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Stability and adaptability evaluation of grain sorghum varieties using GGE biplot

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Authors' Contribution **Saeed, M**, **A. Mumtaz, M. Ihsanullah, A. Hussainn** & **A. Khan** performed research trials. **A. Mumtaz, S. F. Nayab** and **J. Iqbal** performed statistical analysis.

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ABSTRACT

In Pakistan, Sorghum can be a good domestic source of high-quality fodder and feed, because of its high protein and sugar contents. Location-specific adaptation of lines/varieties as found in the current study evidently implies that location-specific breeding needs are more importance than concentrating on wider adaptability. Another point of consideration is that it is essential to recognize location-specific cultivars over location and multi-year data for their consideration before commercial release for the sake of stability of the cultivar. This is important not only to sorghum only but also in other crops as well. The G × E interaction of six Pakistani experimental sorghum lines produced by Pedigree method and two check cultivars were evaluated for days to 50% flowering, stalk weight, grain yield and Brix value along with their stability and/or adaptability across two locations and two years, under randomized complete block (RCB) design. Three replications were used for each treatment. The combined analyses of variance of all the studied characters showed that they were affected significantly by environments (E), genotypes (G) and genotype by environment interaction (G × E) in every year except for the environment in Brix value. The ideal genotype evaluation proved that YSS-10 was the best line for the all four environments. Dera Gazi Khan is an ideal location for testing grain sorghum genotypes. The 'Which-won-where' biplots indicated a crossover type of G × E between experimental lines YSS-10 and YSS-18 for the grain yield.

Keywords: MMRI, GE interaction, ideal genotype, Mega-environment, which-won-where analysis.

INTRODUCTION: The livestock and chicken sectors have been growing rapidly in Pakistan in recent years; for example, from 2.25% in 2021-2022 to 3.78% in 2022-2023 for livestock, as 16304 metric tons of feed an fodder were imported in 2022-2023 at considerable expense (Government of Pakistan, 2022-23). Globally, Pakistan is ranked number 4th, 9th and 28th in in milk, beef and chicken production respectively (FAOSTAT, 2017; USDA, 2017). This ranking could be improved by growing high-quality fodder and feed, which can increase chicken and livestock production. Low-quality feed & fodder is the main cause for animals for late puberty, and also the interval between calving to be shorter (Ali, 2011). Despite the high demand, the area under cultivated for fodder crops is declining rapidly because of housing development (Government of Pakistan, 2022-23). In Pakistan, fodder crops were cultivated on 2.38 million hectares in 2022-2023. Of this cultivated area, 59,000 hectares were devoted to sorghum (*Sorghum bicolor*), with a production of 49,000 tons. This area accounts for 3% of the total cultivated fodder crops area, making sorghum the second largest cultivated crop for fodder production after barseem (45.54%) (Government of Pakistan, 2022-23; Pakistan Bureau of Statistics, 2022–23). Sorghum is a prominent grain and fodder crop in rain-fed and arid zones, particularly because of its dual nature, in that it can be used both as fodder and a grain crop (Bibi *et al.*, 2010). Sorghum ranks 5th amongst the significant cereal crops globally (Motlhaodi *et al.*, 2014). Being a dual-purpose crop, its grain and fodder both are useful to poultry and livestock respectively. Sorghum contains significant amount of protein and carbohydrates (Selle, 2011), and its juicy nature and sweetness make it more palatable to animals (Cifuentes *et al.*, 2014; Mumtaz *et al.*, 2017; Mumtaz *et al.*, 2018). The Genotype (G) x Environment (E) biplot with mega-environment analysis has being applied for crops such as maize (corn) (Fan *et al.*, 2007), and wheat (Mohammadi *et al.*, 2009), barley (Dehghani *et al.*, 2006), lentils (Sabaghnia *et al.*, 2008). Breeders use G × E interactions to estimate the relative ranking and thus to improve the genotype selection. However, assessments based on G x E interactions in distinct environments can be difficult; for example, when the G x E interaction is found to be significant, utmost care is needed to judge its basis, nature and association (Kang and Gorman, 1989). Numerous stability analyses have been used for G x E interaction, including the cluster analysis (Crossa *et al.*, 1991), the multiplicative interaction (AMMI) model and the additive main effects (Gauch Jr, 1992), multivariate analysis (Westcoff, 1987) and the regression analysis (Gauch Jr and Zobel, 1997). However due to its graphical interactions presentation, Genotype (G) x Environment (E) biplot is the most powerful technique.

