



Identification of sorghum parental lines with high phenotypic stability using GGE biplot analysis in Central India

U. SAXENA,¹S. REDDY, M. K. SAXENA AND ²P. KUMARI

All India Coordinated Sorghum Improvement Project, RVSKVV, Indore-452001, M.P.

¹. Indian Institute of Millets Research, Hyderabad, Telagana

². Chaudhary Charan Singh Haryana Agricultural University, Hisar, Haryana

Received : 29.10.2019 ; Revised : 06.02.2020 ; Accepted : 02.03.2020

DOI: <https://dx.doi.org/10.22271/09746315.2019.v15.i3.1230>

ABSTRACT

The experimental material was newly developed sorghum parental lines (25 B-lines and 38 R-lines) which were evaluated in RBD in two trials for two consecutive years (2016 & 2017) at research Farm, College of Agriculture, Indore in rainy seasons. The objective of the present study was to identify stable grain sorghum lines and also evaluate them for grain yield and other agronomic attributes (days to 50% flowering, plant height, leaf length, leaf width, leaf area, panicle length) and suitable for kharif season using GGE biplot analysis. Genetic variation was the major contributor for LL, LA and GY in B-lines and PL in R-lines. Variance due to genotype \times year interaction effect was a major source of variance for only LL in B-lines. The GE influence was seen only for grain yield in both B- and R-lines. The GY per panicle was high in R-lines (52 to 107g) as compared to B-lines (32 to 79g). Three B-lines (E.Nos. 1, 5, 17) has GY greater than 63g panicle⁻¹ while eight R-lines (I 28, I 32, I 40, I 45, I 47, I 50, I 51 and I 56) had GY greater than 90g panicle⁻¹. Based on mean performance and stability, 1, 14, 7 and 5 were desirable B-lines and 142, 134, 156, 155, RS673 and I26 were desirable R-lines for cultivation and use in further breeding programme over the years.

Keywords: Biplot, mega-environment, sorghum, stability, testers and yield

Sorghum bicolor (L.) Moench is a multipurpose cereal having genome size 730Mb. is a traditionally important cereal crop of India being cultivated in around 5.65 million ha with a production of 4.41 million tons and with a productivity of 740 kg ha⁻¹. The major sorghum growing states in India are Maharashtra, Madhya Pradesh, Karnataka, Andhra Pradesh, Tamil Nadu, Telangana, Gujarat and Rajasthan. In the state of Madhya Pradesh, sorghum is important as a food crop, feed crop and also as a fodder crop for rainfed farming. In view of the multiple usage of the crop, sorghum is presently grown in area of about 2.05 lakh hectare with a productivity 1951 kg ha⁻¹ in Madhya Pradesh (Anonymous, 2018). Over the past few years, sorghum has taken a quantum leap in productivity in Madhya Pradesh on account of development of high yielding hybrids and varieties with photo insensitivity, short stature and high yield along with simultaneous improvement in production technology. The development sorghum hybrid has been possible primarily due to the availability of Cytoplasmic Male Sterile lines (CMS lines). Due to the availability of well established CMS system for sorghum, all the national and state released hybrids are based entirely on the three line system viz., the male sterile line *i.e.* A, maintainer line called B and fertility restorer line R. It is a need of time to ensure nutritional security for the large poor masses of the world *via* enhancing production potential of grain sorghum needs using breeding approaches (Shetty *et al.*, 2013).

In the recent times, with uncertainty around the climate conditions and the constantly changing/evolving climatic and/or environmental factors, evaluation of genotypes (parental lines) for consistence of performance in different environment conditions is of utmost importance to enable development of stable high performing hybrids. Change in environmental conditions has major impact on performance of genotypes. The occurrence of large G \times E interaction becomes a major hurdle in direct selection for relative phenotypic performance related to genetic constitution and selection of genotypes becomes extremely onerous. Therefore it is pertinent to understand the type of interaction between genotype and the environment in order to make testing and the ultimately selection of more efficient genotypes. This increased efficiency in selection of genotype will lead to the identification of stable parental lines which are necessary to increase productivity levels.

