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Genotypes selection of *Sorghum bicolor* L. based on interrelationship of quantitative traits using Genotype×Traits and Genotype by Yield×Traits biplot

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Abstract

Sorghum is one of the most important crops grown for human diet and bio-energy. An understanding of genotypes efficiency by evaluating multivariate methods like genotype by traits (GT) and genotype by yield×trait (GYT) biplot is essential to detect suitable genotypes of sorghum. Therefore, traits interrelationship of eighteen sorghum genotypes were investigated based on a randomized complete block design with three replications during 2016-2017. The data of various characters were subjected to ANOVA, Pearson correlation, the GT and the GYT biplot analysis via SAS and GGE biplot software. The analysis of variance depicted that there were significant differences among Genetype×Year interaction based on evaluated variables ($P>0.01$). The evaluation of traits and their association by GT and GYT biplot indicated that there were significant ($P>0.001$) differences among traits and yield-trait combination which was strongly approved by numerical Pearson correlation. Also, the GT biplot indicated that the best-ranked genotypes included G4>G15>G6>G17>G18>G16>G13>G3 and the GYT biplot superiority-ranked genotypes comprised of G4>G6>G17>G3>G15>G10>G2>G7>G11. Both the GT and GYT biplot confirmed that FGCSI04 (G4) was the most suitable and ideal genotype strongly suitable to sorghum production according to prominent performances on plant height, panicle length, panicle width, grain yield and biological yield. This genotype evaluation showed that there were existed a high genetic diversity among genotypes for the studied variables in which GT and GYT approach simultaneously can help breeders to select prominent genotypes and reduce genetic load in the breeding programs.

Key words: Breeding program, Genotype by traits biplot, Genotype by yield trait biplot, Grain yield, Sorghum genotypes.

INTRODUCTION

Sorghum [*Sorghum bicolor* (L.) Moench] is one of the most significant cereal crops in the world (Gebeyehu *et al.*, 2019). It is compatible to a wide magnitude of agro-ecological conditions such as drought-prone semi-arid tropical regions and the adverse environmental conditions (Prakash *et al.*, 2010), and is grown approximately in an area of 40 million hectares with the average grain productivity of 1400 kg. ha^{-1} (FAOSTAT, 2019). Its grains contain 12% protein, 3% fat , and 70% carbohydrates (Hussain *et al.*, 2011; Kaplan *et al.*, 2017; Kaplan, 2019). Therefore, it is widely used as a source of nutrition, fodder, biofuel, fiber, and confection. It is also a good resource for human and animal feeding (Abubakar and Bubuche, 2013; Awan *et al.*, 2015; Kaplan *et al.*, 2017; Gebeyehu *et al.*, 2019). Although it is a much-appreciated cereal, there have not been efficient breeding programs specifically regarding its hybrid production in Iran. Plant breeding is very important to humankind's survival and therefore, genotype evaluation to determine the most suitable cultivars, is an important key part of this process. For the identification of superior genotypes, emphasizing genotypes, environment and traits as well as their association are three vital challenges (Kaplan, 2019; Yan and Frégeau-reid, 2018; Yan and Kang, 2002). To improve sorghum genetically, one needs to know about the nature of its growth and yield related traits (Awan *et al.*, 2015). Some data analysis procedures allow studying analysis of variance, mean comparisons, and correlation coefficients among traits (Abraha *et al.*, 2015; Salihu *et al.*, 2018). The univariate analysis (such as Pearson correlation analysis) depicts relationship between two characters (Paramesh *et al.*, 2016; Abdalla, 2018; Yan and Frégeau-reid, 2018). Meanwhile, multivariate methods (including multiple regression, path coefficient analysis, cluster analysis, genotype by traits and genotype by yield×traits biplot, etc.) have many advantages in evaluating all variables at the same time to clarify the obtained information. Therefore, they have been applied in different experiments (Jobson, 1992; Atnaf *et al.*, 2017; Farid *et al.*, 2017; Gravina *et al.*, 2018; Yan and Frégeau-reid, 2018). Genotypes by traits (GT biplot) (Kaplan *et al.*, 2017; Gravina *et al.*, 2018; Kaplan, 2019) and genotype by yield×traits (GYT biplot) (Yan and Frégeau-reid, 2018) biplot analyses, are two of the best multivariate approaches applied to tackle off the genotypes evaluation challenges. They are based on various variables to recognize superior parents with desirable traits, in which they may be used as potential commercial cultivars or as parents in a breeding program. Furthermore, these analyses can not only graphically visualize the traits and genotypes correlations, but also they can detect the best and the worst traits for the indirect selection of genotype, based on traits of interest (Mohammadi and Amiry, 2013). In light of multivariate approaches specifically GT and GYT biplot, this experiment aimed to evaluate the best genotypes based on interested traits, to select them to be used as parents in a breeding program.

