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Genotype-by-trait association of sorghum (*Sorghum bicolor* (L.) Moench) advanced lines grown under arid and semi-arid regions of Zimbabwe

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Abstract

Inadequate information is available on trait relations and profiles of sorghum genotypes, yet this information is vital for precise decisions to be undertaken in breeding programs. Here, 17 sorghum experimental lines were evaluated together with three checks at five locations, representing the major sorghum production environments in Zimbabwe. Across site analysis of variance (ANOVA) showed significant genotypic effects on grain yield (GYD) as well as the other traits, including panicle length (PL) and stem diameter (SD). Distance-based clustering indicated the possibility of indirectly selecting for GYD using; SD, exertion (EXSTN), panicle length (PL), panicle width (PW) and number of leaves (NL). In addition, the vector view of the genotype-by-trait (GT) biplot also revealed strong correlations between GYD and, PW, SD and FYD, as well as the other physiological traits including, days to male flowering (DMA) and days to physiological maturity (DPM). Genotypes superior for a combination of traits were, G6, G7, G11, G18 and G20, which were strong for GYD, PL and PW, as well as, G5 which was strong for sugar content (SC), number of leaves (NL) and SD. Genotypes 15, 16 and 17, were specifically strong for GYD whereas, genotypes 4 and 9 were strong for FYD. Overall, results revealed the key traits which can be considered singularly or in combination, when selecting suitable sorghum genotypes, either for feed or food purposes, under arid and semi-arid conditions. This information is vital for decision making in sorghum breeding programs.

Keywords Genotype by trait analysis · Trait association · Heritability · Genetic advance

Introduction

Sorghum (*Sorghum bicolor* (L.) Moench) is among the most important food security crop in the arid and semi-arid regions of Africa where climate is characterized by unpredictable weather patterns, mostly dominated by frequent droughts and heat stress conditions (Rincen et al. 2017; Salim et al. 2017; Ajeigbe et al. 2018). It is the fifth most important staple food crop after maize, rice, wheat and barley, worldwide (Mare et al. 2017; Mundia et al. 2019). In countries where it is produced, sorghum is predominantly utilized for food or feed (Hassan et al. 2015; Guo et al. 2017). Besides its importance for food and nutrition security, the sorghum crop is also valuable in industry, where the grain is used for beer and starch production (Xiong 2019). In Zimbabwe, sorghum production is confined to the southern parts, which are geographically classified as, arid or semi-arid, usually characterized by very low rainfalls per annum (Mugandani et al. 2012; Tsusaka et al. 2015). Because of its

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drought resilience capabilities (Gill et al. 2014; Amare et al. 2015; Dube et al. 2018; Chanza 2018), sorghum has traditionally been a crop of choice to these drought prone environments. With the present increased incidences of climate change-induced abiotic stresses, especially drought and heat stress which are actually predicted to increase (Hadebe et al. 2017; Bosire et al. 2018; Eggen et al. 2019), importance of sorghum as a food and nutrition security and an industrial crop may improve (Dahlberg et al. 2003; Rukuni et al. 2015). Hence, efforts should be directed on improving the genetic potential of this crop so that it meets up with these predicted socio-economic and climatic scenarios.

Despite its adaptability under above optimal temperatures as well as water-deficit conditions (Tari et al. 2013; Tack 2017), average yields of sorghum per hectare, in comparison with the other important cereals such as maize and wheat, are very low. When grown under optimal growing conditions, grain yields of between 3 and 4 tha^{-1} are usually reported (Ajeigbe et al. 2018; Phiri et al. 2019) and when grown under severe abiotic stresses (e.g. drought and heat stress), yields ranging between 0.3 and 1 tha^{-1} were reported. These low yields are normally attributed to use of genetically unimproved and low yielding varieties (Ncube et al. 2007). Therefore, developing stress resilient, but high yielding sorghum varieties is a key task for crop breeders of the twenty-first century and those of the unforeseeable future years to come.

In any plant breeding program, testing of the developed materials for adaptation to stress and non-stress conditions in multi-environmental trials (METs) remains a very important step for making accurate decisions (Ramburan et al. 2018; Rincent et al. 2017; Malosetti et al. 2013). But, accurate estimation, interpretation and utilization of METs datasets in decision-making remains a challenge to most plant breeders (Chapman et al. 2000; Yan and Rajcan 2002; Yan and Holland 2010; Hunt et al. 2020). One of the key procedures often ignored or which other breeders are ignorant of is understanding of genotype by trait (GT) associations for a particular set of developed materials (Chapman et al. 2000; Hammer et al. 2014; Wang et al. 2020). Yet, this information is important in making accurate selection decisions in a breeding program.

Over the years, several methods have been used to interpret trait relations and genotype profiles of different crops (Rao et al. 2013; Salim et al. 2017; Patil and Lokesh 2018). Of-recent, the GT biplot which is an application of the genotype–genotype \times environment (GGE) biplot has become an effective tool for analyzing METs datasets, particularly focusing on identifying cultivars that are good for certain group of associated traits (i.e. potential candidates for parents in a plant breeding program) (Yan and Kang 2003). The GT biplot allows for visual display of genetic correlations among traits and was previously used to study trait relations

in crops such as white lupin (Rubio et al. 2004), Duram wheat (Dolatabad et al. 2010) and maize (Musvosvi et al. 2018). In this study, we aim to assess the GT associations of sorghum genotypes grown under the arid and semi-arid sorghum growing environments of Zimbabwe. We hypothesize that grain yield components (e.g. PW and PL), fodder yield and leaf characteristics (e.g. NL), are closely associated with grain yield and can be indirectly used to select for yield in sorghum breeding programs.

