred sorghum cultivars. Further, this will enhance cultivar release and adoption across the sorghum value chain. Previous studies have indicated the presence of a high level of phenotypic variation in sorghum for important traits, such as grain yield and yield-related traits.

Materials and methods

Description of the study area

The study was conducted in Western Ethiopia at Bako Agricultural Research Center (BARC), located at 9° 6' N, 37° 09' E and 1650 m above sea level, during the 2016 and 2017 main crop seasons, from May to October. The Center receives annual rainfall ranging from 1200 to 1600 mm, with mean minimum and maximum temperatures of 13° C and 29° C, respectively. The relative humidity ranges from 46 to 57%. The Center is a known hotspot for sorghum anthracnose because of high temperatures and relative which humidity. favor anthracnose disease development.

Plant materials

The study used 366 sorghum landrace accessions, including three released cultivars (Table 1). The accessions, initially collected by the Ethiopian Biodiversity Institute (EBI) from nine regions in Ethiopia, were provided by the Melkassa Agricultural Research Center. The three improved sorghum cultivars ('Gemedi' and 'Chemeda' released by BARC, and 'Geremew' released by the Melkassa Agricultural Research Center) were used as checks (Table 1).

Experimental design and field management

The experiment was laid out in a 61×6 row by column incomplete block design, with three replications. Genotypes were planted in 2.1 m long single-row plots, with an inter-row spacing of 0.75 m and an intra-row spacing of 0.15 m. Trials were planted on 27 May 2016 and 16 May 2017, depending on the onset of rainfall. The experimental field was fertilized with urea, applied at a rate of 50 kg ha⁻¹, and NPS (nitrogen, phosphorous and sulfur in the ratio of 19% N, 38% P₂O₅ and 7% S), applied at a rate of 100 kg ha⁻¹. Urea was applied in two splits (half at planting and the other half when plants had attained a height of about 60 cm). Other cultural practices were carried out as per standard practices recommended for the study area.

Data collection

Phenotypic traits

Data were collected on the following phenotypic traits using published sorghum descriptors (IBPGR/ICRI-SAT 1993): days to 50% flowering (number of days from sowing to when 50% of the plants had flowered), days to 95% maturity (number of days from sowing to when 95% of the plants had reached physiological maturity), grain-filling period (days from flowering to maturity), plant height (measured in cm from the base of the plant to tip of the panicle), panicle length (cm), panicle width (cm), panicle weight (grams), fresh biomass yield (tons ha⁻¹), thousand-kernel weight (grams), and grain yield (tons ha^{-1}). Harvest index was calculated as the ratio of grain yield to fresh biomass yield plus grain yield. Data were collected from five randomly selected and tagged plants on all traits, except days to flowering, days to maturity, fresh biomass yield, grain yield, and anthracnose resistance, which were estimated based on all plants on each plot basis.

Anthracnose disease severity assessment

Anthracnose severity (%) was determined on a plot basis at physiological maturity. The percentage of total leaf area of plants damaged by anthracnose was estimated, as suggested by Chala and Tronsmo (2012).

Data analysis

The data were subjected to analysis of variance, correlation analysis, and principal component and cluster analyses using SAS software (SAS Institute, 2004). Combined analysis of variance for the two seasons was performed following Bartlett's homogeneity test of variance. Genotypic coefficient of variability (GCV), phenotypic coefficient of variability (PCV), broad-sense heritability (H²), and genetic advance as percent of the mean (GAM) were calculated according to Singh and Chaudhary (1985). Genotypic correlations between yield and yield-related traits were computed using SAS software (SAS Institute 2004). A path coefficient analysis was conducted to deduce direct and indirect effects of agronomic traits on grain yield. The path coefficients