MATERIALS AND METHODS

Experimental methods

For evaluating sorghum genotypes, an experiment was conducted in two successive years (2016-17) at Gorgan Agricultural and Natural Research Station (Table 1). The experimental plant materials comprising of 18 sorghum genotypes had been released from different centers in France and Iran (Table 2). This research was carried out as a Randomized Complete Block Design (RCBD) with three replications in 2017-18 cropping season. The soil was twice cross-plowed up to the 30 cm depth and leveled to perform uniform irrigation. According to soil test recommendations, nutrients such as phosphorus (300 kg. ha^{-1}), urea (300 kg. ha^{-1}) and potassium (300 kg. ha^{-1}) were applied during the soil preparation stage. Each experimental plot included four rows, each with 6 m in length, 60 cm row spacing and 15 cm spacing between plants. Seeds were sown on the 1st June at the rate of 14 kg.ha^{-1} as per the recommendation for sorghum planting. Thinning was done three weeks after seedling emergence to adjust plant density. It is noteworthy that one-third of total amount of urea was added at the sowing time, another one was added when plants reached 30 cm in height, and the remaining urea was added before the flowering stage. The weeds were controlled by hand weeding during the growing period. Generally, the agronomical practices including sowing method, irrigation, nutrient, weed management, etc.

Table 1. Agro-ecological properties of the experimental location.

Location	Geography			Climate			Soil properties			
	Altitude (m.a.s.l)	Latitude	Longitude	Ave. Rain Fall (mm)	Ave. Tem. (^{o}C)		Depth (cm)	pH	EC (dS m^{-1})	Soil texture
					Max.	Min.				
Gorgan Agricultural and Natural Research Station	5.5	36° 54´ N	54° 25´ N	468	23.4	12.8	0-30	7.7	4.2	Silty clay loam
							30-60	7.6	5.1	Silty clay loam
							60-90	7.5	4.1	Silty clay loam

Source: Gorgan Agricultural and Natural Research Station.

were carried out normally and uniformly for the whole plots.

Recording data

The phenological, agronomical, yield, and yield-related traits were collected from the two middle rows and 10 randomly sampled plants based on descriptors for sorghum (ICRISAT and IBPGR, 1993) during sorghum growth. The details of the data collection are presented in Table 3.

Statistical analysis

Homogeneity of residual variances was tested prior to analysis via Bartlett's test (Bartlett, 1937). Combined analysis of variance based on a completely randomized block design for the recorded data were conducted by SAS (ver. 9.4) (SAS, 2017). Genotypes by traits data were used to visualize the association among traits and traits profile of the genotypes. The mean values were used for each genotype-trait combination across years. The GT biplot was based on the first two principal components (PC) of trait-standardized GT data resulting from "Scaling=1", "Centering=2" and "SVP (Singular Value Decomposition)=2" (Yan and

Table 2. Accession name and origin of the evaluated genotypes.

No.	Varieties	Seed Breeder/Maintainer
1	FGCSI01	ES
2	FGCSI02	ES
3	FGCSI03	ES
4	FGCSI04	ES
5	FGCSI05	ES
6	FGCSI07	ES
7	Fast green 400	NAVAJOSEEDS
8	Dravotolernet 600	NAVAJOSEEDS
9	High yield 700	NAVAJOSEEDS
10	Drought Tolerant	NAVAJOSEEDS
11	Human900	NAVAJOSEEDS
12	FS Double	NAVAJOSEEDS
13	PGS1	Pajpal
14	Payam	SPII
15	Kimia	SPII
16	Sepide	SPII
17	KGS23	SPII
18	KGS32	SPII

ES: Euralis seed company, NAVAJOSEEDS: Navajo seeds LLC company, Pajpal: Pajpal seed company, SPII: Seed and plant improvement institute.

Table 3. Description, full name and abbreviation of the investigated traits in the experiment.

No.	Traits name	Abbreviation	Description
1	Days to 50% flowering	DF	The date when 50 percent of the plants produced flowers was recorded and converted to the number of days from date of planting up to the date of heading.
2	Plant height	PH	Heights of five plants were determined from the base of the plant to the tip of the panicle in cm at physiological maturity.
3	Stem diameter	SD	Stem diameter from 10 cm above the base of 5 plants per plot in cm at maturity.
4	Panicle length	PL	Panicle length measured (cm) from the base of the panicle to the tip measured from five randomly selected plants per plot at maturity.
5	Panicle width	PW	Panicle width measured in the widest diameter of the panicle on five randomly selected plants per plot at maturity.
6	Grain feeling period	GFP	The number of days from flowering to maturity including watery ripe stage, milk stage, soft dough stage, hard dough stage and ripening stage.
7	Effective Grain feeling rate	GFR	It was estimated based on methodology described by (Pireivatlou *et al.*, 2011).
8	Thousand grain weight	TGW	A sample of 500-grain was taken randomly from five plants in two inner rows at each plot, cleaned, dried up to standard moisture level at 12.5% and then converted to 1000 grain weight.
9	Grain yield	GY	All panicles from the two inner rows in each plot were threshed, cleaned and dried up to standard moisture level at 12.5% and weighed to get grain yield per plot then converted to tons. ha^{-1}.
10	Biological yield	BY	The total plants in the two middle rows threshed and weighed to get grain yield per plot then converted to tons. ha^{-1}.
11	Harvest index	HI	The ratio of grain yield to the biological yield computed as harvest index in percent.