Materials and methods

Evaluation sites and germplasm

Twenty genotypes comprised of 17 experimental sorghum lines developed by the Crop Breeding Institute (CBI), a research entity, under the Department of Research & Specialist Services (DR & SS) of Zimbabwe, one landrace variety (Chimupositori), collected from the Masvingo province, and two commercial check varieties (i.e. SV-2 and SV-4) were tested in METs (Table 1). The METs were conducted at five sites representing areas where sorghum is predominantly grown in Zimbabwe (Table 2), during the 2018–2019 rainy seasons.

Experimental layout and agronomic management

The 20 sorghum genotypes (17 experimental lines + 3 checks) were laid out at all the five locations using an alpha (0.1) lattice design with three replications. Each replication accommodated a total of four incomplete blocks of size five. A gross plot size of 11.25 m^2 was used (i.e. 4 rows of 5 m length), with an inter row spacing of 75 cm and an intra-row spacing of 20 cm.

Land was disc ploughed and a disc harrow was used to make a fine tilth. A tractor drawn row marker was used to mark the row at spacing of 75 cm. Compound D (8% N: 14% P_2O_5 : 7% K_2O) was applied as basal fertilizer at a rate of 75 kg/ha. Basal fertilizer was banded into the furrows before planting. A seeding rate of 8 kg/ha was used with the seed being drilled along the furrows. The crop stand was thinned 15 days after emergence (DAE) to achieve an intra-row spacing of 20 cm. Top dressing with Black Urea (36% N) was done, 30 DAE at a rate of 50 kg/ha. A mixture of Super dash dash (Emamectin benzoate 20 g/l + Acetaprimid 50 g/l), Ampligo 150EC (Lambda cyhalothrin 15 g/l) and Lambda at a rate 20 ml/knapsack was used to control fall armyworm, while thionex granules were applied for stalk borer control, five weeks after crop emergence.

A net plot of 4 m by 2 rows was used with 0.5 m being left out at either ends along the 5 m plot and two outer rows

Table 1 Description of the planting materials evaluated at four locations during the 2018–2019 rainy seasons in Zimbabwe

Code	Genotype	Description	Origin	Treatment type
G6	NL 2022	Grain cultivar	Zimbabwe	Experimental line
G15	NL2033	Grain cultivar	Zimbabwe	Experimental line
G13	NL9966	Grain cultivar	Zimbabwe	Experimental line
G11	NL9834	Grain cultivar	Zimbabwe	Experimental line
G17	NL2008	Grain cultivar	Zimbabwe	Experimental line
G7	SV-4	Released Variety	Zimbabwe	Check
G1	SV-2	Released Variety	Zimbabwe	Check
G9	NL9932	Grain cultivar	Zimbabwe	Experimental line
G12	NL312	Grain cultivar	Zimbabwe	Experimental line
G5	NL2045	Grain cultivar	Zimbabwe	Experimental line
G14	SDSL90004	Grain cultivar	Zimbabwe	Experimental line
G18	NL2014	Grain cultivar	Zimbabwe	Experimental line
G16	NL2007	Grain cultivar	Zimbabwe	Experimental line
G3	NL9948	Grain cultivar	Zimbabwe	Experimental line
G19	NL2041	Grain cultivar	Zimbabwe	Experimental line
G4	NL2034	Grain cultivar	Zimbabwe	Experimental line
G2	NL9847	Released variety	Zimbabwe	Experimental line
G20	NL2044	Grain cultivar	Zimbabwe	Experimental line
G8	Chimupositori	Land race collected	Zimbabwe	Check
G10	NL2040	Grain cultivar	Zimbabwe	Experimental line

Table 2 Description of testing sites used to evaluate experimental sorghum lines during the 2018–2019 rainy season in Zimbabwe

Site code	Testing site	NR	Altitude	Soil type	Average rainfall (mm)	Geographic location	
						Latitude	Longitude
Env1	Gwebi VTC	Ila	1448	Red clay	> 1000	17° 41' S	30° 32' E
Env2	Kadoma	Iib	1149	Red clay	700–1000	18° 19' S	29° 53' E
Env3	Matopos	IV	1338	Black clay	550–750	20° 23' S	28° 30' E
Env4	Makoholi	IV	1204	DAS	450–650	19° 50' S	30° 47' E
Env5	Chisumbanje	V	421	Basalt	< 500	20° 48' S	32° 14' E

being left out on either side of the plot. The net plot area was used for record taking and yield component analysis.

Data collection and statistical analysis

Plant characteristics recorded were: days to 50% flowering (DMA), days to physiological maturity (DPM), plant height (PHT), exertion (EXTN), number of fully extended leaves (NL), stem diameter (SD), panicle length (PL), panicle width (PW), sugar content (SC), grain yield (GYD) and fodder yield (FYD) (see Table 3).