72564, 72998, 73003, 73006, 73007, 73008, 73019, 73026, 73643,

70436, 70844, 70864, 231179, 231199, 231201, 231204, 231458

SC283-14, ETSL100375, PML981475, 29832

73645, 206212, 206210

Gemedi and Chemeda

Geremew

Type of genotype	Source (Administrative Region or Research Center in Ethiopia)	No. of accessions	Name or designation
Landrace accessions	Oromia Region	127	9110, 9116, 15830, 15832, 15877, 15890, 15897, 15904, 15908, 15914, 15932, 15935, 15956, 16113, 16116, 16133, 16135, 16152, 16162, 16163, 16168, 16171, 16173, 16176, 16177, 16180, 16206, 16208, 16212, 16213, 16440, 16450, 16451, 16477, 16487, 16489, 17518, 69534, 69540, 69553, 70282, 70471, 70704, 70842, 70859, 70943, 70967, 70998, 71044, 71110, 71137, 71154, 71165, 71168, 71169, 71177, 71194, 71319, 71334, 71337, 71363, 71372, 71374, 71392, 71395, 71466, 71500, 71502, 71503, 71507, 71513, 71516, 71524, 71555, 71556, 71557, 71558, 71559, 71560, 71562, 71563, 75003, 75004, 75006, 75114, 75115, 75118, 75119, 75120, 75123, 75132, 75143, 75146, 75147, 200126, 200193, 200306, 200307, 200308, 208740, 211251, 213201, 214110, 223552, 223562, 228179, 228916, 228920, 228922, 234858, 237550, 237804, 241221, 241265, 241267, 241282, 241283, 245062
	Tigray Region	59	19613, 19619, 19621, 19641, 31309, 71420, 71424, 71425, 71476, 71479, 71480, 71484, 71489, 71497, 73799, 73802, 73805, 73955, 73963, 73964, 74061, 74101, 74130, 74133, 74145, 74157, 74168, 74177, 74181, 74183, 74191, 74203, 74220, 74222, 74225, 74231, 74933, 207876, 220014, 234088, 234112, 235468, 237300, 238388, 238391, 238392, 238394, 238396, 238397, 238403, 238405, 238408, 238425, 238428, 238445, 238449, 238450, 242043, 243670
	Amhara Region	54	69252, 70376, 72443, 72467, 72477, 72520, 72524, 72526, 72616, 73037, 73041, 73048, 73045, 75274, 73079, 73049, 73095, 75455, 73074, 73042, 228115, 72474, 200539, 229887, 214845, 211237, 212640, 210971, 213354, 210949, 214852, 210945, 210974, 226057, 226054, 226047, 226048, 239179, 239180, 239197, 239188, 239184, 239194, 239187, 239154, 239219, 228112, 239182, 239250, 239228, 243657, 243650, 242052, 243645
	Gambela Region	39	69372, 69412, 70027, 70028, 70051, 71569, 71570, 71571, 71574, 71623, 71624, 71625, 71628, 71631, 71635, 71642, 71643, 71644, 71648, 71653, 71654, 71656, 71658, 71698, 71700, 71701, 71708, 71711, 71712, 71714, 71720, 74914, 200522, 201433, 206149, 206154, 211209, 211210, 222885
	†SNNP Region	38	69088, 69178, 69326, 70161, 70187, 70636, 70795, 70874, 70891, 74649, 74651, 74653, 74656, 74663, 74665, 74666, 74670, 74681, 74685, 74686, 74687, 204622, 204626, 204631, 204633, 204636, 210903, 210906, 241706, 241708, 241709, 241715, 241720, 241721, 241722, 241723, 241725, 241728
	Dire Dawa City Administration	22	70742, 71161, 71180, 228840, 239114, 239115, 239116, 239117, 239118, 239119, 239123, 239124, 239125, 239126, 239127, 239129, 239131, 239132, 239133, 239134, 239135, 239137

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[†]SNNP, Southern Nations, Nationalities, and Peoples

Benishangul Gumuz Region

[‡]ARC, Agricultural Research Center

Afar Region

Somali Region

Bako ARC‡

Melkassa ARC

Released

cultivars

were calculated following Shimelis and Hugo (2011) using genotypic correlation coefficients. Grain yield was considered as the response variable, while the agronomic traits were treated as causal variables. Also, a path diagram was constructed to depict the direct and indirect effects of agro-morphological traits on grain yield (Fig. 1).

Results and discussion

Combined analysis of variance for quantitative traits.

Results of the study indicated the presence of a substantial level of genetic variation in the current population, which could be exploited in sorghum improvement programs in western Ethiopia or similar agro-ecologies. Combined analysis of variance showed that variation attributable to the genotype \times year interaction was significant (p < 0.05) (Table 2). This implies that the test genotypes had different performances, while individual performances were also affected by seasonal variability. Genotype variation for agronomic traits is attributable to differences in genetic make-up of the test populations, the environment and their interaction. Derese et al. (2018) also reported significant differences for yield and yield components among 196 sorghum genotypes collected and evaluated at Kobo, Ethiopia.

The mean performance of the sorghum landraces showed significant variation in agronomic traits, grain yield and anthracnose reaction (Table 3). The days to 50% flowering ranged from 72.3 to 94.7 days, with a mean of 86.6 days, while the days to 95% maturity had





minimum, mean and maximum values of 150.2, 169.1 and 181.3, respectively. The wide variation in days to flowering and maturity offers an opportunity to select suitable genotypes for various environments in Ethiopia. Early flowering and maturing varieties should be more suitable for environments with short and erratic rain seasons. Early flowering and maturity are well-known drought escape mechanisms. Therefore, the accessions evaluated in our study can be good candidates for drought tolerance breeding. However, it has been reported that early flowering and early maturing genotypes have low yield potential due to reduced rate of photosynthesis (Disasa et al. 2017). Ethiopia has been experiencing progressively shorter rain seasons due to climate change (Belay et al. 2017) and selection for early flowering and maturing genotypes is highly recommended despite the potential yield penalty. Late flowering and maturing genotypes identified in this population will only be selected for use in sorghum breeding programs if they harbor favorable yield influencing genes that can be introgressed into early flowering and maturity genotypes. Alternatively, accessions with late flowering and maturity can be recommended for environments with

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longer rain seasons.