Frégeau-reid, 2018). SVD decomposes the GT table into genotype eigenvalues, trait eigenvalue and singular value according to Yan and Frégeau-reid, (2018). A genotype by yield×trait biplot (GYT biplot) was also another biplot procedure used to deal with independent culling and index selection obstacles (Yan and Frégeau-Reid, 2008; Xu *et al.*, 2017) in breeding programs. A GYT biplot is founded based on yield as the most important trait and other traits are important, if they are associated with high yield. Therefore, genotype ranking will be carried out according to their overall superiority across the yield trait combination in order to select the superior genotypes by their combining yield levels with other traits (Yan and Frégeau-reid, 2018). The data for genotypes by yield×traits (GYT) was obtained by multiplying the grain yield value with the traits value including stem diameter, panicle length, panicle width, thousand grain yield and harvest index (for example GY×SD). For the traits such as days to flowering, plant height, grain filling period, grain filling rate and biological yield in which the larger value means are less desirable, the yield-trait combinations data were obtained by dividing the yield value with the trait value for each genotype (e.g., GY/DF) (Yan and Frégeau-reid, 2018). GYT biplot was constructed in the same manner as constructing a GT biplot; but, the term "traits" is replaced with the term "yield-traits combination" (Yan and Frégeau-reid, 2018). Both GT and GYT biplot were established by the GGEbiplot software (Yan, 2014; Yan and Kang, 2002).

RESULTS AND DISCUSSION

Analysis of variance

When homogeneity of the error variance was approved (Figure 1), the combined analysis of variance was proceeded, revealing that genotype×year interactions had different effects on traits ($P>0.01$) (Table 4). These significant differences among evaluated genotypes revealed that there are diverse genetic variabilities for sorghum breeding programs, indicating that the evaluated traits were different in each genotype (Badu-Apraku and Akinwale, 2011; Kaplan *et al.*, 2017; Kaplan, 2019). Therefore, classification of the abovementioned genotypes is necessary (Abraha *et al.*, 2015; Woldesemayat *et al.*, 2015; Abdalla, 2018; Udoh *et al.*, 2018). Furthermore, Pearson correlation of variables depicted that traits may favorably or unfavorably be associated with each other, significantly (Table 5). Significant correlations among favorable traits facilitate improvement of two associated traits, simultaneously (Awan *et al.*, 2015).

Assessment of traits association based on GT and GYT biplot

The GT and GYT biplot analysis represented 68% and 92.4% of total variables variation among genotypes (Figure 2).

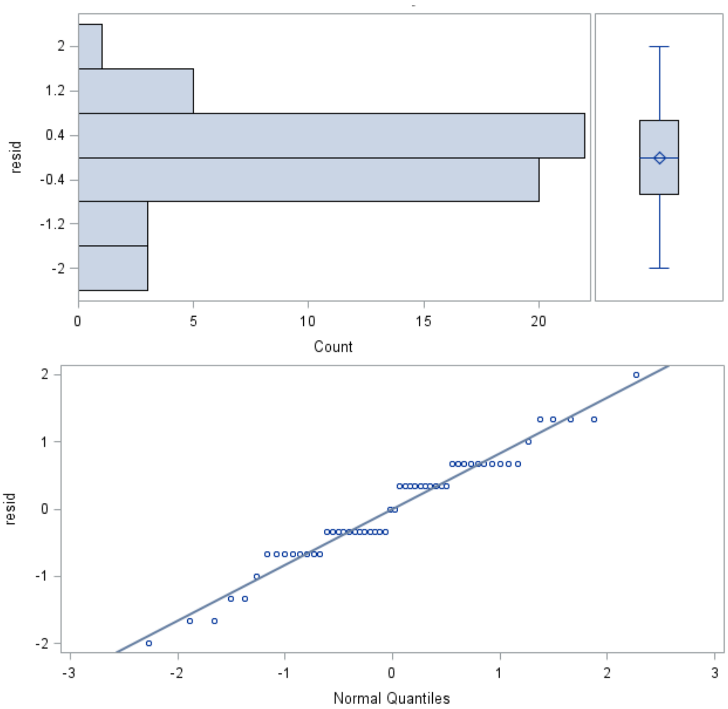

Figure 1. Normal distribution and probability plot for the residuals of the investigated variables.

Table 4. Analysis of variables variance in 18 sorghum genotypes assessed in the experiment.