Gathered MET data were subjected to across site analysis of variance (ANOVA) using Genstat Software, 17th Edition (Payne et al. 2009). Means for the agronomic traits were compared using the Tukey's HSD tests, using the '*HSD.test*' function in the agricolae R package (De Mendiburu and Simon 2015). Genotypic and environmental variance as well as the broad-sense heritability estimates was predicted in the Multi Environment Trial Analysis with R (META-R) software v2.1 (Alvarado et al. 2015). The phenotypic coefficients of variation (PCV) and the genotypic coefficient of variation (GCV) estimates were obtained using formulas coined by Alvarado et al. (2015). Genetic advance as well as the expected genetic gain was calculated following procedures in Alvarado et al. (2015). To identify traits correlated to each other, a heat map with a dendrogram was graphed using the '*heatmap.2*' function in the gplots R package (Warnes et al. 2009). In brief, dissimilarity matrices between yield as well as the other agronomic traits were calculated using the 'Manhattan' method (Payne et al. 2009), while clustering of the correlated traits was done based on the 'Ward.D' method (Ward Jr 1963). GT associations were performed following procedures in Payne et al. (2009) using the Genstat Software. This was done using trait means (see Table 5) computed from each environment. The genotype–genotype \times environments (GGE) biplot model, based on singular value decomposition was used to determine GT associations. Two types of graphs were created to achieve two objectives. Firstly, to identify traits closely associated with GYD in sorghum, the 'vector view' of the GT biplot was plotted. On this plot, traits that are closely associated are those where the angle between the vectors of two traits is smaller than 90° indicating a positive correlation, an angle greater than 90° indicates a negative correlation, whereas an angle of 90°

Table 3 List of sorghum plant characteristics recorded during the 2018–2019 rainy season in Zimbabwe

Variable	Abbreviation and unit of measurement	Description
Days to 50% flowering	DMA (days)	Number of days from planting until half of the plants has started blooming (show exerted stigmas)
Days to physiological maturity:	PHT (days)	Number of days from planting until a black layer has been formed above the hilar region of the seed
Plant height	PHT (cm)	The length between the lap and the apex of the panicle measured at physiological maturity
Exertion	EXTN (cm)	The distance from the flag leaf to the base of the head (panicle)
Number of fully extended leaves	NL (counts)	Number of fully extended leaves per plant record as an average of 10 plants per plot
Stem diameter	SD (cm)	Measure the diameter of the plant stem recorded
Panicle length	PL(cm)	Measure the panicle/head length from the base of the panicle to the tip
Panicle width	PW(cm)	Measure the diameter of the panicle
Sugar content	SC (%)	Measured using the brix meter by putting a drop of juice squeezed from the plant and taking a reading
Grain yield	GYD (kg)	After threshing and adequate drying, grain weight (GW) per net plot was recorded (i.e. in grams) and was converted into kilograms per hectare as follows: Kg/ha = [(Area per ha/Net plot area)*GW per plot]/1000]
Fodder yield	FYD (g)	Mass of dry plant material (g) at harvesting (i.e. fodder weight; FW) and was converted into kilograms per hectare as follows: FYD = [(Area per ha/gross plot area)*FW per plot]/1000]

indicates zero correlation. The angle between a genotype and a trait indicates the relative level of performance of the genotype for the trait. Thus, an acute angle indicates that the genotype is above-average for the trait; an obtuse angle indicates that the genotype is below-average for the trait; and a right angle indicates that the genotype is average for the trait. The distance to the biplot origin (i.e. vector length) of a trait indicates how well the trait is represented in the biplot, while a relatively short vector indicates that the variation of the trait across genotypes is either small or not well presented in the biplot, which is due to its weak or lack of correlation with other traits. The vector length of a genotype indicates whether it is intermediate for all traits or has clear strengths and/or weaknesses in its trait profile. And lastly, to identify key traits for breeding as well as genotypes harbouring the traits, the ‘ideal tester view’ of the GT biplot was plotted. Here, key traits are those with the most recognition and representation capabilities among other traits and are located closer to the ideal tester of traits represented by the innermost concentric circle, while genotypes harbouring these important traits are those with the highest mean performance across traits [i.e. longest projection onto the average tester axis (ATC abscissa) and shortest entry-vector], therefore it should be close to the ideal genotype represented by the innermost concentric circle with an arrow pointing to it (Payne et al. 2009).

Results

Performance of experimental sorghum lines across arid and semi-arid conditions

Significant genotypic effects were observed on GYD performance as well as on the other agronomic traits, including DPM, PL and SD. Additionally, significant genotype \times environment interaction (GEI) effects on most of the measured traits, GYD included, were also observed. Genotype variance was more important than environmental variance for most of the traits, including GYD, SC, NL, PW, PL, PHT, DPM and DMA, except for EXTN and SD ($p < 0.05$, Table 4). Broad-sense heritability (H^2) was also very high (i.e. $H^2 > 50\%$) for most of the traits, with the exception of EXTN and SD, that showed H^2 values below 50%. Moderate genetic advance of 10.9% was exhibited on DPM, NL, and SD. Low genetic advance (i.e. 7.1%) was observed for DMA (Table 4).