The GGE biplot is one of the most reliable method for stability analysis over the mega-environments (ME) data analysis and it pin points that only GEI and G are the most relevant factors and must be considered simultaneously when evaluating genotypes over mega environments even though the measured yield is a result of combination effect by Genotype (G), Environment (E) and genotype \times environment interaction (GEI). Yan *et al.*, 2000 reported that GGE it very easy for one to see which genotype won in which environments because it is based on singular value decomposition of

environment centered yield data. GGE is a better way to underline all genotypic interactions and visualize them simultaneously (Rakshit *et al.*, 2012). Keeping above points in view, Indore AICSIP centre has developed a number of B and R lines. The present study has been conducted for identification of stable B and R parental lines which can contribute towards.

MATERIALS AND METHODS

Location

The present research experiment was conducted out during *kharif* 2016-17 and 2017-18 at Research Farm of College of Agriculture, RVSKVV, Indore. Indore is in Madhya Pradesh, India and situated in western part of Malwa plateau. Its geographical location is between latitude 22°43' N and longitude 75°58' E and at an altitude of 555.7 meters above the mean sea level. The semi-humid and subtropical climate of Indore is having temperature ranges from 23° to 42°C in summer and 7° to 29°C in winters, respectively. Most of the rainfall is received during in June to early October months of the year and it receives 936 mm of average annual rainfall. More specifically, during the experimental year 2016, the annual rainfall was 1108.4 mm with a total of 43 rainy days and in the year 2017 the annual rainfall was 705.1 mm with a total of 42 rainy days.

Experimental material

In present study, 25 sorghum maintainer lines (B lines) including 24 recently developed B lines which were developed at Indore, AICSIP centre during 2004-2015 were used and one previously existing B line (IMS 9B). The material also comprised of 38 sorghum restorers (R lines) including 33 restorers developed at Indore, AICSIP centre and the remaining from other AICSIP canters.

The two separate experiments during each year were conducted out in a RBD(Randomized Block Design) having three replication. The material was sown in the last fortnight of June, 2016 and 2017 at Research Farm, College of Agriculture, RVSKVV, Indore.

Each genotype was sown in two rows, 5 m long with row to row distance of 45 cm and plant to plant distance of 12-15 cm. Recommended package of practices was followed for raising the experimental crop.

Observations recorded

Seven biometrical observations *i.e.* days to 50% flowering, plant height (cm), leaf length (cm), leaf width (cm), leaf area (cm²), panicle length (cm) and grain yield per plant (g) were recorded on five randomly selected plants of the B and R lines in each replication in each trial and mean was obtained.

Statistical analysis

ANOVA for individual years were done following standard procedure for analyzing Randomized Block Design. Bartlett's homogeneity test was used to determine homogeneity of residuals variance. Year and replication were treated as random effects and genotype was treated as fixed effects. Later on pooled analysis of variance was performed to partition out environment (E), genotype (G) and the GE interaction (Yan *et al.*, 2000). For analysis of variance and biplots generation GenStat v. 10 was used.

RESULTS AND DISCUSSION

Analysis of variance

Analysis of variance for pooled year for B and R-lines is tabulated in table 1, which gives a clear measure of the relative magnitudes of the G (genotype), E (year), and GE (genotype × year) variance terms and showed that genotype and year effects were significant for all the traits in both season. Environment was always the most important source of variation, accounting for 1 to 98% of the G+E+GE and major source of variation for days to 50% flowering (DF) and plant height (PHT) in both B- and R-lines, panicle length (PL) in B-lines and leaf length (LL), leaf width (LW), leaf area (LA) and grain yield (GY) in R-lines. Gauch and Zobel (1997) reported that normally in MET(multi-environment trials) data, environment accounts for about 80 per cent of the total variation. Similarly, about 83 to 94 per cent of variability was explained by environment for sorghum MET data in several studies (Rakshit *et al.*, 2012, Reddy *et al.*, 2014). Genetic variation was the major contributor for LL, LA and GY in B-lines and PL in R-lines. Variance due to genotype × year interaction effect was a major source of variance for only LL in B-lines. However, it contributed to more than 10% of the G+E+GE for leaf width, leaf area in B-lines, PL in R-lines and GY in both B- and R-lines (Table 1). Since GE was smaller than G and E for almost all the traits, the results are discussed with respect to pooled data. The GE influence was seen only for grain yield in both B- and R-lines. Hence, GGE is presented only for grain yield.