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Variability for plant height ranged from 297.7 to 401.5 cm, with a mean of 355.9 cm. The presence of variable plant height is important for selection of fitfor-purpose genotypes. For instance, short plant height has been identified as an important trait for drought tolerance (Seyoum et al 2019; Birhan et al 2020). Also genotypes with shorter plant height are useful as a source of height reducing genes and to select genotypes with a higher harvest index. Conversely, tall genotypes are important genetic resources for fodder production and for house construction and as a thatching material in Ethiopia (Venkateswaran et al. 2019). Yield determining components, such as panicle length, panicle weight, harvest index and thousandkernel weight showed wide variability that could be exploited in cultivar development through selection and hybridization. Panicle length and weight and thousand-kernel weight have been reported to be critical determinants of grain yield (Khadakabhavi et al. 2017). Genotypes 71571, 71644, 71425 and 70161 exhibited relatively high performance for traits such as panicle weight, panicle width, thousand kernel weight and harvest index, which contributed to the high grain yield production.

) years in western Et	hiopia											
source of variation	Traits											
	DF	DM	GFP	Hd	PL	PW	PWT	TKW	H	FBY	GY	Anth
Genotype (G)	277.9^{**}	477.6^{**}	$168.2^{\ast\ast}$	5465.8^{**}	115.0^{**}	28.7^{**}	1484.9^{**}	29.1^{**}	44.1^{**}	1348.2^{**}	3.3**	628.2^{**}
(ear (Y)	1613.3^{**}	16287.6^{**}	7641.6^{**}	52950.1^{**}	147.8**	3275.7^{**}	7351.7^{**}	40.0ns	1304.3^{**}	29098.0^{**}	122.8^{**}	0.57^{**}
$3 \times Y$	110.1^{*}	40.0ns	98.3ns	3325.6^{**}	40.3^{**}	20.3^{**}	1077.8**	26.3^{**}	28.5^{**}	807.8**	2.5^{**}	263.2^{**}
, ** Significant at <i>p</i> DF, days to flowering veight; HI, harvest ir	\leq 0.05 and $_{I}$; DM, days to dex; FBY, fr	$p \le 0.01$, respe o maturity; GF resh biomass y	ectively; ns de 'P, grain-fillin _i ield; GY, grai	notes non-sigr g period; PH,] in yield; Anth,	nificant plant height: Anthracnos	; PL, panicle se severity	length; PW,	panicle wid	th; PWT, par	nicle weight; T	KW, thousa	nd kernel

Fable 2 Mean squares and significance tests for 11 agronomic traits and anthracnose severity among 363 sorphum landrace accessions and three released cultivars evaluated in

Values in that column are mean squares and significant tests

 $G\,\times\,Y,$ genotype by year interaction

Table 3 Mean values for
agro-morphological traits
and anthracnose severity
score of 22 selected
sorghum lines evaluated at
Bako during 2016 and 2017

Accession	Traits	5										
	DF	DM	GFP	PH	PL	PW	PWT	TKW	HI	FBY	GY	Anth
High yieldi	ng 10	accessic	ons									
71571	90.8	174.5	83.7	326.3	27.6	13.1	93.1	20.7	12.8	45.8	5.0	24.0
71425	79.7	163.7	84.0	376.8	32.5	13.2	58.5	19.5	9.6	45.9	4.1	29.3
71644	93.3	182.2	88.8	366.5	35.7	13.9	69.4	20.6	10.2	44.6	4.4	34.2
243645	87.2	171.2	84.0	311.5	27.8	10.7	61.0	21.3	7.5	69.0	5.0	33.3
71524	72.3	150.2	77.8	345.8	24.3	10.1	79.1	24.8	11.3	41.7	4.3	31.5
70161	88.5	162.8	74.3	339.5	28.8	13.6	73.3	21.7	7.0	63.7	4.5	22.7
204622	94.7	175.8	81.2	297.7	31.9	12.2	96.1	22.7	6.6	66.9	4.5	23.2
71653	90.0	175.0	85.0	381.8	29.7	9.6	57.6	18.3	7.1	56.5	3.9	25.0
71551	83.2	165.5	82.3	361.2	24.8	11.9	106.4	21.0	6.3	78.7	4.7	29.7
71559	87.2	172.8	85.6	384.8	31.4	14.6	108.8	22.4	10.5	48.7	4.9	23.0
Low yieldir	ng 9 ac	cession	5									
70859	88.5	166.5	78.0	353.8	15.6	7.4	31.1	18.7	1.7	85.0	1.4	32.8
73007	83.8	166.2	82.3	349.0	27.5	10.9	70.5	17.6	1.9	77.8	1.4	27.7
70874	87.5	165.2	77.7	377.0	28.7	12.1	61.0	19.9	3.4	46.9	1.5	42.4
71516	79.8	162.7	82.8	347.3	29.0	12.4	48.9	20.7	3.7	47.8	1.5	36.5
70998	91.5	176.8	85.3	391.5	25.1	8.8	73.6	22.2	2.9	57.1	1.5	31.3
71547	90.5	175.5	85.0	374.2	19.4	9.7	83.4	23.8	3.4	47.9	1.7	23.8
73095	94.5	179.5	85.0	374.1	21.6	8.9	80.7	17.3	2.2	81.7	1.7	30.3
70891	81.5	157.5	76.0	401.5	29.3	10.7	41.7	22.0	2.9	62.6	1.7	28.4
239137	84.7	160.8	76.2	328.2	23.7	10.8	64.4	22.1	3.2	55.2	1.7	33.7
Standard c	hecks											
Geremew	80.5	167.2	87.0	350.7	29.5	8.5	81.6	20.3	3.7	48.3	1.8	21.8
Gemedi	94.3	181.3	87.0	350.7	29.5	8.5	81.6	20.3	4.8	48.3	2.3	21.8
Chemeda	80.5	167.2	86.7	340.8	15.7	9.8	44.2	20.8	3.7	81.5	3.0	43.5
Mean	86.6	169.1	82.5	355.9	26.8	11.0	71.2	20.9	5.7	59.2	3.0	29.5