Source of variation	Mean of Square											
	df	DF	PH	SD	PL	PW	GFP	GFR	TGW	GY	BY	HI
Years	1	2821.33**	2194.47^{ns}	0.08^{ns}	27.39**	4.74**	189.34*	0.07^{ns}	54.04**	54.76**	447.98**	598.36**
Error1 [Block(Year)]	2	8.08	440.86	1.45	0.24	0.33	8.92	0.04	7.75	0.16	6.18	6.67
Genotype	17	885.51**	1507.87**	12.78**	46.73**	0.74*	144.39**	0.28**	33.21**	4.14*	26.47**	270.50**
Genetype×Year	17	25.56**	529.69**	16.45**	9.82**	1.10**	20.26**	0.05**	19.84**	1.81**	13.70**	81.24**
Error (Residual)	68	4.59	104.46	4.01	2.81	0.37	3.70	0.01	4.17	0.33	2.13	14.39
Coefficient of variation (%)	-	3.49	8.06	12.77	6.83	14.15	7.69	11.70	8.34	22.41	13.71	15.45

*, ** and ^{ns}: Significant at the 5% and 1% probability levels and non-significant, respectively.

DF: Days to 50% flowering, PH: Plant height, SD: Stem diameter, PL: Panicle length, PW: Panicle width, GFP: Grain feeling period, GFR: Effective grain feeling rate, TGW: Thousand grain weight, GY: Grain yield, BY: Biological yield, HI: Harvest index.

Table 5. Pearson correlation analysis of the assessed variables in the experiment. Below the orthogonal traits correlation and above the orthogonal yield×traits combination correlation are presented.

Variables (code)		GY×GY (a)	GY/DF (b)	GY/PH (c)	GY×SD (d)	GY×PL (e)	GY×PW (f)	GY/GFP (g)	GY/GFR (h)	GY×TGW (i)	GY/BY (j)	GY×HI (k)
		1	2	3	4	5	6	7	8	9	10	11
DF (1)	a	1	0.92***	0.86***	0.90***	0.89***	0.97***	0.89***	0.84***	0.83***	0.58**	0.93***
PH (2)	b	0.61***	1	0.96***	0.90***	0.90***	0.96***	0.98***	0.75***	0.92***	0.76***	0.94***
SD (3)	c	0.32***	0.10^{ns}	1	0.92***	0.87***	0.91***	0.93***	0.77***	0.92***	0.84***	0.94***
PL (4)	d	-0.08^{ns}	0.20*	-0.03^{ns}	1	0.93***	0.92***	0.84***	0.87***	0.93***	0.68***	0.87***
PW (5)	e	-0.05^{ns}	0.23**	-0.12^{ns}	0.28**	1	0.94***	0.87***	0.83***	0.91***	0.63***	0.84***
GFP (6)	f	0.81***	0.47***	0.26***	-0.07^{ns}	-0.08^{ns}	1	0.92***	0.86***	0.90***	0.70***	0.95***
GFR (7)	g	-0.60***	-0.37***	-0.21*	0.07^{ns}	0.03^{ns}	-0.82***	1	0.65***	0.88***	0.71***	0.91***
TGW (8)	h	-0.07^{ns}	-0.14^{ns}	-0.03^{ns}	0.07^{ns}	-0.07^{ns}	-0.14^{ns}	0.62***	1	0.71***	0.58***	0.78***
GY (9)	i	-0.19^{ns}	-0.05^{ns}	-0.09^{ns}	0.21*	0.51***	-0.25**	0.15^{ns}	0.09^{ns}	1	0.74***	0.86***
BY (10)	j	0.38***	0.58***	0.12^{ns}	0.28***	0.40***	0.18^{ns}	-0.12^{ns}	0.02^{ns}	0.61***	1	0.82***
HI (11)	k	-0.51***	-0.39***	-0.20*	0.01^{ns}	0.26***	-0.42***	0.28***	0.10^{ns}	0.71***	-0.06^{ns}	1

*, **, *** and ^{ns}: Significant at the 5%, 1% 0.1% probability levels and non-significant, respectively.

DF: Days to 50% flowering, PH: Plant height, SD: Stem diameter, PL: Panicle length, PW: Panicle width, GFP: Grain feeling period, GFR: Effective grain feeling rate, TGW: Thousand grain weight, GY: Grain yield, BY: Biological yield, HI: Harvest index.

In the biplot analysis, it is proposed that the first two PCs explain more than 60% of data variation (Yang *et al.*, 2009). In this experiment, the data total variation was elucidated by the PC1 and PC2, suggesting that GT and GYT graphs efficiently showed the nature and the magnitude of data, raising a comprehensive and precise explanation of the evaluated variables. As it is clear from Figure 2, GYT biplot is more powerful in traits evaluation than GT biplot, because of its higher representation of data variations. The Pearson correlation of individual traits and yield×traits combination is depicted in Table 5. Both GT (Figure 2A) and GYT (Figure 2B) were applied to show the visualized traits correlation for assessing the association among traits and the traits profile of genotypes (Yan and Rajcan, 2002).

The cosine angle between two variable vectors; however, approximates the Pearson correlation (Kaplan, 2019; Yan, 2014; Yan and Frégeau-reid, 2018), in which the angles smaller or greater than 90^{o} depicts a positive and negative traits correlation respectively, and a 90^{o} angle shows that there is no correlation between the two traits. An acute and an obtuse angle between genotypes and traits; furthermore, represents that the genotype is above average and below average for the traits, respectively. A right angle between genotypes and traits indicates that the genotype is average for the traits (Yan, 2014; Yan and Frégeau-reid, 2018). Also, the length of the vector represents that how well traits and genotypes are represented in the biplot (Yan and Frégeau-reid, 2018).