OBJECTIVES: The purpose of the research was to evaluate the performance (stability & adaptability) of sorghum varieties in two successive years at both locations, and to propose the ideal varieties and the ideal location.

MATERIAL AND METHODS: Six experimental sorghum lines developed by the Pedigree method and two check cultivars (YSS-16 and YSS-98) (table 1) were assessed at two locations in Pakistan, at the Maize and Millets Research Institute, Yusafwala, Sahiwal (MMRI) and the Sorghum Research Sub-Station Dera Gazi Khan (DG Khan).

Code	Name	Variety definition	Maturity group
1.	YS-16©	Registered check pure line variety	Medium
2.	YSS-10	Line	Medium
3.	YSS-18	Line	Early
4.	YSS-19	Line	Medium
5.	YSS-23	Line	Late
6.	YSS-25	Line	Late
7.	YSS-31	Line	Medium
8.	YSS-98©	Registered check variety	Early

Table 1: Genotype code and name of grain sorghum experimental lines and check cultivars.

Yusafwala (30°40'53.4''N/73°12'54.7'') which is located at 174 m above the sea level, has clay loam while Dera Ghazi Khan (30°3'22.1''N/70°8'5.17''E) is located at 129 m above the sea level, and is characterized by clay loam. Sorghum lines were sown in succeeding years (2015 and 2016) and in three (3) replications, for a total of four (4) environments: DG Khan-15, DG Khan-16, MMRI-15, MMRI-16. In all four (4) environments. The experiment was conducted in a RCB design. While the plot size was 4 × 0.75 × 2 m. The new lines and the check cultivars were sown in end of July and harvested in early December. The sorghum lines were sown in plots of 5 × 3.75 m with 0.75 m spacing between the rows and 1.15 m between the plants. An Amamectin Benzoate pesticide was applied after germination. The stem was treated with a granular pesticide Carbofurawhen the stems were 0.50 m high. The trials were irrigated six times.

Data Recording and Statistical Analysis: The traits under consideration for this research were days to 50% flowering, stalk weight, grain yield and grain Brix value. Five (5) plants were selected at random from every plot for data gathering. To find out the dry weight of stalk, the 5 randomly selected plants were harvested at 5 cm above the soil surface, then the leaves and panicles were removed, and fresh stalks were weighed. The Brix value (sugar content in %) was measured from the fourth and sixth internodes below the panicle using a hand-held refractometer. The meteorological data for both locations and years are found in table 2a&b. The locations and the years were different in average monthly and seasonal rainfall as well as their maximum and minimum monthly temperatures (table 2a&b). Thus, the locations in every year were counted as different environments because the locations, years and interaction were determined significantly different.

Month	Average temperature ^{0}C				Rainfall (mm)	
	Maximum		Minimum			
	2015	2016	2015	2016	2015	2016
July	39.60	39.12	27.46	28.61	108.45	92.12
August	39.45	39.08	27.89	27.10	111.28	75.11
September	40.10	37.30	23.10	23.89	50.12	1.12
October	36.45	34.67	18.89	18.55	4.78	-
November	28.78	27.09	13.49	12.39	-	-
December	24.67	26.37	7.49	9.12	-	-
Total rainfall (mm)					**274.50**	**168.30**

Table 2a: Meteorological data (average temperature (°C) and monthly rainfall (mm) of MMRI, Pakistan in 2015 and 2016.

Month	Average temperature ^{0}C				Rainfall (mm)	
	Maximum		Minimum			
	2015	2016	2015	2016	2015	2016
July	40.5	40	21.0	21.8	432.2	341.9
August	37.0	38	21.5	21.5	180.3	128
September	37.0	37	18.0	21.5	79.9	4.2
October	34.2	36.2	10.5	11.00	193.0	24.5
November	27.5	28.9	6.5	6.5	15.2	0.0
December	24.0	26.5	2.0	1.5	20.0	0.0
Total Rainfall (mm)					**920.6**	**498.6**

Table 2b: . Meteorological data (average temperature (°C) and monthly rainfall (mm) of SRSS, DG Khan, Pakistan in 2015 and 2016.

Data of both locations and years was analysed for the analysis of variance (ANOVA) with the help of Software statistix 8.1. A combined ANOVA and heritability estimates were used for explanation. The genotype main effect along with G x E interaction (GGE) biplot model was applied (Yan and Kang, 2002; Sabaghnia *et al*., 2008), using. The multilocation (ML) trial data were analysed and investigated with the help of GEA-R software for genotypes biplots according to methods described Yan and Tinker (2006) and for location assessment by Yan (2001). For identification of ideal lines and mega-environments, which-won-where' option was utilized

RESULTS: The ANOVA results for days to 50% flowering, stalk weight, grain yield and brix valus are shown in table 3.