DF, days to flowering; DM, days to maturity; GFP, grain-filling period; PH, plant height; PL, panicle length; PW, panicle width; PWT, panicle weight; TKW, thousand kernel weight; HI, harvest index; FBY, fresh biomass yield; GY, grain yield; Anth, Anthracnose severity

The genotypes showed marked variation for grain yield that ranged from 1.4 to 5.0 t ha^{-1} . Yield is the product of key yield components (Oladejo et al. 2011, Aliyu and Makinde 2016). The wide variation recorded for grain yield is concomitant with the variation observed in the agronomic traits assessed among the test genotypes. Genotypes such as 71571, 70161, 71644 and 71425 had higher yield potential due to superior performance in traits such as panicle weight, panicle width, thousand kernel weight and harvest index, and were therefore selected for further sorghum breeding.

Anthracnose severity ranged from 22.7 to 42.4%. Landrace accessions, such as 71571, 71425, 70161, 204622, 71653, 71551 and 71559, were moderately resistant to anthracnose (< 29.7%) and had grain yield > 4.0 t ha⁻¹, whereas some accessions, such as

73007, 71547, 73095 and 70891, were also moderately resistant to anthracnose (< 30.3%) but were lowyielding (< 1.7 t ha⁻¹). These accessions can be exploited for enhancing anthracnose resistance and yield potential. The release of novel genotypes with high yield potential and anthracnose resistance should increase sorghum productivity in anthracnose prone environments. The landraces 71571, 70161, and 71425 had relatively low anthracnose severity values of 24.0, 22.7 and 29.3%, respectively. These and the genotypes 73007, 70891 and 73095 are ideal candidates for anthracnose resistance breeding programs.

The significant genotype \times year interaction effects on anthracnose severity suggested differential response of the tested sorghum accessions under the prevailing disease pressure over the seasons. Most assessed genotypes developed higher levels of

Parameters	$\bar{\mathbf{X}}$	$\delta^2{}_g$	$\delta^2_{\ gy}$	$\delta^2_{\ p}$	δ^2_{e}	PCV (%)	GCV (%)	H ² (%)	GA (%)
Days to flowering (days)	86.5	28.0	5.6	46.3	93.4	7.9	6.1	60.4	9.8
Days to maturity (days)	168.7	72.9	41.1	79.6	163.5	5.3	5.1	91.6	10.0
Grain-filling period (days)	82.2	11.6	0.3	28.0	97.3	6.4	4.2	41.5	5.5
Plant height (cm)	347.4	356.7	291.6	911.0	2450.9	8.7	5.4	39.2	7.0
Panicle length (cm)	25.9	12.4	8.2	19.2	15.8	16.9	13.6	64.9	22.6
Panicle width (cm)	10.0	1.4	5.5	4.8	3.7	20.0	10.8	29.5	12.1
Panicle weight (g)	62.3	67.9	314.4	247.5	134.7	25.3	13.2	27.4	14.2
Thousand kernel weight (g)	21.6	0.5	4.8	4.8	12.0	10.2	3.1	9.5	2.0
Harvest Index (%)	6.3	2.6	8.9	7.4	1.9	43.2	25.7	35.4	31.4
Fresh biomas yield (t ha ⁻¹)	56.6	90.1	235.7	224.7	100.6	26.5	16.8	40.1	21.8
Grain yield (t ha ⁻¹)	3.0	0.1	0.8	0.6	0.1	24.6	11.9	23.5	11.9
Anthracnose severity (%)	35.7	60.8	77.2	104.7	31.6	28.6	21.8	58.1	34.2

