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Identification of superior parental lines for seed quality and storability through GGE biplot analysis of line × tester data in grain sorghum

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Abstract

Identification of superior parental lines and their hybrid combinations for seed quality traits pave the way for enhancement of crop stand and yield *per se*. A line × tester analysis was carried out using GGE biplot to identify best combiners for seed quality and storability in 6 A and 9 R grain sorghum lines. ANOVA showed significant effects of lines, testers and their interactions for all the traits. L2 (296A) proved to be a poor combiner for all the traits both in fresh (FS) and aged seeds (AS), while L1 (2219A) was the best combiner for germination (G) and field emergence (FE) in FS, and L6 (IMS 9A) for seedling vigour index (SVI) of FS. 'Which-won-where' analysis proved that L1 (2219A) gave the best or near the best cross combination with all testers for G-FS, G-AS, FE-FS and FE-AS. L6 (IMS 9A) combined well with majority of testers for SVI-FS and SVI-AS. It was observed that the SCA effect of lines which come out in 'mean-versus-stability' analysis may not necessarily identify lines with SCA in favorable direction. Polygon view gives a better visualization of the heterotic pattern. T6 (C43) proved to be the best tester for G-FS and G-AS, and was near ideal tester for all other traits except for SVI-FS. For SVI-AS, T1 (CS 3541) proved to be better than T6 (C 43). Among all testers T3 (RS 29) was relatively less informative for being non-discriminatory or non-representative in most of the cases.

Key words: GGE biplot analysis, line x tester data, seed quality and storability traits, grain sorghum

Introduction

World over sorghum [*Sorghum bicolor* (L.) Moench] is the fifth most important cereal crop after wheat, rice, maize and barley. It is extensively cultivated in the semi-arid tropics of Africa, Asia and America predominantly as source of food, feed, fodder and recently as biofuel. It is highly valued for its adaptation ability to different abiotic stresses, including drought, heat, salinity and flooding (Harris et al. 2006; Ejeta and Knoll 2007). In five yearly average India tops the list among the sorghum producing countries in terms of area, and ranks third to the USA and Mexico in total production (FAO, accessed on Dec 08, 2015). In India sorghum is cultivated in 6.18 mha area with an annual production of 5.28 mt. India has two distinct adaptive types, rainy season (*kharif*) and post-rainy season (*rabi*) sorghum to be cultivated. Rainy season sorghum with higher acreage under hybrids has higher productivity as compared to post-rainy sorghum with lesser acreages under hybrids (Rakshit et al. 2014b).

The success of sorghum hybrids in India has necessitated the production of sorghum hybrid seeds on large scale. Initial establishment of good crop stand is the prerequisite for maximizing the yield potentials of a cultivar. Quality seed leads to establishment of good crop stand by influencing good germination and supply of nutrients to the growing seedlings through a better root system (Dhillon and Kler 1976). Vigour of the seedlings influences nutrient uptake from the soil, there by enhances the vegetative growth. Simply by improving crop stand through better seed germination, significant improvement in yield can be achieved. For genetic improvement in seed quality traits the choice of right parents with desired traits has much significance in sorghum breeding program. Little work has been reported on combining ability analysis of seed quality traits in sorghum (Garcia et al. 1999; Kannababu et al. 2005). Identification of superior parental lines and their hybrid combinations for enhanced crop establishment and planting value shall pave the way for enhancement of commercial yield on per hectare basis. Evaluation of cytoplasmic genic

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male sterile lines and restorer lines for better hybrid seed vigour, storability along with productivity remains to be streamlined in hybrid seed research in order to identify the best general and specific combiners for subsequent utilization to formulate suitable breeding programmes for the improvement of these traits.

In assessing inbred lines to develop hybrid cultivars information on general combining ability (GCA) and specific combining ability (SCA) are important indicators (Abdel-Moneam et al. 2014; Hallauer, 1990). Differences in GCA effects are attributed to additive and epistatic genetic effects, *vis-à-vis* SCA effect are attributed to non-additive genetic variance, including dominance and epistatic genetic effects (Falconer 1981). Diallel and line × tester analysis, are the two most commonly used biometric tools to establish dominance-recessive relations, various types of gene effects, and combining abilities of the parents. Though diallel analysis (Jinks and Hayman 1953; Hayman 1954) is a very potent tool to decipher genetics of trait across the parents studied, it is very labor-intensive, particularly in case a higher number of genotypes are to be evaluated (Fotokian and Agahi, 2014). Line × tester analysis, as suggested by Kempthorne (1957) is a faster and reliable method in which large number of parental lines are crossed to few broad based testers to estimate combining ability and selecting lines for hybrid development (Ruswandi et al. 2015). The method has extensively been used in various crop plants including sorghum (Thakare et al. 2014; Padmashree et al. 2014; Sandeep et al. 2010).