Source of of variation	DF	MS			
		Days to 50% flowering	Stalk weight (kg)	Grain yield (kg ha-1)	Brix value (%)
Replication	**2**	31.89	8102916**	240997	0.375
Genotype (G)	**7**	70.83**	239900000**	1779013**	361.439**
Location (L)	**1**	651.04**	107700000**	135902^{NS}	0.094^{NS}
Year (Y)	**1**	170.67**	588500000**	782287*	3.01^{NS}
G x L	**7**	13.69*	73740000**	781460**	6.713*
G x Y	**7**	8.64^{NS}	29040000**	337449*	5.344^{NS}
L x Y	**1**	22.04*	2212819^{NS}	2666667**	1.76^{NS}
G x L x Y	**7**	14.78**	48170000**	373972**	5.427^{NS}
Residual	**62**	5.55	7518695	117799	2.751
Total	**95**				
CV		**3.00**	**10.75**	**11.61**	**20.34**

Table 3: ANOVA for the data across locations and over years (combined).

DF = degree of freedom, MS = mean square, ** and * significant at 0.01 and 0.05 probability levels, NS= non-significant, respectively.

The analysis illustrated a highly significant ($P<0.01$ and significant ($P<0.05$) difference for genotypes and G x L effects for all traits. The G x Y was highly significant ($P<0.01$) for stalk weight, and significant ($P<0.05$) for grain yield. Except the Brix value, the G x L x Y effect was highly significant ($P<0.01$) for all the studied traits. The combined ANOVA and proportion of variation for G, E and G × E are given in Table 4. G, E and G × E effects were found to be significant for all the traits except the environment in Brix value. The genotype ascribed a higher proportion of the variation in the data (31.0-75.3%). The location contributed to 0.20-52.76 % of the total variation. The contribution of the genotype x environment interaction was 16.24-39.45%. The genotype was the most important factor for grain yield, Brix value and stalk weight, whereas the environment was the most important one for days to 50% flowering. For Brix value, the contribution of G (75.32%) was higher than G x E (24.48%) and E (0.20%). For stalk weight, the contribution of G (48.90%) was higher than G x E (30.77%) and E (20.34%) (table 4). For grain yield, the contribution of G (47.01%) was high in comparison to E (13.53%) and G x E (39.45%). For days to 50% flowering, the contribution of E (52.76%) was higher than G (31.00%) and to G x E (12.37%).

Performance of the genotypes: The mean values of experimental lines and check cultivars for days to 50% flowering, stalk weight, grain yield and Brix values are shown in Table (5). YSS-10 possessed the highest grain yield (3551 kg/ha) followed by YSS-18 with and 3448 kg/ha while YSS-23 was the lowest productive line with a grain yield of 2538 kg/ha. YSS-31 was the earliest line (76 days) while YSS-23 was the latest one (83 days). YSS-10 was the medium (79 days). YSS-23 possessed the highest stalk weight (31958 kg/ha) while the line having the lowest stalk weight (19238 kg/ha) was YSS-19. The sweetest variety containing the highest Brix value (15.467%) was one of the check cultivar YSS-98© followed by the other check YSS-16© (12.325) and YSS-18 (10.225). Two lines (YSS-25 and YSS-23) were non-juicy (tables 5 and 6).