Mean performance

The B-lines flowered from 67 (E. No. 1 and 7) to 82 days (E. No. 24) and had a plant height ranging from 106 (E. No. 4) to 180cm (E. No. 25). The R-lines flowered from 66 (I 3) to 83 days (I 56) and had a plant height ranging from 129 (I 29) to 220cm (I 54). For photosynthetically active parts, wide variability was noted among the parental lines with LL ranging from 59 to 90 cm, LW from 5 to 9cm and LA from 226 to 586 cm². Wide variation was also noted among the yield

Table 1: Analysis of variance for agronomic and yield traits in B- lines for pooled data

Source of variation	d.f.	DOF	Ph (cm)	LL (cm)	LW (cm)	LA (cm ²)	PL (cm)	GY per plant (g)
Genotype	24	39.7**	1513.0**	49.8**	3.2**	13747**	33.2**	395.1**
Year	1	1705.7**	6855.8**	13	0.0	497	388.1**	22.1
Genotype x Year	24	9.4**	157.0**	76.9**	1.2**	7963**	14.7*	167.6**
Residual	49	2.3	58.3	18.6	0.4	2566	7.4	46

* DOF: days to 50% flowering, PH: plant height (cm), LL: leaf length (cm), LW: leaf width (cm), LA: leaf area (cm²), PL: panicle length (cm) and GY/Plant: grain yield /plant (g)

Table 2: Analysis of variance for agronomic and yield traits in R- lines for pooled data

Source of variation	d.f.	DOF	Ph (cm)	LL (cm)	LW (cm)	LA (cm ²)	PL (cm)	GY per plant (g)
Genotype	37	56.3**	1961.7**	185.8**	2.6**	25354**	45.1**	797.3**
Year	1	3710.5**	29652.2**	3344.5**	144.7**	1048732**	4.1	1982.9**
Genotype x Year	37	8.8**	334.5**	75.1**	1.8**	13756**	10.2**	483.7**
Residual	75	1.8000	39.1	24.6	0.3	1877	2.6	164.4

Table 3: Mean performance of B-lines evaluated for pooled data

E. No.	Genotype	DOF	Ph (cm)	LL (cm)	LW (cm)	LA (cm ²)	PL (cm)	GY per plant (g)
1	13-1-3-6-3-1B	67	136	69	8.2	421	25.5	78.8
2	22-1-6-2-2-7B	70	178	59	5.0	226	27.5	32.3
3	33-2-3-1-1B	75	177	68	8.0	400	27.5	52.3
4	34-2-2-2-1B	77	106	70	8.0	416	25.3	36.8
5	40-1-1-1-3-2-20B	71	163	78	8.4	487	26.8	63.8
6	44-2-4-3-13B	74	174	69	7.8	397	26.8	49.5
7	6-1-1-1-3-1-3B	67	126	72	9.3	497	20.0	53.8
8	IMS 15B	76	169	70	7.8	405	26.3	51.3
9	IMS 16B	71	179	73	6.9	373	24.8	55.5
10	IMS 17B	74	166	69	7.1	363	24.5	44.0
11	IMS 18B	70	156	67	7.5	377	24.5	35.5
12	IMS 19B	73	173	70	7.5	387	28.5	50.3
13	IMS 20B	74	175	70	8.3	429	27.0	50.0
14	IMS 22B	72	166	75	8.6	475	30.8	58.0
15	IMS 23B	72	151	76	9.2	522	35.8	53.8
16	IMS 26B	75	169	69	8.0	409	28.3	50.8
17	IMS 27B	77	152	69	8.1	417	28.5	65.5
18	IMS 28B	75	123	69	8.7	441	27.5	46.3
19	IMS 29B	75	175	71	8.2	430	28.5	41.0
20	IMS 30B	75	176	68	7.7	389	27.5	41.0
21	IMS 31B	75	169	70	8.0	416	27.5	48.3
22	IMS 32B	74	156	68	6.9	345	25.8	41.8
23	IMS 34B	76	170	70	8.5	438	31.3	49.5
24	IMS 35B	82	151	67	7.5	374	24.8	50.8
25	IMS 9B	72	180	69	6.8	345	28.5	50.3
Mean		73	161	70	7.8	407	27.2	50.0
CV(%)		2.1	4.8	6.2	8.3	12.4	10	13.6
LSD(0.05)		3	15	9	1.3	102	5.5	13.6