The highest yielding experimental genotypes were identified as NL2007 (3551 kg ha⁻¹), NL9834 (3501 kg ha⁻¹), NL2014 (3251 kg ha⁻¹) and NL2041 (3261 kg ha⁻¹). Mean GYD performance of these sorghum lines significantly differed with one of the check cultivars SV-2 (i.e. GYD = 1585 kg ha⁻¹) and SV-4 (i.e. GYD = 1632 kg ha⁻¹) ($p < 0.05$; Table 5). Although the experimental genotype, NL2007 was high in GYD, it was significantly shorter (i.e. PHT = 134.29 cm) than one of the check cultivars, i.e. SV-2 (162.79 cm). These genotypes also have good

Table 4 Across site analysis of variance (ANOVA) of the experimental sorghum lines evaluated under the arid and semi-arid conditions of Zimbabwe during the 2018–2019 cropping season

Source of variation	DMA	DPM	EXTN	PHT	PL	PW	NL	SD	SC	GYD	FYD
Site	5625.15**	9111.36**	1100.908**	12,052**	98.421**	53.358**	162.9753**	54.5742**	17.936*	61,128,636**	2,668,086,645***
Replication (site)	11.20	118.46	5.579	239.9	3.692	1.040	0.8614	0.00901	3.861	921,591*	463,830,092***
Block (replication × site)	30.48**	158.21**	21.183**	854.5**	19,009**	6.113**	2.1663**	0.08636*	14.541**	1,112,743**	37,817,764***
Genotype	46.79**	246.68**	76.105**	1677**	72,415**	12.713**	7.7154**	0.56249**	132.752**	5,748,039**	525,151,541***
Genotype × site	43.84**	275.01**	55.404**	647.2**	36.16**	7.640**	0.1382	0.02099	3.411	2,530,282**	13,311,719
Residuals	101.11	275.98	39.842	725.4	22,455	5.478	3.5223	0.81206	14.670	2,260,213	10,224,833
Phenotypic variance	18.78	94.77	8.48	456.5	7.2	2.17	0.88	0.09	5.15	531,405	9,231,541
Genotypic variance	10.02	56.83	3.94	329.7	5.49	1.41	0.63	0.04	3.44	332,279	2,591,442
Environmental variance	8.76	37.94	4.54	126.8	1.71	0.76	0.25	0.05	1.71	199,126	6,640,099
PCV (%)	6.48	8.88	40.43	15.8	13.62	20.74	7.39	12.1	17.73	30.04	48.20
GCV (%)	4.73	6.88	27.57	13.43	11.89	16.72	6.25	8	14.49	23.75	25.54
Broad-sense heritability (%)	53.34	59.97	46.49	72.22	76.27	65.01	71.59	43.72	66.78	62.53	28.07
GAM (%)	7.12	10.97	38.72	23.51	21.4	27.78	10.89	10.9	24.39	38.69	27.87
Grand mean	66.9	109.6	7.2	135.2	19.7	7.1	12.7	2.5	12.8	2427	6304
Minimum	36	18	0	79.5	9	3	8.3	0.8	0.8	153.3	1167
Maximum	89	140	30	317	31.3	18.3	16.9	4.7	23.04	7465	11,687
SEm (±)	0.581	0.959	0.365	1.558	0.274	0.135	0.108	0.052	0.221	86.8	363

DMA days to 50% flowering, *DPM* days to physiological maturity, *EXTN* exertion, *PHT* plant height in centimetres, *PL* panicle length in centimetres, *PW* panicle diameter in centimetres, *NL* number of leaves, *SD* stem diameter in centimetres, *SC* sugar content in grams, *GYD* grain yield in kilograms per hectare, *PCV* phenotypic coefficient of variation, *GCV* genotypic coefficient of variation, *SEM* standard error of mean, *GAM* genetic advance as percent of mean

*, **Significant at 0.05 and 0.01 probability levels, respectively

Table 5 Across site means of agronomic traits measured in experimental sorghum lines evaluated under arid and semi-arid conditions during the 2018–2019 rainy season in Zimbabwe