Table 4 Estimates of variance components, heritability and genetic advance for major quantitative traits of 363 sorghum landraceaccessions and three released cultivars

 \overline{X} , mean; δ^2_{g} , genotypic variance; δ^2_{gy} , genotype by year variance; δ^2_{p} , phenotypic variance; δ^2_{e} , error variance; PCV, phenotypic coefficient of variation; H², heritability in broad-sense; GA, genetic advance

anthracnose severity, suggesting a lack of durable resistance genes. Breeding for partial but durable resistance to anthracnose is required to increase sorghum productivity. Accessions such as 71571, 70161, 204622, 71653 and 71559, with low disease severity scores of $\leq 25\%$ are suitable for anthracnose resistance breeding programs. Variation in disease pressure across the two test years allowed selection of these genotypes with minimal disease escape.

Estimation of variance components, heritability and genetic advance

Estimates of variance components, broad-sense heritability and genetic advances for the different traits are presented in Table 4. Generally, GCV values were lower than PCV values for all traits, implying that environmental effects on the studied traits were more prominent than genotypic effects. Higher PCV values than GCV are expected (Khan et al. 2005; Warkad et al. 2008; Dhutmal et al. 2014) due to the confounding effect of genotype performance across environments. The magnitude of the discrepancy has implication on selection and genetic advancement. Large discrepancies between PCV and GCV values for the same test populations indicate that trait performance is significantly affected by the test environment, necessitating multi-environmental selection to maximize genetic values (Tuhina-Khatun et al. 2015). Panicle width and weight, harvest index, fresh biomass and grain yield had large discrepancies for PCV and GCV, showing that they had greater environmental plasticity than the other traits.

Response to selection is also dependent on trait heritability and genetic advances. According to Singh (2001), heritability values may be categorized as low $(H^2 \le 40\%)$, medium (40 < $H^2 \le 59\%$), moderately high ($60 \le H^2 \le 79\%$) and very high ($H^2 \ge 80\%$). In the present study, days to flowering, days to maturity and panicle length exhibited moderately high heritability ($H^2 \ge 60\%$). The high heritability estimates suggested that these traits could be selected directly across seasons with relatively high efficiency. The high heritability estimates also indicate that the test environments exerted little effects on these traits. Heritability estimates for grain-filling period, plant height, anthracnose severity, harvest index and fresh biomass yield was intermediate $(40 < H^2 \le 54\%)$. The environment and genetic impact on these traits was almost similar. Traits with low heritability estimates ($H^2 < 35\%$), including panicle width, panicle weight, thousand-kernel weight, and grain yield, would be difficult to select directly over seasons due to the strong environmental influence. The low heritability estimates can be attributed to $G \times E$ interactions, which are known to negatively affect the heritability of quantitative traits (Nzuve et al. 2013). Traits with low heritability values can be selected indirectly via proxy traits that have high heritability and favorable correlations.

Anthracnose severity had a moderate heritability estimate of 58%. Several authors have reported heritability values for sorghum anthracnose resistance, with values ranging from 36 to 94% (Burrell et al. 2015; Beshir et al. 2016; Patil et al. 2017). The moderate heritability for anthracnose resistance found in this study indicated the reliability of the test location for selection. This presented an opportunity to select for anthracnose resistant breeding parents and progenies. The efficiency of identifying anthracnose resistant genotypes would be subject to multiple selection cycles to ensure the homogeneity of the new population and homozygosity of genes conditioning anthracnose resistance and agronomic traits.

Genetic advancement of breeding populations for yield and its component traits are dependent on the extent of trait heritability. Therefore, broad-sense heritability estimates are key in accurately estimating genetic advance and yield gains. In this study, GAM ranged from 5.5% for grain-filling period to 34.2% for anthracnose severity (Table 4). Genetic advance was relatively high for anthracnose severity (34.2%), harvest index (31.4%), panicle length (22.6%) and fresh biomass yield (21.8%). Traits with intermediate GAM included panicle weight (14.2%), panicle width (12.1%), and grain yield (11.9%). The lowest GAM was observed for thousand-kernel weight (2.0%). High values for genetic advances indicates that there is a high potential for improvement of the trait under selection. High heritability and high GA show that yield-influencing trait under selection is predominantly conditioned by its genes and is less affected by environmental influences, and can be used to select for yield improvement (Akinwale et al. 2011). A trait with low heritability and low genetic advances has a low response to selection (Hefny 2011). In the present test population traits such as days-to-flowering, -grain filling and -maturity would have low response to selection, given their low values for genetic advance. Therefore, the present populations should be further selected for high panicle length, harvest index and fresh biomass, and low anthracnose severity scores under multiple environments.