Stability of the genotypes: The performance & the stability of the lines were illustrated as principal components (PCs) with their graphically presentation through GGE biplot in figures 1a-d. Tester-centered G + G x E biplots were generated with no scaling for days to 50% flowering, stalk weight, grain yield and Brix value. In figures 1a-d the cumulative of the first two PCs explained 89.4% variation for days to 50% flowering, 88.1% for stalk weight, 86.5% for grain yield and 97.6% for Brix value (table 4 and figures 1a-d). The ideal genotypes (i.e. those that give the best performance) stay closer to the abscissa (AEC abscissa line: the single arrowhead vertical line, passing through the origin). The environmental situation can be considered normal because of near-average values of PC1 and PC2 scores on AEC ordinate (The perpendicular line that passes through the origin). The shorter the projection of a cultivar on AEC ordinate line, the better performer the cultivar is expected to be. For days to 50% flowering, the earliest and most stable lines were YSS-31 and YSS-19, being located at the end of the AEC ordinate line and having a shorter projection of the AEC abscissa. YSS-23 also had a short abscissa, meaning that it is stable, but this line was the latest one, as shown by its position on the AEC ordinate. YSS-10 and YSS-18 are stable and have a medium growing period as cleared by their positions on the AEC ordinate andon the AEC abscissa (figure 1a). For stalk weight, the highest yield was achieved by YSS-23, followed by check cultivar YS-16© and line YSS-10. The most stable experimental line was YSS-10, as shown by having the lowest projection on the AEC abscissa. The experimental line YSS-25 and the check cultivar YSS-98© were also stable but they had the lowest yields, as indicated by their farthest position on the AEC ordinate and the lowest projection on the AEC abscissa. YSS-31 YSS-18 were medium stalk yielders, but they were the least stable, as indicated by their higher projections on the AEC abscissa (figure 1b). YSS-10 showed the highest grain yield followed by YSS-18. Among them, YSS-18 (having shorter AEC ordinate) was more stable than YSS-10 at both locations in both years. The experimental line YSS-23 and YSS-31 were poor grain yielders, but the latest experimental line was more stable than other varieties, because it has the shortest AEC ordinate. The check cultivar YSS-16© was also one of the most stable varieties, as shown by its shorter AEC ordinate but its yield was lower than that of the three other varieties, which is shown by the fact that it is behind them on the AEC abscissa (figure 1c). The GGE biplot of the Brix value was ambiguous and could not be used for further interpretation (figure 1d).

Environmental assessment (ideal and discriminating environments): For better understanding about the adaptability of the genotypes, we compared the studied environments. The correlation among them was studied by an environment centered preservation of data (SVP = 2) without scaling. The combined analysis performed over two years ranked the four (4) environments according to days to 50% flowering (figure 1e), stalk weight (figure 1f), grain yield (figure 1g), and Brix value (figure 1h). The correlation among the environments was determined with the help of cosine of angles between their vectors (Yan and Tinker, 2006). DG Khan-16 and MMRI-16 were highly correlated for grain yield, whereas MMRI-15 and DG Khan-15 were divergent. The DG Khan location in 2016 was the ideal environment for sorghum, as shown by its closeness to the AEC circle. There was two mega-environments; the first one comprised of DG Khan-16, DG Khan-15 and MMRI-16 whereas second one have only MMRI-15. This means that environmental conditions in 2016 at DG Khan and MMRI, and in 2015 at MMRI, were similar whereas they were different in 2015 at MMRI. Similar patterns were noted for days to 50% flowering; but for stalk weight and Brix value, DG Khan-15, MMRI-15 and DG-Khan-16 and MMRI-16 correlated strongly with one another (figure 1.e,f,g,h).