Small or unfavorable representation of variables variation among genotypes in GT and GYT biplot which were shown by comparatively short vectors may be raised by either its weak or lack of variables association as well as insufficient goodness of fit of biplot (Yan, 2014; Yan and Frégeau-reid, 2018). In addition, the genotypes vector length reveals either genotypes strength, weakness or intermediate for assessing variables (Yan and Frégeau-reid, 2018). Based on Figure 2A, the traits such as days to flowering (DF) exhibited a highly significant and positive correlation with plant height (PH), stem diameter (SD), grain filling period (GRP), biological yield (BY) and it has a significant negative correlation with grain filling rate (GFR) and harvest index (HI); however, it was not favorably correlated with others. Earliness is an important trait in summer crops such as sorghum, in which grain yield was not well associated (Figure 1A). Furthermore, PH had a positive correlation with DF, panicle length (PL), GFP, BY and had a negative correlation with GFR and HI, significantly, but was not correlated strongly with other traits. The SD had an unfavorable positive association with DF and GFP and a positive one with GFR and HI. The PL and PW not only had a significant positive correlation with each other but also had a significant positive correlation with PH, grain yield (GY), BY as well as HI for PW (Figure 1A). The GFP was unfavorably associated with DF, PH, SD, GFR, GY and HI, significantly. In addition, GFR had a significant positive associated with TGW, HI, and a significant negative relationship with DF, PH, SD, kowever, GFP was not well associated with other traits. Thousand grain weight (TGW) positively correlated with GFR, meaning that if the higher GFR will occur, the higher TGW will achieve. On the other hand, GY, as an important trait had a positive significant correlation with PL, PW, BY, HI; meaning that higher PL, PW, BY, HI could increase higher grain yield; However, it, had a negative correlation with GFP. BY positively and significantly was well associated with

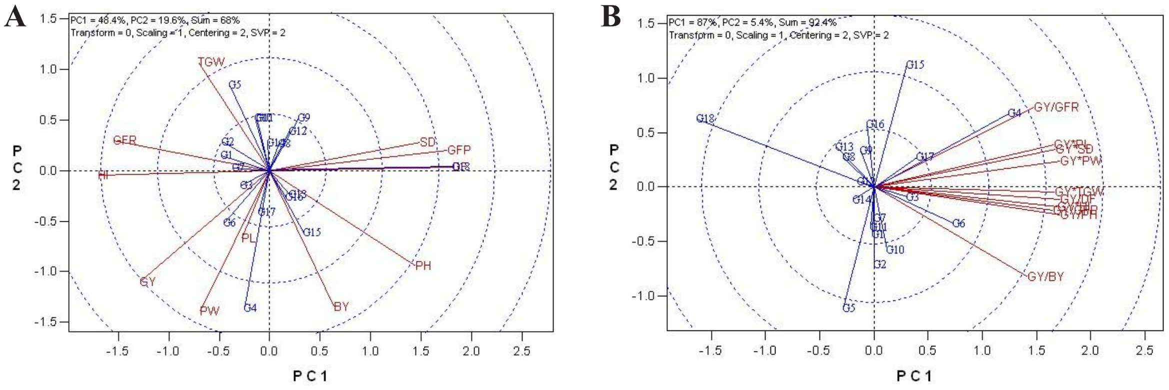

Figure 2. Association among traits and traits profile of genotypes visualized by **A:** GT and **B:** GYT biplot based on singular value decomposition of trait-standardized data (Scaling=1, Centering=2) and trait-focused singular value partition (SVP=2). Note: for abbreviated traits, refer to Table 2.

DF, PH, PL, PW and GY. Moreover, HI strongly and positively was correlated with PW, GFR, GY and it had a significant negative correlation with DF, PH, SD, and GFP (Figure 2A). Despite the fact that GT biplot has advantages in depicting traits associations as well as the existence of unfavorable association among traits, it is not suitable in making a decision that which trait could be selected as a selection index. In order to evaluate genotypes based on various variables, it is very essential that genotypes be evaluated according to yield×traits combinations. Because yield is a prominent variable and other variables are only significant when they are joined with the high yield (Yan and Frégeau-reid, 2018). These findings could be proven to be true from the Pearson correlation of traits (Table 5), although the goodness of fit of the biplot was suitable (sum of PCs=68%). In GT biplot all traits had long vectors, except PL which had a medium vector, revealing that the variation of the assessed variables across traits is well presented in the biplot (sum of IPCs=68%). In GT chart, G18, G4, and G15, G6, G5, G9 and other genotypes had long, medium and short vectors, indicating strong, intermediate and weak in traits profile, respectively (Figure 2A).