Table 4: Mean performance of R-lines evaluated for pooled data

Genotype	DOF	Ph (cm)	LL (cm)	LW (cm)	LA (cm ²)	PL (cm)	GY per plant (g)
I3	66	159	71.3	7.1	377	26.5	60.5
I12	75	151	75.8	8.8	499	26.3	58.0
I14	68	173	68.0	6.5	327	26.8	55.2
I26	77	166	77.5	8.9	513	27.3	88.2
I27	73	170	67.0	7.6	385	26.0	84.7
I28	80	190	84.8	8.5	538	33.5	106.7
I29	75	129	76.3	8.2	470	27.5	69.5
I30	77	152	84.0	8.0	504	27.0	72.7
I31	75	146	76.8	8.5	493	30.0	84.0
I32	75	148	75.0	8.1	453	30.0	91.5
I33	71	145	66.8	8.0	395	27.0	60.5
I34	77	157	70.8	8.0	418	32.8	82.5
I35	80	153	75.5	7.6	425	29.5	67.2
I36	79	141	71.0	6.9	361	27.5	79.7
I37	72	165	73.8	8.0	449	25.8	82.7
I38	76	174	77.5	8.7	503	30.5	86.0
I39	71	192	70.8	8.0	426	25.3	74.2
I40	78	173	80.5	8.8	532	33.5	90.7
I42	80	170	80.0	7.9	467	32.3	82.7
I43	78	162	79.3	8.9	521	29.0	74.5
I44	75	167	77.0	7.5	432	27.5	62.2
I45	73	209	81.8	8.1	501	28.8	94.2
I46	73	164	75.8	7.8	446	27.3	60.5
I47	78	186	81.8	9.2	585	28.5	92.2
I48	78	189	67.0	7.3	367	24.8	67.0
I49	68	204	69.5	7.1	368	25.0	76.7
I50	79	173	73.0	7.9	429	30.0	97.8
I51	76	171	90.0	8.8	586	30.3	95.2
I52	70	156	82.5	7.6	476	25.0	55.0
I53	76	200	69.0	6.6	336	24.3	67.5
I54	76	220	72.3	6.8	365	24.5	69.2
I55	74	218	74.0	7.5	417	30.5	85.7
I56	83	186	88.8	8.6	576	37.0	90.7
C 43	76	140	62.5	6.5	301	22.5	52.0
C 85	75	145	62.5	5.5	255	24.0	57.5
KR 125	71	174	70.3	7.6	396	22.5	63.2
RS 673	77	173	70.3	7.4	387	32.5	87.5
SU 8-4	77	144	63.0	7.5	352	23.3	70.5
Mean	75	169	74.6	7.8	438	27.9	76.2
CV(%)	1.8	3.7	6.7	6.8	9.9	5.8	16.8
LSD(0.05)	3	12	9.9	1.1	86	3.2	25.5

Mean performance vs. stability of the genotypes

traits with PL ranging from 20 to 36cm among B-lines and 23 to 37cm among the R-lines. The GY per panicle was high in R-lines (52 to 107g) as compared to B-lines (32 to 79g). Three B-lines (E.Nos. 1, 5, 17) has GY greater than 63g/panicle while eight R-lines (I 28, I 32, I 40, I 45, I 47, I 50, I 51 and I 56) had GY greater than 90g/panicle. The high yielding B- and R-lines can be utilized for development of high yielding hybrids.