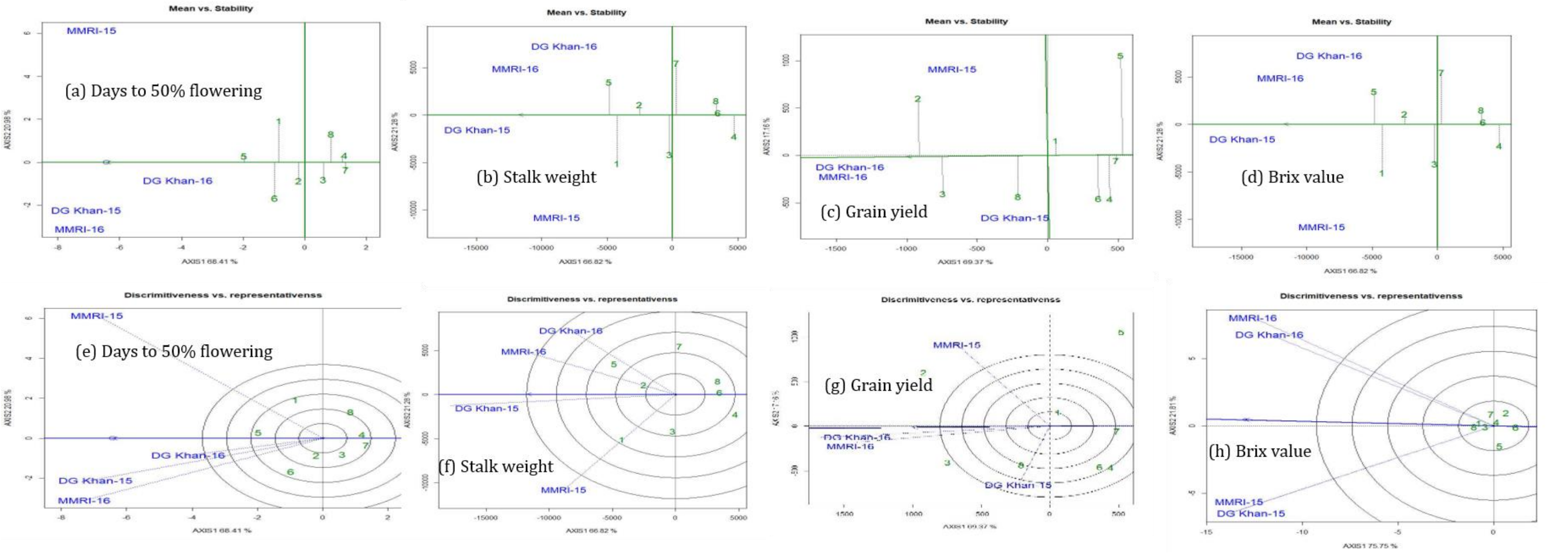

Figure 1: GGE biplots of the combined analysis for all traits. a-d Mean versus stability of the genotypes. e-h Relation among the test locations.

Trait		G	E	G × E	Contribution of PC1 +PC2
Grain yield	MS	1779013*	1194952*	497626*	91.57%
(kg/ha)	Proportion of G + E + G × E (%)	47.01	13.53	39.45	
Days to 50% flowering	MS	70.83*	281.25*	12.37*	88.56%
	Proportion of G + E + G × E (%)	31.00	52.76	16.24	
Stalk weight	MS	23.9 ×10⁷*	23.2 ×10⁷*	50.3 ×10⁷*	94.02%
(kg/ha)	Proportion of G + E + G × E (%)	48.90	20.34	30.77	
	MS	290.74*	1.82 NS	31.49*	99.95%
Brix value (%)	Proportion of G + E + G × E (%)	75.32	0.20	24.48	

Table 4: Combined ANOVA and proportion of variation in Genotype (G), Environment (E) and G × E.

Variety	Days to 50% flowering	Stalk Weight (kg)	GrainYield (kg/ha)	Brix Value (%)
YSS-10	79[bcd]	28102[bc]	3551[a]	8.4833[c]
YSS-18	77[cde]	26444[cd]	3448[ab]	10.225[c]
YS-16©	80[abc]	30245[ab]	3086[bc]	12.325[b]
YSS-98©	77[de]	22014[ef]	3002[cd]	15.467[a]
YSS-25	81[ab]	21518[ef]	2741[cde]	Non Juicy
YSS-31	76[e]	24583[de]	2639[de]	9.3833[c]
YSS-19	76[de]	19238[f]	2638[de]	9.2333[c]
YSS-23	83[a]	31958[a]	2538[e]	Non Juicy

Table 5: Sorghum genotypes value (Mean) for the al traits.

Genotype/Year	Days to 50% flowering			Brix value (%)			Stalk weight (kg/ha)			Grain yield (kg/ha)		
	2015	2016	Comb.	2015	2016	Comb.	2015	2016	Comb.	2015	2016	Comb.
YS-16©	78.8	81.8	80	12.2	12.5	12.3	31444.5	29046.3	30245	3193.3	2979.2	3086
YSS-10	78.2	80.0	79	7.7	9.3	8.5	32444.4	23759.4	28102	3468.8	3633.3	3551
YSS-18	76.7	78.0	77	11.3	9.2	10.2	27999.9	24888.9	26444	3686.6	3209.8	3448
YSS-19	74.8	77.8	76	9.5	9.0	9.3	20688.8	17787.1	19238	2847.8	2427.8	2638
YSS-23	79.8	85.5	83	0.0	0.0	0.0	35111.0	28805.0	31958	2328.9	2747.2	2538
YSS-25	80.5	81.0	81	0.0	0.0	0.0	23666.6	19370.4	21518	2973.3	2509.7	2741
YSS-31	75.0	76.7	76	8.7	10.1	9.4	29666.6	19500.0	24583	2851.1	2426.4	2639
YSS-98©	74.8	79.2	77	14.6	16.4	15.5	22888.9	21138.9	22014	3015.5	2987.4	3002
Genotype/Location	**MMRI**	**DG Khan**	**Comb.**	**MMRI**	**DG Khan**	**Comb.**	**MMRI**	**DG Khan**	**Comb.**	**MMRI**	**DG Khan**	**Comb.**
YSS-16©	80.5	80.2	80	12.0	12.6	12.3	24962.9	35527.8	30245	2722.5	3450.0	3086
YSS-10	82.2	76.0	79	7.5	9.5	8.5	26481.4	29722.3	28102	3796.7	3305.5	3551
YSS-18	80.0	74.7	77	10.6	9.8	10.2	23222.2	29666.7	26444	3707.5	3188.8	3448
YSS-19	80.0	72.7	76.4	9.9	8.6	9.3	16925.9	21550.0	19238	2531.1	2744.5	2638
YSS-23	85.3	80.0	83	0.0	0.0	0.0	33111.1	30805.5	31958	2331.7	2744.5	2538
YSS-25	84.2	77.3	81	0.0	0.0	0.0	21370.3	21666.7	21518	2577.5	2905.5	2741
YSS-31	78.3	73.3	76	10.5	8.3	9.4	26111.1	23055.5	24583	2405.3	2872.2	2639
YSS-98©	79.7	74.3	77	14.5	16.5	15.5	23444.4	20583.3	22014	3269.7	2733.2	3002