Furthermore, traits in the GYT biplot tend to be associated positively with each other, because they have yielded as the main component in yield-trait combination (Figure 2B)(Yan and Frégeau-reid, 2018). Nevertheless, all types of trait correlations including positive, negative and zero were strongly and positively correlated in GYT biplot (Figure 2B), as shown by the acute angle between traits, e.g., GY×PL and GY×PW, etc. despite their statistical significance which was observed in GT biplot (Figure 2A). These results could also be confirmed by numerical Pearson correlation of traits (Table 5), although the goodness of fit of the biplot was suitable (sum of PCs=92.4%). In the GYT biplot all traits had a long vector, revealing that the variation of assessed variables across traits are well presented in the biplot (sum of PCs=92.8%, respectively). In the GYT biplot, genotypes G18 and G4 with long vectors, G15, G5, G10 and G2 with medium vectors, and other genotypes with short vectors indicated strong intermediate and weak in their trait profiles (Figure 2B). Jankovic *et al.* (2012) reported a significant and positive correlation among morphological and productive traits. A significant correlation was reported for green leaf length, fodder yield, plant height and leaf number per plant in *Sorghum bicolor* (Jain and Patel, 2013). Kumar (2013) showed a significant and positive correlation between days to 50% flowering and yield in sorghum.

Trait profile of the genotypes based on GT and GYT biplot

The polygon or "which-won-where" view (Yan, 2001) (Figure 3) is effectively practical to visualizing the variables brief description of genotypes. By connecting the genotypes with the longest vectors in all directions, the irregular polygon was formed with a line that starts from biplot origin that divided the genotypes, traits, or yield-trait combination (Yan, 2001). Therefore, genotypes located in the biplot vertex indicate the best performance in one or several traits and those placed within the polygon are the least responsive to these traits (Paramesh *et al.*, 2016; Gravina *et al.*, 2018; Yan and Frégeau-reid, 2018). The GT and GYT biplot (Figure 3) showed the accuracy of eleven assessed traits profile across eighteen genotypes depends on the goodness of fit of the biplot (in this experiment sum of PCs for GT and GYT were 68% and 92.4%, respectively).

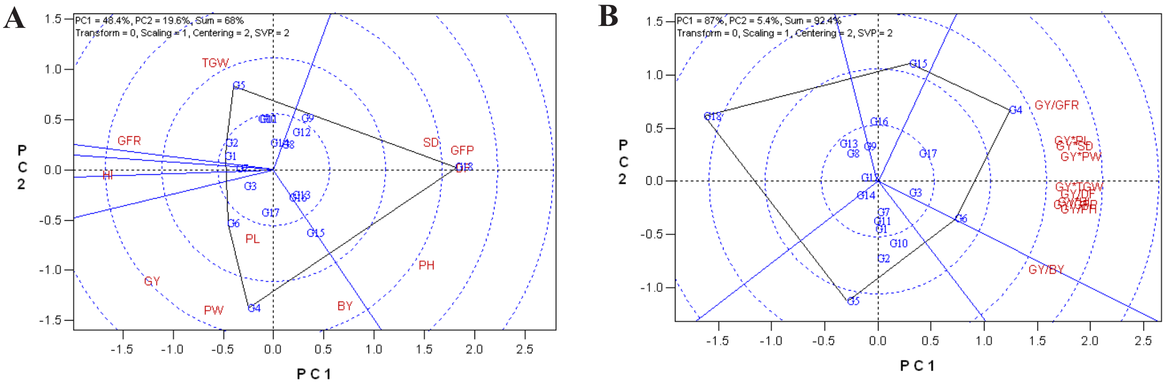

Figure 3. The which-won-where view of **A:** the genotype by traits (GT) and **B:** genotype by yield×traits (GYT) biplot to highlights traits profile of genotypes. These biplots are based on singular value decomposition of trait-standardized data (Scaling=1, Centering=2) and trait-focused singular value partition (SVP=2). Note: for abbreviated traits, refer to Table 2.

The polygon view of the GT biplot divided traits into four mega-traits in which some genotypes were superior in some traits. The first mega-trait including SD, GFP, DF, and PH showed that genotype G18 was the most responsive to these traits. Oppositely, G18 had the lowest level of BY, PW, PL, GY, HI, GFR and TGW. The second mega-trait comprising of only two traits such as TGW and GFR that G5 was the strong responsive genotype, but other traits were low in this genotype. The third mega-trait consisted of GY, PW, PL and BY in which G4 was the strong responsive for those traits and G6, G15 and G17 were the most responsive for PL. Genotype G4 had the least HI, GFR, TGW, SD, GFP as well as DF. The same trend was observed for G6, G15 and G17. Finally, only genotype G7 outstood for HI in the fourth mega-trait in moderate strength (Figure 3A).

Despite its efficiency in indicating trait profiles of genotypes, the GT biplot is not very helpful in making decisions on which cultivars could be selected or recommended and which one breeders could discard. The GYT biplot approach could tackle this problem (Yan and Frégeau-reid, 2018).