GGE biplot was used for graphical presentation of performance and stability of B-lines (Fig. 1) and R-lines (Fig. 2) and evaluated by using average environment coordination (AEC) method described by (Yan, 2002). For grain yield, environment centered and genotype metric biplot is presented. As the first 2 PCs explained 100% of the (G+GE) variability in the data, the biplot adequately approximated the variability in G × E data

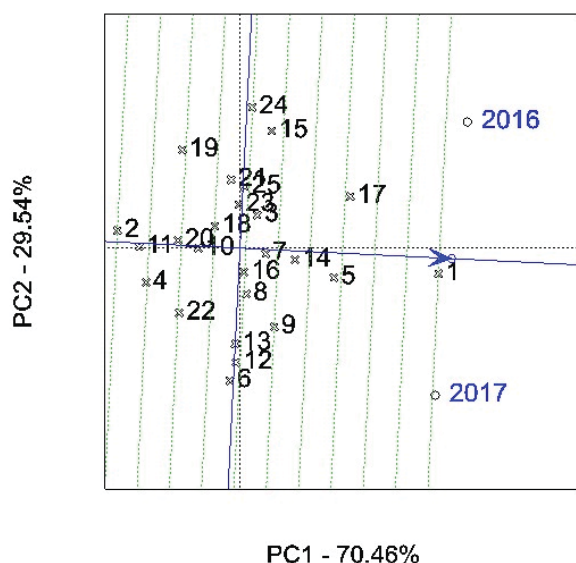


Fig. 1: Pooled data analysis for grain yield and GGE Biplots: Mean vs. stability of the B-Lines (B-Lines codes are in table 3)

(Yan *et al.*, 2010). In Fig.1 and 2, the line with single arrow head is the AEC abscissa. It pointed towards higher mean values and passes via the biplot origin and marker for average environment. The perpendicular lines which are passing through the biplot origin are referred as AEC ordinate represents the stability of genotypes. The absolute length of the projection of a cultivar determine its stability more length less stability. The projections of their markers to the AEC abscissa, further represents the average yield performance of genotypes (Yan *et al.*, 2010). The AEC ordinate separates entries with below-average means from those with above-average means.

Based on the mean performance, the B-lines 1, 17, 5 had grain yield above 60g/plant and the B-lines 14,9,7,15,3 and 8 had grain yield above 50g/plant. This can also be visualized in the Figure 1 as they are present towards the arrow head and away from origin. From among these entries, the B-lines, 1, 14 and 7 are highly stable having minimal projection from the AEC abscissa followed by the B-line 5. On A-axis, either direction away from the biplot origin indicates reduced stability and greater G×E interaction (Yan, 2002). Similarly, from the mean performance for grain yield, 17 R-lines had GY greater than 80g/panicle. Among them, I 42, I 34, I 56, RS 673, I 55 and I 26 were stable for grain yield across years with low projection from AEC abscissa. Swapna *et al.*, 2017 had reported similar results in a set of 8 x 8 diallel cross in well watered and water stressed conditions and analyzed using GGE biplot and identified that IS23514 found to be the best specific combiner in