Table 6: Mean days to 50% flowering, stalk weight (kg), grain yield (kg/ha), Brix value (%) of 8 sorghum genotypes tested in 2 years and in 4 environments.

Ideal genotype*:* As discussed above, the major emphasis of this study was grain yield, thus in comparison to ideal genotype, the genotypes were ranked according to grain yield for all the genotypes. The ideal genotype can be found by its position closest the centre of the concentric circles, and the genotypes nearest to the ideal genotype are the most desired ones (figure 2). This analysis is supported by the information described in table 4a&b. Figure 2 shows that the experimental line YSS-10 was the closest to the ideal genotype, and it was followed by line YSS-18. The experimental lines YSS-10 (3551.0 kg/ha) and YSS-18 (3448.2 kg/ha) had the highest grain yields. Both of them significantly over yielded the check cultivars YSS-16 (3068.2 Kg/ha) and YSS-98 (3001.4 Kg/ha) table 5).

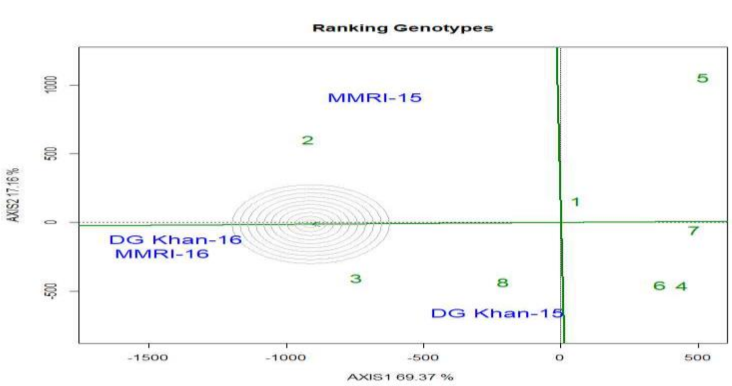

Figure 2: Ranking of different genotypes.

Mega-environment identification: The performance of genotypes is estimated by the 'which-won-where' diagrams in which a polygon is drawn to show the performance of the genotypes in distinct environments for summarizing the multi-environment data. They are created first by connecting the farthest genotypes creating a polygon. Equality lines are sketched in a perpendicular style to the source of the biplot via the sides of the polygon. Genotypes are recognized as desirable or less desirable based on their position at the polygon peaks. The best one genotype are those falling within the sectors. 'Which-won-where' biplots for days to 50% flowering stalk weight, grain yield and Brix value over two years are presented in figures 3a-d. Tables 4a&b, furthermore, figure 3c indicated the presence of the crossover GE and the presence of the mega-environment, specifically for grain yield. From biplots it is assessed that the grain yield biplot (figure 3c) is the most helpful, as it could recognize the environment more efficiently. The polygons for days to 50% flowering (figure3a), stalk weight (figure 3b) and Brix value (figure 3d) could not separate the locations much more effectively. Thus, being less helpful and informative they were not studied more. Therefore, only the grain yield is worth of discussion which will be discussed in the next section.