However, the "which-won-where" view of GYT biplot divided yield×trait combination into two mega-traits. The first mega-trait including all yield-trait combinations except GY×BY in the G4 was the most responsive to these traits. The second group was formed by GY×BY, which did not present any genotype responsive to these traits (Figure 3B). As it is clear, GYT biplot by representing acute traits for some genotypes helps breeders to reduce genetic load that should be investigated in the breeding programs. Furthermore, the genotypes that give raise to the vertices, but do not hold grouped traits or weak response to them are unfavorable for breeding programs focused on increasing the expression of these traits. Therefore, except the above-mentioned genotypes for the given traits, all other genotypes were considered inefficient in the current evaluated traits (Figure 3). The genotypes that were placed in the biplot peak may be examined in sorghum breeding programs to help developing genotypes responsive to the traits of interest.

Superiority rank of genotypes based on GT and GYT biplot

Figure 4A was constructed to focus on comparisons among genotypes representativeness and discriminating capacity towards the evaluated variables based on GT and GYT, respectively (Yan, 2002; Yan and Frégeau-reid, 2018). The small circle in GT and GYT biplot represents the means placement of traits and yield-trait combination, determined by the coordinates of both traits and yield-trait combinations that included in the biplot. The average tester axis (ATA) is a line with a single arrow passing through the biplot origin and the average yield-trait combination. The arrow points the higher mean values for the genotypes across all traits and yield-trait combinations. The ATA serves the purpose of ranking the genotypes based on their overall superiority or usefulness. The distance of the genotype and the mean measure the representativeness power, therefore, the closer to the mean, the greater the genotype representativeness towards the traits.

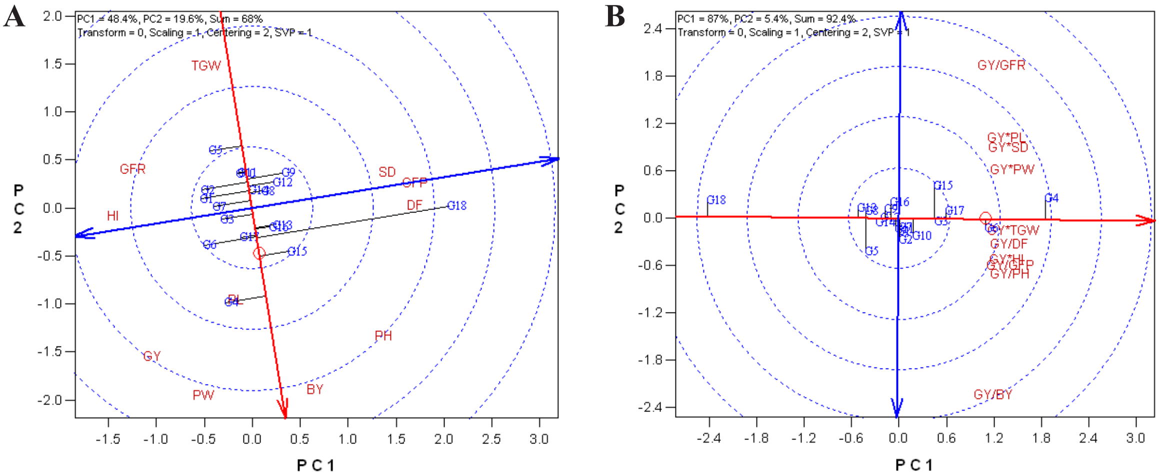

Figure 4. The average tester coordination view of the **A:** GT and **B:** GYT biplots to rank the genotypes based on their overall superiority, mean and stability to superiority rank of genotypes. These biplots were constructed based on singular value decomposition of the standardized GT and GYT ("Scaling-1, Centering=2"). The genotype-focused singular value partition ("SVP=1") was applied. Note: for abbreviated traits, refer to Table 2.

Conversely, the length of the projection from a line towards the Y-axis (straight line passing through the origin) shows the discrimination line (Yan, 2001). The line with two arrows pointing outward passes through the biplot origin and is perpendicular to the ATA. This double-arrowed line serves to separate genotypes better than average (placed on its right, on the same side as the ATA arrow) from those poorer than average (placed on the left side)(Yan and Frégeau-reid, 2018). This separation intuitively suggests the researcher focus on the genotypes ranked better than average. The double-arrowed line also helps to indicate whether a genotype has an all-rounded or balanced trait profile or has obvious strengths and/or weaknesses, the latter determines how a “useful” genotype should be used in terms of environmental adaptation and/or end-use (Yan and Frégeau-reid, 2018). Genotypes placed close to ATA (i.e., with short projections to the double-arrow line) tend to have balanced trait profiles whereas those placed away from the ATA in either direction tend to have obvious strengths and/or weaknesses (Yan and Frégeau-reid, 2018).