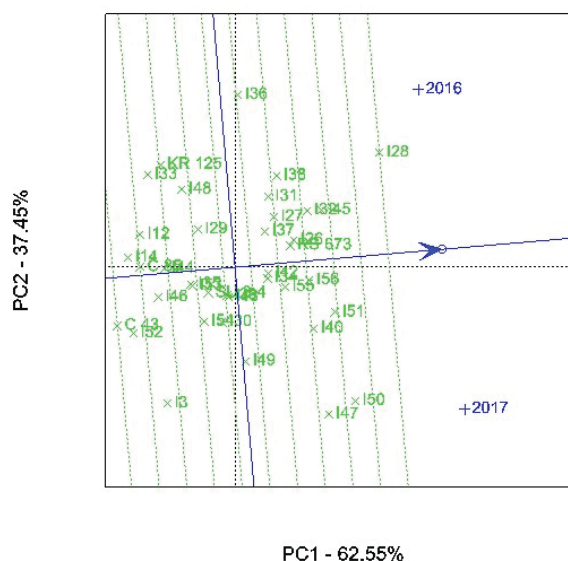


Fig. 2: Pooled data analysis for grain yield and GGE Biplots: Mean vs. stability of the R-Lines (R-Lines codes are in table 4)

well watered condition while IS40752 found to be the best specific combiner in water stressed condition for the trait plant height. The biplot also helped in identifying promising specific combiners, like P. Anuradha x IS40752 for the trait Days to flowering.

For broad selection, genotypes having high mean yield and high stability will be considered as ideal. In the biplot, they are close to origin and have the shortest vector from the AEC abscissa. Based on mean performance and stability, the order of stable and desirable B-lines are 1, 14, 7 and 5 and the order of R-lines is I42, I34, I56, I55, RS673 and I26 which can be used further for hybrid/varieties development for high grain yield.

REFERENCES

- Anonymous, 2018. Directorate of Farmer Welfare & Agriculture Development, Bhopal.
- Gauch, H.G. and Zobel, R.W. 1997. Identifying mega-environment and targeting genotypes. *Crop Sci.*, **37**: 381-85.
- Rakshit, S., Ganapathy, K.N., Gomashe, S.S., Rathore, A., Ghorade, R.B., Kumar, N.M.V., Ganesmurthy, K., Jain, S.K., Kamtar, M.Y., Sachan, J.S., Ambekar, S.S., Ranwa, B.R., Kanawade, D.G., Balusamy, M., Kadam, D., Sarkar, A., Tonapi, V.A. and Patil, J.V. 2012. GGE biplot analysis to evaluate genotype, environment and their interactions in sorghum multi-location data. *Euphytica* : **185** : 465-479.

Identification of sorghum parental lines

- Reddy, S.P., Reddy, B.V.S and Rao, S. P. 2014. Genotype by sowing date interaction effects on sugar yield components in sweet sorghum (*Sorghum bicolor* (L.) Moench). *SABRAO J. Breeding Genetics*, **46** (2): 241-55.
- Shetty, P.K., Ayyappan, S. and Swaminathan, M.S. 2013. Climate Change and Sustainable Food Security. Editors Shetty PK, Ayyappan S and Swaminathan MS, Published by National Institute of Advanced Studies. ISBN: 978-81-87663-76-8.
- Swapna, M., Rakshit, S., Ganapathy, K.N. and Talwar, H.S. 2017. Biplot analysis of combining ability in elite Rabi sorghum genotypes under irrigated and drought situations . *Agric. Update*, **12** (8):2164-2170.
- Yan, W. 2002. Singular-value partitioning in biplot analysis of multi environment trial data. *Agron. J.* **94**: 990-96.
- Yan, W., Frégeau-Reid, J.A., Pageau, D., Martin, R.A., Mitchell Fetch, J.W., Etienne, M., Rowsell, J., Scott, P., Price, M., De Haan, B., Cummiskey, A., Lajeunesse, J., Durand, J. and Sperry, E. 2010. Identifying essential test locations for oat breeding in eastern Canada. *Crop Sci.* **50**: 504-15.
- Yan, W., Hunt, L.A., Sheng, Q. and Szlavnic, Z. 2000. Cultivar evaluation and mega-environment investigation based on GGE biplot. *Crop Sci.* **40**: 597-605.