Genotype	Type	DMA	DPM	EXTN	PHT	PL	PW	GYD (kg ha ⁻¹)	FYD (kg ha ⁻¹)	NL	SD	SC
Chimupositori	L. race	62 ^a	104 ^a	10.3 ^{gh}	158.0 ^{hi}	15.7 ^a	4.6 ^a	1232 ^a	7525 ^{ab}	12.6 ^{bc}	2.3 ^{ab}	13 ^{cde}
NL2007	E. line	66 ^{bcdefg}	113 ^{bcd}	4.1 ^{ab}	140.1 ^{efg}	16.1 ^a	7.4 ^{bcdef}	3551 ^h	20928 ^h	12.6 ^{bc}	2.5 ^{cde}	7.7 ^a
NL2008	E. line	69 ^{gh}	119 ^d	5.7 ^{bcdef}	141.3 ^{efg}	24.3 ^f	7.3 ^{bcdef}	2662 ^{ef}	8701 ^{ab}	12.6 ^{bc}	2.4 ^{bc}	15.7 ^f
NL2014	E. line	66 ^{bcdefg}	113 ^{bcd}	7 ^{ef}	142.5 ^{fg}	20.3 ^d	7.7 ^{bcdefg}	3251 ^{gh}	16523 ^{efg}	13.3 ^{cd}	2.6 ^{defgh}	11.1 ^b
NL2022	E. line	69 ^{efgh}	108 ^{abc}	5.7 ^{bcdef}	125.6 ^{abcde}	20.8 ^{de}	8.7 ^g	2788 ^{efg}	7002 ^a	13.3 ^{cd}	2.3 ^{bc}	11.8 ^{bcd}
NL2033	E. line	69 ^{efgh}	113 ^{bcd}	4.3 ^{abc}	147.2 ^{gh}	20.7 ^d	8.2 ^{fg}	2780 ^{efg}	11461 ^{cd}	12.2 ^b	2.6 ^{defgh}	12.4 ^{bcd}
NL2034	E. line	68 ^{cdefgh}	110 ^{abc}	7 ^{def}	120 ^{ab}	17.5 ^{ab}	6.7 ^{bc}	2706 ^{efg}	16737 ^{fg}	12.9 ^{bcd}	2.4 ^{bc}	11.5 ^{bcd}
NL2040	E. line	66 ^{bcdefg}	108 ^{abc}	6.2 ^{cdef}	130.3 ^{abcdef}	17.9 ^{ab}	6.9 ^{bcde}	1748 ^{abc}	17901 ^g	12.5 ^{bc}	2.6 ^{defgh}	22.6 ^g
NL2041	E. line	70 ^h	115 ^{cd}	7.7 ^f	140.4 ^{efg}	19.4 ^{bcd}	6.4 ^b	3261 ^{gh}	14364 ^{ef}	10.9 ^a	2.1 ^a	8.1 ^a
NL2044	E. line	70 ^h	112 ^{bcd}	7 ^{ef}	134.3 ^{bcdefg}	21.4 ^{de}	8.0 ^{defg}	2060 ^{bcd}	23272 ^h	12.3 ^b	3 ⁱ	11.2 ^{bc}
NL2045	E. line	66 ^{bcdefg}	104 ^a	5 ^{abcd}	121.9 ^{abc}	18 ^{abc}	6.2 ^b	2898 ^{fg}	25919 ⁱ	13.5 ^d	2.5 ^{cdefg}	15.2 ^f
NL312	E. line	67 ^{bcdefgh}	107 ^{abc}	7.6 ^f	137.6 ^{defg}	23 ^{ef}	6.7 ^{bc}	1962 ^{bcd}	15051 ^{ef}	12.9 ^{bcd}	2.5 ^{cdef}	14.1 ^{ef}
NL9834	E. line	68 ^{cdefgh}	113 ^{bcd}	10.2 ^{gh}	142.6 ^{fg}	20.4 ^{cd}	6.7 ^{bc}	3501 ^h	16871 ^{fg}	13.6 ^d	2.7 ^h	11.5 ^{bcd}
NL9847	E. line	65.1 ^{abc}	103 ^a	11.8 ^h	126.2 ^{abcde}	19.1 ^{bcd}	7.1 ^{bcdef}	2278 ^{cde}	7620 ^{ab}	14.3 ^e	2.7 ^{egh}	15.2 ^f
NL9932	E. line	67 ^{bcdefgh}	109 ^{abc}	6.6 ^{def}	118.2 ^a	20.4 ^d	8.1 ^{efg}	2305 ^{cde}	10109 ^{bc}	12.9 ^{bcd}	2.5 ^{cdefg}	11.7 ^{bcd}
NL9948	E. line	65 ^{abcde}	110 ^{abc}	6.5 ^{def}	124.1 ^{abcd}	17.8 ^{ab}	6.4 ^b	1849 ^{bc}	8723 ^{ab}	12.3 ^b	2.8 ^h	15.5 ^f
NL9966	E. line	66 ^{bcdef}	103 ^a	3.4 ^a	136.6 ^{cdefg}	19.2 ^{bcd}	6.9 ^{bcd}	2450 ^{def}	14855 ^{ef}	12.9 ^{bcd}	2.3 ^{ab}	13.24 ^{de}
SDSL90004	E. line	65 ^{abcd}	106 ^{ab}	12 ^h	134.4 ^{bcdefg}	23.8 ^f	6.2 ^b	2038 ^{bcd}	13857 ^{de}	12.6 ^{bc}	2.6 ^{defgh}	13.2 ^{de}
SV-2	Check	64 ^{ab}	110 ^{abc}	9.7 ^g	162.8 ⁱ	17.8 ^{ab}	7.3 ^{bcdef}	1685 ^{ab}	8051 ^{ab}	10.5 ^a	2.4 ^{bc}	9.3 ^a
SV-4	Check	69 ^{defgh}	114 ^{bcd}	5.5 ^{bcde}	131.1 ^{abcdef}	20.6 ^d	8.5 ^g	1535 ^{ab}	8572 ^{ab}	13.2 ^{cd}	2.5 ^{cd}	12.1 ^{bcd}
Grand mean	–	66.9	109.6	7.2	135.2	19.7	7.1	2427	13,702	12.7	2.5	12.8
SEm (±)	–	2.2	5.3	5.3	10.5	1.6	0.8	407.4	1994	0.6	0.1	1.3
LSD	–	6.3	14.8	3.9	29.3	4.6	2.3	1136.1	5560.9	1.5	0.4	3.6
CV	–	5.8	8.4	34	13.4	14.6	20.5	29.1	25.2	7.5	9.2	17.7
P	–	***	***	***	***	***	***	***	***	***	***	***

The trait abbreviations are: *E. Line* experimental line, *L. race* land race, *DMA* days to 50% flowering, *DPM* days to physiological maturity, *ESN* exertion, *PHT* plant height, *PW* panicle width, *PL* panicle length, *SD* stem diameter, *SC* sugar content, *FW* fodder yield, *GYD* grain yield. *F-pr* significance level, *LSD* least significant differences, *CV%* coefficient of variation, *SE* standard error of means, ***significant at <0.001, **significant at <0.01, *significantly at <0.05, *NS* not significant, NB: The Grand mean, F-pr, LSD and CV% values displayed above are means across five sites. Differences in mean performance of two or more genotypes for a particular trait like grain yield (GYD) are considered as statistically significant ($p < 0.05$) if they do not share a similar letter (e.g., letter a or b). Mean separations were done using Tukey HSD test