Clustering of sorghum accessions

The sorghum accessions were grouped into five clusters, with two outliers, based on the mean values of traits (Table 5). The largest number of accessions (263) were found in Cluster I, including 82 accessions from the Oromia region. Cluster II had 85 accessions, of which 40 were from Oromia. Although the number of accessions from various regions was variable across clusters, accessions from all regions were distributed across clusters (Table 5), which indicated significant variation among test genotypes within the same region of collection. The grouping of diverse genotypes across clusters provides an opportunity for designed hybridization for sorghum improvement. Designation of genotypes into clusters is a significant step towards characterization of these genotypes as they form a part of vital genetic resources for sorghum improvement in Ethiopia. Also, clustering allows selection of divergent parental genotypes to exploit heterosis during breeding (Swamy et al. 2018).

Principal component analysis (PCA)

Principal component analysis revealed that the first four principal components with eigenvalues greater than unity explained 63% of the total variation (Table 6). PC1, PC2, PC3 and PC4 explained 25%, 16%, 12% and 10% of the total variation, respectively. Days to maturity, days to flowering, plant height, grain-filling period, fresh biomass yield, panicle width, panicle weight, and panicle length were the major contributors to the variation explained by the first principal component. The highest contributors to PC2 were harvest index, grain yield, panicle width, panicle length, panicle weight, and thousand-kernel weight. Derese et al. (2018) reported that two principal components contributed 79.41% of the total variation for yield and yield-related traits among sorghum populations evaluated under irrigated condition in Ethiopia. Abraha et al. (2015) noted a variation of 74.6% among 25 Eritrean sorghum genotypes for grain yield and yield-components, which was highercompared to the present study. The traits mostly associated with PC1 accounted for much of the variation among the test genotypes and could be used as the basis for selection. In this population, the genotypes were differentiated by their differences in days to maturity, days to flowering, plant height and

Collection region	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	outlier 1	outlier 2
Afar	73645, 73006, 72998, 73007, 73008, 72564, 206212, 73003, 73026, 73643, 73019	206210					
Amara	226054, 210974, 239180, 211237, 239154, 75274, 72477, 239194, 239179, 73045, 73049, 214852, 228115, 69252, 239188, 210949, 72467, 73074, 73079, 243650, 73041, 200539, 226048, 210945, 75455, 226047, 239250, 228112, 242052, 73037, 239184, 239187, 243645, 212640, 213354, 72616, 210971, 72526, 73042, 73048, 72524,	72443, 243657, 70376, 239197, 72474, 73095, 72520, 214845, 229887	226057, 239228, 239219	239182			
Benshangul	229832, PML981475	ETSL100375		SC283- 14			
Dire Dawa	70742, 239135, 239137, 239123, 71161, 228840, 239124, 239117, 71180, 239129, 239119, 239126, 239125, 239118, 239116, 239133, 239134, 239131	239114, 239127, 239132	239115				
Gambella	71708, 71700, 71648, 71654, 71643, 201433, 200522, 71574, 71658, 222885, 71644, 211209, 71631, 69372, 71698, 70051, 71711, 206154, 71642, 74914, 71714, 71624, 71571, 71656, 71625, 206149, 70028,	71720, 71635, 70027, 69412, 71653, 71569, 71712, 71570, 71623	71628	71701	211210		
Oromiya	$\begin{array}{r} 71177,\ 16116,\ 241267,\ 71169,\\ 245062,\ 71363,\ 71466,\ 70842,\\ 16171,\ 16162,\ 70704,\ 70471,\\ 71516,\ 71168,\ 15908,\ 71556,\\ 75146,\ 16113,\ 71194,\ 15897,\\ 71502,\ 75115,\ 71165,\ 16450,\\ 71337,\ 16477,\ 16176,\ 214110,\\ 228179,\ 75147,\ 16487,\ 70967,\\ 16451,\ 241265,\ 15877,\\ 200193,\ 208740,\ 69553,\\ 71154,\ 16177,\ 71503,\ 15904,\\ 200306,\ 75006,\ 71553,\ 16135,\\ 71137,\ 71395,\ 211251,\ 70282,\\ 71392,\ 75114,\ 228916,\ 16208,\\ 75120,\ 71563,\ 15935,\ 71500,\\ 71558,\ 17518,\ 241283,\\ 234858,\ 71507,\ 16213,\\ 241282,\ 69534,\ 75143,\ 15914,\\ 241221,\ 75123,\ 16489,\ 75118,\\ 75119,\ 237804,\ 71524,\ 15832,\\ 70859,\ 15956,\ 228920,\ 71555,\\ 71513,\ 15830\\ \end{array}$	70998, 71374, 200126, 71372, 71545, 71544, 71044, 71319, 75132, 223552, 71549, 16440, 71546, 71560, 16206, 15890, 75004, 15932, 16152, 71110, 75003, 228922, 71547, 213201, 71334, 16133, 16212, 223562, 9110, 71559, 16173, 16180, 70943, 71562, 9116, 16168, 200307, 69540, 237550, 71548	200308, 71557, 71551			71550	