The GT biplot (Figure 4A) indicated that the best-ranked genotypes based on the GT included G4>G15>G6>G17>G18>G16>G13>G3 which depicted good representativeness. Besides, only G17, G14, G10 and G11 showed good discrimination. The other genotypes depicted means below the general mean. Moreover, the best-ranked cultivars based on the measured traits included G4 and G15 (Figure 4A). G5 placed on the far left side of the biplot was ranked the poorest even though it was among the best in TGW and GFR (Figure 2A and Figure 3A). Furthermore, Figure 4A depicted that G4 was strong in some traits including PH, PL, PW, GY and BY. Regardless of their overall superiority, all genotypes placed above the ATA tend to have relatively good levels of BY, PH, DF, GFP and SD; but relatively low levels of PW, PL, GFR, TGW, GY, and HI. The opposite of that is also true for genotypes placed below the ATA (Figure 4A). Figure 4B revealed that the best-ranked genotypes based on GYT comprised of G4>G6>G17>G3>G15>G10>G2>G7>G11 and showed good representativeness; however, only G6, G8 and G14 showed good discrimination. The other lines showed means below the general mean. The best-ranked cultivars based on yield-trait combination included G4 and the G6 (Figure 4B). G18 placed on the far left side of the biplot was ranked the poorest even though it was among the best in DF, GFP, SD and PH (Figure 2A and Figure 3A). Furthermore, Figure 4B depicted that the G4 was balanced for various traits and G6 was strong in all other traits, but in PW, SD, PL, GFR. Regardless of their overall superiority, all genotypes placed above the ATA tend to have relatively good levels of PW, SD, PL and GFR, but relatively low levels of TGW, DF, HI, GFP, PH and BY. The opposite is true for genotypes placed below the ATA (Figure 4B). This information is important for deploying the superior but different cultivars to their most suitable environment and end-use (Yan and Frégeau-reid, 2018). The GT and the GYT biplots revealed that G4 was the superior genotype for using in breeding programs.

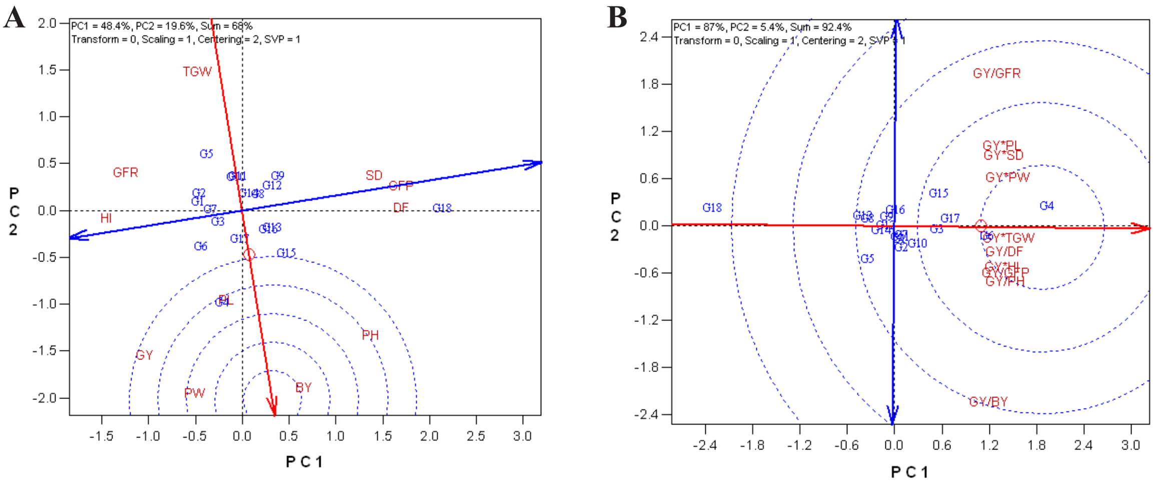

Figure 5. The **A:** GT and **B:** GYT biplots comparing the 18 sorghum genotypes with the estimate of an ideal genotype based on their overall superiority, mean and stability to identify an ideal genotype. These biplots were constructed based on singular value decomposition of the standardized GT and GYT (“Scaling-1, Centering=2”). The genotype-focused singular value partition (“SVP=1”) was applied. Note: for abbreviated traits, refer to Table 2.

Identification of the ideal genotype based on GT and GYT biplot

The ideal genotype is the one presenting high means for all the traits and it is identified based on the length of the vector. Therefore, the more PC1 and PC2 without projection and the closest to the concentric circle, represent the better genotype (Gravina *et al.*, 2018) (Figure 5). According to this, G4 was identified as an ideal genotype by both GT and GYT biplot (Figure 5A and Figure 5B, respectively). Thus, this genotype could be applied as a parent in breeding programs because this was particularly desirable in many traits.

CONCLUSION

This research revealed that many genotypes have suitable characteristics in terms of phenological, agronomical, yield and yield components. These genotypes depicting superior traits could be applied into field sorghum cultivation based on usage aim (e.g., earliness, plant height, grain yield, etc.). Besides, the GT and GYT biplot were superior tools to visualize sorghum genotypes based on traits and yield-trait combination to identify the best genotypes to use as a parent in breeding programs or release as superior cultivars. In the current experiment; however, based on both GT and GYT biplot, it is confirmed that FGCSI04 (G4) was a superior genotype that was able to present higher PH, PL, PW, GY and BY which is essential to economic sorghum production.

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