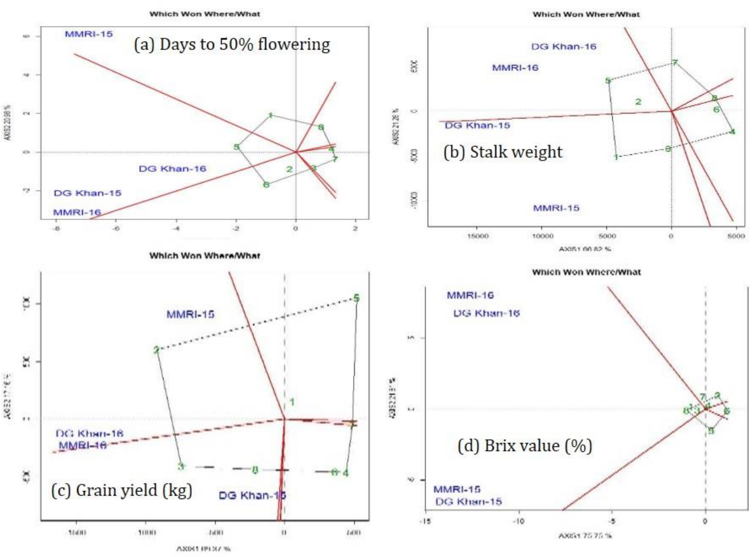

Figure 3: Analysis of the genotypes (a-d).

DISCUSSION: In every plant breeding programme, GE interaction effects are of special attention for recognizing the most favourable genotypes, the mega-environments, the representative locations and other adaptation targets. The visual presentation of interactions of genotype x environment interactions (G x E) make is favourable for breeders to use it for estimation of the relative ranking in crops such as lentils (Sabaghnia *et al.*, 2008), wheat (Mohammadi *et al.*, 2009), barley (Dehghani *et al.*, 2006) and maize (Fan *et al.*, 2007).

In this study, the comparison of the performance (adaptability and stability) of sorghum varieties in two successive years at both locations was done for recommending the best varieties and the best location. The ANOVA analysis illustrated a highly significant (*P<0.01* and significant (*P<0.05*) difference for genotypes and G x L effects for the traits except the Brix value. So, we can predict from this that analysis of all the traits can be further evaluated significantly except brix value. The genotype was the most important factor for grain yield, Brix value and stalk weight, whereas the environment was the most important one for days to 50% flowering. The results were in coincide with the findings of Human *et al.* (2011); Teodoro *et al.*, (2016); Mumtaz *et al.*, (2019); Worede *et al.*, (2020). They found significant differences for year, location, genotype and interactions for grain yield. While significant differences were observed for year, location, Y x L, Genotype and L x G by Gasura *et al.*, (2015). Filho *et al.* (2014) found significant differences for genotype, location, and G x L effects for grain yield. Hassan *et al.* (2015), Nida *et al.* (2016), and Admas and Tesfaye (2017) observed significant differences for grain yield and interactions. The presence of significant genotype and environment interaction in this study needs further analyses to ascertain the magnitude of G x E.

The complex genotype and environment interaction were considered as principal components (PCs) and are given graphically through GGE biplot for better understanding. According to Yang *et al.* (2009) and Yan *et al.* (2010), the G x E data are reliable for further interpretation with the average environment coordination (AEC) method if the first two PCs explained more than 60% variability and G x E explained more than 10% variability. In this study, the cumulative of the first two PCs explained 89.4% variation for days to 50% flowering, 88.1% for stalk weight, 86.5% for grain yield and 97.6% for Brix value. These results suggest that our G x E data is useful for additional analysis. With the help of AEC abscissa and AEC ordinate, In the current study, YSS-31 and YSS-19 were the early maturing and stable lines, YSS-23 was stable but late maturing while YSS-10 and YSS-18 are stable and have a medium maturity period (figure 1a). For stalk weight, the highest yield was achieved by YSS-23, followed by check cultivar YS-16© and line YSS-10. While YSS-10 was the stable one so it is better to select YSS-10 than YSS-23 in spite of its higher production (figure 1b). YSS-10 showed the highest grain yield followed by YSS-18. Among them, YSS-18 (having shorter AEC ordinate) was more stable than YSS-10 at both locations in both years (figure 1c). The GGE biplot of the Brix value was ambiguous and could not be used for further interpretation (figure1d).