 Table 5 Genetic relatedness of 363 sorghum landrace accessions and three released cultivars based 11 quantitative traits and anthracnose reaction

Table 5 continued

Collection region	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	outlier 1	outlier 2
SNNP	210903, 241721, 74663, 210906, 70636, 74681, 70874, 241709, 74649, 74651, 241722, 241723, 74685, 70161, 241725, 74656, 241706, 74670, 204636, 241715, 241708, 74653, 69326, 241728, 204631, 70795, 74665, 204633	69088, 70187, 74666, 74686, 204626, 70891, 74687, 69178	241720				204622
Somali	231204, 70436, 231201, 70844, 231199, 231458, 231179, BTx623	70864					
Tigray	74168, 238403, 74222, 238391, 234088, 238394, 31309, 71479, 19641, 74145, 71420, 207876, 71497, 74225, 242043, 73964, 238405, 238445, 71425, 74130, 238392, 74101, 74933, 234112, 73805, 19613, 73963, 238388, 74181, 238408, 235468, 243670, 74203, 74177, 74220, 74157, 74231, 74133, 237300, 73802, 19621, 238449, 238428	74061, 71484, 238396, 74183, 238425, 238397, 73799, 71489, 71476, 74191, 220014, 238450, 71480		71424, 19619	73955		
Released cultivars	Chemeda, Gemedi, Geremew						

SNNP, Southern Nations, Nationalities and Peoples

Table 6Principalcomponents (PCs) for 12traits of the 363 sorghumaccessions and 3 releasedcultivars

Variables	Principal co	omponents (PCs	5)	
	PC1	PC2	PC3	PC4
Days to flowering (days)	0.422	- 0.031	0.238	0.149
Days to maturity (days)	0.471	-0.064	0.437	- 0.099
Grain-filling period	0.250	- 0.068	0.429	- 0.357
Plant height (cm)	0.356	0.062	-0.147	0.174
Panicle length (cm)	0.218	0.351	-0.379	- 0.362
Panicle width (cm)	0.226	0.375	-0.325	- 0.254
Panicle weight (g)	0.221	0.303	- 0.049	0.346
Thousand-kernel weight (g)	0.034	0.178	- 0.183	0.227
Harvest Index	- 0.261	0.521	0.374	0.005
Fresh biomass yield (t ha^{-1})	0.248	-0.378	-0.242	0.426
Grain yield (t ha^{-1})	-0.037	0.408	0.242	0.508
Anthracnose disease severity (%)	-0.361	- 0.135	0.061	0.063
Eigen value	2.99	1.94	1.44	1.17
Individual variation explained (%)	25	16	12	10
Cumulative variation explained (%)	25	41	53	63

Table 7 Genotypic correlati	on coefficient	s for 12 majo	or traits of 36:	3 sorghum ac	ccessions and	3 improved e	cultivars					
Traits	DF	DM	GFP	Hd	PL	PW	PWT	TKW	IH	FBY	GY A	nth
Days to flowering (days)	1											
Days to maturity (days)	0.804^{**}	1										
Grain-filling period (days)	0.068 ^{ns}	0.648^{**}	1									
Plant height (cm)	0.403^{**}	0.349^{**}	0.068 ^{ns}	1								
Panicle length (cm)	0.076 ^{ns}	0.091 ^{ns}	0.055 ns	0.227^{**}	1							
Panicle width (cm)	0.131^{*}	0.121^{*}	0.035 ns	0.220^{**}	0.533^{**}	1						
Panicle weight (g)	0.209^{**}	0.168^{**}	0.015 ^{ns}	0.237^{**}	0.180^{**}	0.214^{**}	1					
Thousand kernel weight (g)	- 0.018 ^{ns}	- 0.023 ^{ns}	- 0.016 ^{ns}	0.095 ^{ns}	0.110^{*}	0.089 ^{ns}	0.072 ns	1				
Harvest Index (%)	-0.192^{**}	-0.205^{**}	- 0.097 ^{ns}	-0.228^{**}	-0.041 ns	0.013 ^{ns}	0.065 ns	0.033 ns	1			
Fresh biomass yield $(t ha^{-1})$	0.197^{**}	0.197^{**}	_{su} 620.0	0.211^{**}	— 0.066 ^{ns}	– 0.019 ^{ns}	0.062 ^{ns}	– 0.019 ^{ns}	-0.710^{**}	1		
Grain yield (t ha ⁻¹)	-0.012 ns	- 0.012 ^{ns}	-0.006 ns	-0.003 ns	0.014 ^{ns}	0.092 ^{ns}	0.204^{**}	0.093 ^{ns}	0.528^{**}	0.027 ^{ns}	1	
Anthracnose severity (%)	-0.326^{**}	-0.367^{**}	-0.199^{**}	-0.272^{**}	-0.290^{**}	-0.261^{**}	-0.283^{**}	- 0.031 ^{ns}	0.154^{**}	-0.158**	0.013 ^{ns} 1	
ns,* and ** denote non-signi DF, days to flowering; DM, c weight; HI, harvest index; FI	ficant, signific lays to maturi 3Y, fresh bior	cant correlatio ity; GFP, grai mass yield; G	ons at 0.05 an in-filling peric 'Y', grain yield	ıd 0.01 proba od; PH, plant d; Anth, anth	ubility levels, height; PL, p racnose sevel	respectively; anicle length; ity	; PW, panicle	e width; PWT	, panicle we	ight; TKW,	thousand ker	nel