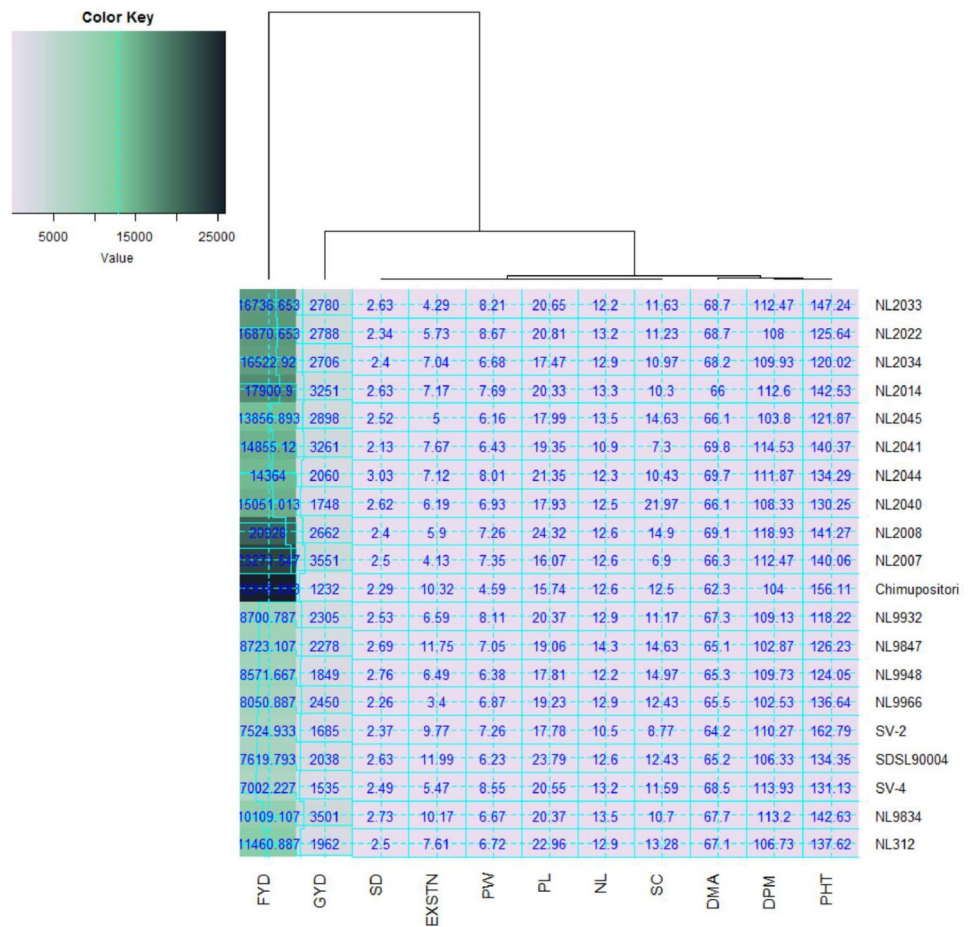
agronomic attributes like early maturity, strong stalk (high values for stem diameter) to resist lodging and large panicle (high values for panicle length and width) and high fodder yield. NL2041, NL2044 and NL2008, observed as the highest yielders all significantly matured within the same range (110 = 115 days) with the check genotypes with the check SV-2 maturing earlier (i.e. DMP = 110 days) than all other genotypes. Number of leaves seemed to have a very strong effect on GYD performance as the highest yielders (i.e. NL2041, NL9834 and NL2007) had significantly more leaves than the least yielding genotypes such as Chimupositori (a landrace). The trait, SD, did not show strong relationship with GYD as some of the highest yielders (e.g. NL2014) showed the least SD whereas the other highest yielder, NL2014, had the highest SD. This

trend was also similar between GYD with other traits (i.e. SC, PL and PW) (Tables 5, S1). These results corroborated with trends observed on the heat map (Fig. 1), where correlations were shown between GYD and traits, including; SD, EXSTN, PW, PL and NL. No correlations were observed between GYD and the other measured traits such as SC, and PHT (Fig. 1).

Traits associated with grain yield in sorghum

To visualise traits associated with GYD, the ‘vector view’ of the GT biplot was used and it showed interesting results (Fig. 2). Traits closely associated with GYD were identified as NL, SD, PL, PW, SD and DMA, whereas those not associated with GYD were: SC, EXTN and PHT. The experimental genotypes with superior performance for

Fig. 1 A heat map showing correlations between agronomic traits of sorghum with the grain best performing genotypes for each trait measured in the experiment. Dissimilarities between the sites as well as the agronomic traits were calculated using the Manhattan method, while clustering was done based on the Ward method. *DMA* days to 50% flowering, *DPM* days to physiological maturity, *EXTN* exertion, *PHT* plant height in centimetres, *PL* panicle length in centimetres, *PW* panicle diameter in centimetres, *NL* number of leaves, *SD* stem diameter in centimetres, *SC* sugar content in grams, *GYD* grain yield in kilograms per hectare



GYD as well as its associated traits were noted as G20 (NL2044), G19 (NL2041) and G17 (NL2008). Genotypes ideal for the other traits not associated with GYD were also identified. For instance, G8 (Chimupositori, a check cultivar) was the best for EXTN, whereas G2 (NL9847) and G5 (NL2045), showed the highest SC. The tallest genotype was noted as G1 (SV-2) and this was used as a check variety (Fig. 2).