So, keeping in consideration of summary of above results and emphasizing on the major aspect of this study i.e, grain yield; therefore, to select a good line, we gave priority to the high performance and the stability of the grain yield. Our results showed that experimental line YSS-10 achieved the highest grain and stalk yield, and it has a medium growing period. That experimental line is stable for those traits. Different studies have estimated the genotype stability in a variety of crops for prediction of good lines; for example, in barley and rapeseed (Dehghani *et al.*, 2006; Dehghani *et al.*, 2008), in wheat (Kaya *et al.*, 2006), in lentil (Sabaghnia *et al.*, 2008), in sorghum (Khalil *et al.*, 2011; Mitrovic *et al.*, 2012), and in maize (Munawar *et al.*, 2013). Rakshit *et al.* (2012) found a 70% contribution of variation from the first two PCs in four grain yield, fodder yield, days to 50% flowering and harvest index. The authors also observed that G x E interaction clarified only 10% of the whole variation for all traits. For finding out the ideal environment, we compared the studied environments.

Testing environments can be easily understood by using biplots, with the help of consideration of the angle between vectors. Vector of the environment can be defined as a line connecting its markers to the origin of the biplots. While cosine of the angle between the vectors represents the correlation between them (44). It was observed that that environmental conditions in 2016 at DG Khan and MMRI, and in 2015 at MMRI, were similar whereas they were different in 2015 at MMRI. Similar patterns were noted for days to 50% flowering; however, for stalk weight and Brix value, DG Khan-15, MMRI-15 and DG-Khan-16 and MMRI-16 correlated strongly with one another (figure 1.e,f,g,h). The main advantage of this such graphical representation is that we can identify very conventional the generally adapted and specific environments. This point is very important for optimizing the scarce resources while considering the environment for Multi location trials. The results suggest that DG Khan is the ideal location to evaluate different experimental lines/varieties. The environment at MMRI fluctuated more strongly than at DG Khan for sorghum. Previously, similar studies of environmental evaluations have been testified (Khalil *et al.*, 2011; Mitrovic *et al.*, 2012; Rakshit *et al.*, 2012; Munawar *et al.*, 2013).

Keeping the major emphasis of this study on grain yield, the genotypes were ranked accordingly for ideal genotype. Ideal genotype (Greater stability and higher yield) is described by having longest vector length of high yielding genotype with zero. The experimental line YSS-10 is the closest to the ideal genotype followed by YSS-18. They significantly over yielded the check cultivars YSS-16 and YSS-98 (table 5). Previously, similar methods to identify ideal genotypes by means of this method were used (Dehghani *et al.*, 2006; Kaya *et al.*, 2006; Dehghani *et al.*, 2008; Sabaghnia *et al.*, 2008; Khalil *et al.*, 2011; Mitrovic *et al.*, 2012; Rakshit *et al.*, 2012; Munawar *et al.*, 2013).

In the end, we summarize the multi-location data with the help of the 'which-won-where' diagrams in which the polygons were drawn to demonstrate the performance of the genotypes in discrete environments. The suitable and le-desirable genotypes were identified according to their positions at the vertex as mentioned in results (Yan, 2002; Yan and Tinker, 2006). From the results it was observed that out of the four 'which-won-where' biplots the grain yield biplot (figure 3c) is the most enlightening, as it could categorise the environments more effectively, the other three polygons could not separate the locations much more effectively. Therefore, here we discuss only the grain yield for which the rectangle has four genotypes (figure 3c), lines YSS-10, YSS-18, YSS-19 and YSS-23. Line YSS-10 achieved best results at DG Khan-16, MMRI-16 and MMRI-15, while line YSS-18 performed the best at DG Khan-15. Four sectors were identified with the help of the equality

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lines, two of which contain all the environments. Two mega-environments were identified, one with DG Khan-16, MMRI-16 and MMRI-15, and one with DG Khan-15. The former mega-environment was the best for YSS-10 and the latter one was the best for YSS-18, as discussed earlier. Previously, a similar method to mega-environment recognition and specific adaptation was exploited (Gauch and Zobel, 1988; Yan and Tinker, 2006; Putto *et al.*, 2008; Yan *et al.*, 2010; Khalil *et al.*, 2011; Rao *et al.*, 2011; Mitrovic *et al.*, 2012; Munawar *et al.*, 2013). Rakshit *et al.* (2012) studied the performance of ten grain sorghum hybrids in a rainy season at12 locations for 2 years using GGE biplot, and out of the four 'which-won-where' biplots, like in our experiment, only the grain yield one was informative. This study has conveniently aided the breeders in prioritizing the trait for breeding programme. Location-specific adaptation of lines/varieties as found in the current study evidently implies that location-specific breeding needs are more importance than concentrating on wider adaptability. Another point of consideration is that it is essential to recognize location-specific cultivars over location and multi-year data for their consideration before commercial release for the sake of stability of the cultivar. This is important not only to sorghum only but also in other crops as well.

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