panicle width, which had high PC1 loadings. This will allow for the identification of genotypes suitable for the target production environments with different growth periods and diverse uses. Anthracnose severity was linked with PC4.

Correlation analysis

The present study found positive and significant correlations between grain yield and harvest index (r = 0.528), and panicle weight (r = 0.204) (Table 7). This suggests that direct selection of these traits will result in yield improvement. A strong correlation was previously reported between panicle width and grain yield (Warkad et al. 2010; Khadakabhavi et al. 2017). Simple correlations provide opportunities for direct selection of genotypes based on mutual traits associations. For instance, higher panicle weight and harvest indices were beneficial traits that can be simultaneously selected for improvement in the current population.

relative importance of the casual factor individually, which is useful in identifying target traits for yield improvement (Akram et al. 2016). Harvest index (1.11) had the highest significant direct effects on grain yield. Harvest index negatively influenced grain yield through fresh biomass (Table 8 and Fig. 1). This suggests that genotypes with high fresh biomass are likely to attain less grain yield. This could be due to a competition between early vegetative and yield influencing traits during partitioning of assimilates (Akinseve et al. 2017). This would hinder selection of sorghum genotypes with high fresh biomass and yield to fulfil the need for dual-purpose types in Ethiopia, where grain is used for human consumption and straw is used for livestock feed, and thatching. Detailed genetic analysis and identification of genes causing linkage drag between biomass and grain yield is required to develop dual-purpose sorghum genotypes. Also, mutation breeding techniques can be explored to enhance genetic variation and identify novel mutants with high yield and biomass production potential. Panicle weight had the highest indirect effect on grain yield through plant height, suggesting that taller plants were more likely to have higher panicle weights.

Path coefficient analysis

Path analysis partitions the total correlation coefficient into direct and indirect effects, and measures the

 Table 8
 Path coefficients based on genotypic correlation analysis of 10 quantitative traits indicating direct effect (diagonal and bold) and indirect effect (off diagonal) on grain yield in sorghum

Traits	DM	GFP	PH	PL	PW	PWT	TKW	HI	FBY	GY
DM	0.014	0.014	0.012	0.007	0.004	0.008	- 0.001	- 0.228	0.159	- 0.012
GFP	0.009	0.022	0.002	0.004	0.001	0.001	- 0.001	- 0.108	0.064	- 0.006
PH	0.005	0.001	0.034	0.016	0.006	0.011	0.005	- 0.254	0.171	- 0.003
PL	0.001	0.001	0.008	0.073	0.016	0.009	0.006	- 0.046	- 0.053	0.014
PW	0.002	0.001	0.008	0.039	0.029	0.010	0.005	0.014	-0.015	0.092
PWT	0.002	0.000	0.008	0.013	0.006	0.047	0.004	0.072	0.050	0.204**
TKW	0.000	0.000	0.003	0.008	0.003	0.003	0.055	0.037	- 0.015	0.093
HI	- 0.003	- 0.002	- 0.008	- 0.003	0.000	0.003	0.002	1.113	-0.574	0.528**
FBY	0.003	0.002	0.007	- 0.005	- 0.001	0.003	- 0.001	- 0.790	0.809	0.027

**Denote significant correlations at the 0.01 probability level

DM, days to maturity; GFP, grain-filling period; PH, plant height; PL, panicle length; PW, panicle width; PWT, panicle weight; TKW, thousand kernel weight; HI, harvest index, FBY, fresh biomass yield; GY, grain yield

The last column denote genotypic correlation value of the trait with GY, grain yield corresponding to the sum of the direct and indirect path coefficients in that row

Conclusions

Significant variation was detected among the tested genotypes for the assessed traits, which will be useful for further breeding. Accessions such as 71559, 71571, 71425, 71644, 243645, 71524, 70161, 204622, 71653 and 71551 were identified as having high yield potential and moderate resistance to anthracnose. The selected accessions are distantly related and complementary and, recommended for breeding. Simultaneous selection for a high harvest index and panicle weight will potentially improve grain yield in the test populations.

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