Key traits for selection in a sorghum breeding program

For identification of key traits for use in a sorghum breeding program, the ‘ideal tester view’ of the GT biplot further showcased important results (Fig. 3). It was interesting to note that GYD, together with other agronomic traits such as DPM, DMA, PW, PL, SD and SC, seemed to be the most important traits in sorghum breeding programs. The experimental genotype with superior performance for a combination of these traits was shown to be G20 (NL2044; GYD = 2060 kg ha^{-1}), but other experimental sorghum genotypes, for example, G6 (NL2022; GYD = 2788 kg ha^{-1})

and G9 (NL9932; GYD = 2305 kg ha^{-1}), as well as, a check genotype identified as G7 (SV-4; GYD = 1535 kg ha^{-1}), also proved their prowess for these important traits across the arid and semi-arid environments of Zimbabwe (Fig. 3). On the other hand, the check genotypes, G1 (SV-2; GYD = 1685 kg ha^{-1}) and G8 (Chimupositori; GYD = 1232 kg ha^{-1}) were observed as the weakest genotypes for GYD, together with all the other traits associated with it (Fig. 3; Tables 5, S1).

Discussion

Undesirable associations among traits complicate selection decisions in plant breeding programs (Yan and Fréreau-Reid 2008; Michel et al. 2019). As for sorghum, an important crop for the arid and semi-arid regions of the world (Murungweni et al. 2016; Zhao et al. 2019), limited information is available on its trait relations and profiles, yet this information is vital for precise decisions to be undertaken in its breeding programs. To assess GT associations of this important crop, we evaluated 17 sorghum experimental lines, planted

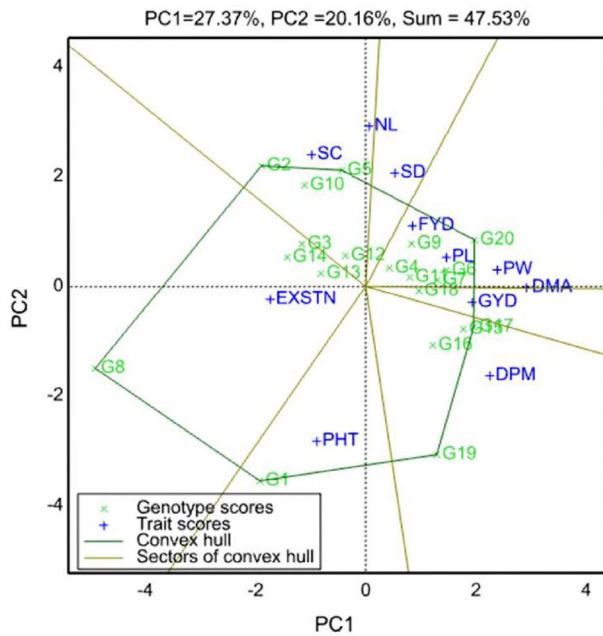


Fig. 2 Polygon view of the Sorghum genotype-by-trait biplot, showing which cultivar had the highest values for which traits. Names of genotypes are presented in Table 2. *DMA* days to 50% flowering, *DPM* days to physiological maturity, *EXTN* exertion, *PHT* plant height in centimetres, *PL* panicle length in centimetres, *PW* panicle diameter in centimetres, *NL* number of leaves, *SD* stem diameter in centimeters, *SC* sugar content in grams, *GYD* grain yield in kilograms per hectare

together with three checks at five, arid and semi-arid locations in Zimbabwe. Results revealed the genetic variation that exists in sorghum germplasm available in Zimbabwe and also identified the experimental sorghum lines strong for some specific agronomic traits, solely or in combination with others, as well as traits that can indirectly be used to select for *GYD* performance.

To start with, it is common knowledge in breeding cycles that the effectiveness of selection mainly depends upon the extent of genetic variability present in the plant population (Holme et al. 2019; Bhandari et al. 2017). The present study showed wide genetic variability among the tested sorghum genotypes for the several agronomic traits measured, including *GYD* and *FYD* (Table 4), indicating chances of making effective selections for improvement of sorghum in Zimbabwe. As reported by Ezzat et al. 2010), results revealed significant GEI effects for the different agronomic traits measured on the experimental sorghum lines. Quantification of GEI effects is usually practiced by plant breeders to determine an effective strategy for selecting genotypes suitable to target environments (Nowosad et al. 2016).

Apart from quantification of GEI, genotype selections can also be efficiently done using broad-sense heritability (H^2), combined with genetic advance estimates of the measured

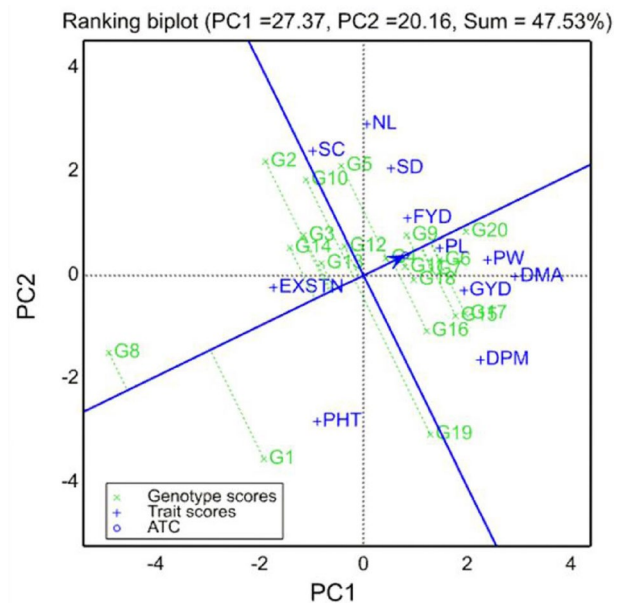


Fig. 3 An entry/tester genotype \times trait biplot of 11 measured traits of sorghum genotypes evaluated, ranking cultivars in order of their trait performance. Names of genotypes are presented in Table 2. *DMA* days to 50% flowering, *DPM* days to physiological maturity, *EXTN* exertion, *PHT* plant height in centimetres, *PL* panicle length in centimetres, *PW* panicle diameter in centimeters, *NL* number of leaves, *SD* stem diameter in centimeters, *SC* sugar content in grams, *GYD* grain yield in kilograms per hectare

traits (Annicchiarico et al. 2010). Results indicated high H^2 estimates for *PHT*, *PL*, *PW*, *NL*, *SC* and *GYD*. A study by Ali et al. (2012), also reported high estimates of heritability in broad sense for *PHT* and *GYD* in sorghum. The low H^2 estimates observed for traits including, *DPM*, *EXSTN* and *SD*, exhibits predominance of additive and non-additive gene action in controlling these traits (Vagadiya et al. 2013), therefore direct selection for these traits is not rewarding. Since high H^2 estimates does not always guarantee high genetic gain from selection, heritability should be considered, but combined with genetic advance in predicting selection for superior genotypes (Patil and Lokesha 2018). According to Ubi et al. (2001), a combination of high H^2 estimates, coupled with high genetic advance as shown for traits such as, *PL*, *PW*, *SC* and *GYD*, are desirable. Accordingly, the presence of high estimates for *GCV*, H^2 and genetic advance, as percent of mean for *GYD*, shown in this study, depicts presence of additive gene action in governing the expression of this trait, therefore high genetic gain can be expected through selection for this important trait in sorghum. To add on this point, high H^2 , genetic advance and *GCV* estimates, proposes less influence of environmental variance in the inheritance of traits, hence characters exhibiting this phenomenon can be improved by means of simple selection. Contrary, moderate H^2 estimates with

low/moderate GAM, as observed for traits such as; DPM, EXSTN and SD, points out to non-additive gene action for these traits (Chikuta et al. 2017). According to Shegro et al. (2013), high H^2 estimates are not always coupled with high genetic advance, and this claim is also supported by the current findings. Traits exhibiting this phenomenon cannot be improved through selection; heterosis breeding can be a viable option.

In plant breeding, breeders have traditionally made it a habit to identify traits that are correlated to the trait(s) of economic importance, and for crops like sorghum, yield is of economic significance. In the current study, traits correlated with yield were identified as SD, EXSTN, PW, PL and NL (Fig. 1), suggesting that yield improvement of sorghum can be indirectly achieved through improving these traits (Alam et al. 2001). With a perspective to managing selection criteria to breed new sorghum varieties for high yield, our study adds to an understanding of the associations between yield and other agronomic traits. A previous study (see Jimmy et al. 2017) reported correlations between GYD with traits such as; PW, panicle weight and 100 seed mass and these findings (particularly, on PW) corroborate with our results.

The GT biplots also showed interesting trends (Figs. 2, 3). For instance, correlations noted between GYD and DMA, and also with DPM (Fig. 2), was not surprising since it is widely accepted that cereal crop varieties that take long days to flower matures late and are usually high yielding compared to the short seasoned types (Oluwaranti et al. 2008). On the other hand, negative correlations between GYD and traits such as SC and EXSTN may posit that these traits cannot be used to indirectly select for yield. An ideal tester of a trait is regarded as the one that combines various desirable traits in its genetic constitution (Sharifi and Ebadi 2018). Using the ideal tester view of the GT biplot (Fig. 3), our results revealed that traits including; GYD, PL, PW and DMA are the most important in sorghum breeding programs. This implies that, a concomitant of these traits can be used as selection indices when selecting for yield in sorghum.

Finally, it was delightful to note that some sorghum lines can be recommended for dual purposes. For instance, G2, G5 and G10 showed both, high GYD potential as well as high SC (i.e. a trait associated with high fodder quality) (Fulgueira et al. 2007; Schmidt et al. 1997), therefore these lines can be used in crossing programs for development of dual-purpose cultivars (i.e. for food and feed). Similar results were reported by Sharifi and Ebadi (2018).

In conclusion, results exposed the wide genetic variation that exists in sorghum germplasm in Zimbabwe, highlighting opportunities for its improvement. Furthermore, the key traits which can be considered singularly or in combination, when selecting for sorghum genotypes suitable, either for

feed or food purposes, under arid and semi-arid conditions were also identified. These details are vital for crafting of an efficient sorghum breeding program.

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Compliance with ethical standards

Conflict of interest The authors declare no conflict of interest.

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