Conventional line x tester analysis is limited to obtain general combining ability (GCA) for each genotype and specific combining ability (SCA) for each cross while a biplot displays the most important entry by tester patterns of the data and allows the visualization of GCA of each genotype, SCA of each genotype, groups of parents with similar genetics, and superior hybrids (Yan and Hunt, 2002). Thus, biplot representation of any two way data aids in visualization of complexity of interaction in the data in a convenient way (Yan 2001). Yan and Hunt (2002) demonstrated the applicability of GGE biplot, which originally developed to analyze and visualize two-way genotype x environment data, in visualization of combining abilities of lines. Since then GGE biplot has been employed in analysis and interpretation of diallel data in various crop plants (Anido et al. 2004, Yi et al. 2006, Bertoia et al. 2006, Malla et al. 2009). Narro et al. (2003) indicated possibility to deploy AMMI and SREG models toward effective visualization of GCA and SCA of genotypes in line × tester data. Akinwale et al. (2014) further demonstrated use of GGE biplot analysis in analyzing line × tester data. Fotokian and Agahi (2014) reported identification of suitable parents, heterotic crosses and the best hybrids in rice line × tester data using GGE biplot. Ruswandi et al. (2015) successfully employed GGE biplot in heterotic grouping and combining ability analysis of 46 maize mutant lines crossed to three testers. However, this method is not used for line x tester analysis in sorghum specially for its seed quality and storability traits. In this background the current work was carried out with two objectives: (1) to identify the best combiners for seed quality and storability traits, (2) to identify group of parents based on heterotic relationships for seed quality and storability traits using GGE biplot analysis.

Materials and methods

Experimental material

The study material consisted of six male sterile (MS) lines, *viz*., 2219A, 296A, 14A, 104A, 27A and 9A and nine restorer (R) lines, *viz*., CS3541, MR750, RS29, AKR150, RS585, C43, RS673, Indore 12 and R354. Pedigree details of the genotypes used in the study are given in Table 1. The six MS lines and nine R-

Table 1. Details of the lines and testers used in the study

Code	Name	Pedigree
Lines		
L1	2219A	Selection from Kharif Shallu
L2	296A	IS3922 x Karad local
L3	14A	(MR 760 × BT 632) × AKMS 2B
L4	104A	296B x Swati
L5	27A	83B × 199B
L6	IMS 9A	2077A × (MA9B × Vidisha 60-1) 11-4-2-5-5A
Testers		
T1	CS 3541	IS 3675 × IS 3541
T2	MR 750	Sel. MR 841 (SC 108-3×CS 3541-27)
T3	RS 29	SC 108 × SPV 126
T4	AKR 150	CS 3541 × 900
T5	RS 585	[(CS3541x M35-1) x Nandyal Rabi Local]
T6	C 43	CS3541 × IS23549
T7	RS 673	SPV 544 × K 24-1
T8	Indore 12	(SSV 53 × SPV 475) -7-1-1-1
T9	AKR 354	[SPV 504x(SPV 504x R 263) x R 67-4]

lines were crossed in line × tester mating design through controlled pollinations leading to 54 cross combinations (F_1 seed).

Seed trait evaluation

The fresh seeds of the parents and their crosses with initial moisture content of 10% were used for the experiment. The experiments were conducted during 2008 to 2010 at the ICAR-Indian Institute of Millets Research (formerly Directorate of Sorghum Research), Rajendranagar, Hyderabad under the ambient storage conditions. For accelerated ageing studies,a sub-set from each seed sample was used in an ageing chamber as described (Delouche and Baskin 1973). The fresh seeds and accelerated aged seeds were tested for seed germination, and seedling vigour index in paper towels (between paper method) as per International Seed Testing Association (ISTA 2004) protocols. The vigour index was calculated by multiplying mean germination percentage by mean dry weight of single seedling and expressed in the nearest whole number. The field emergence of fresh and accelerated aged seeds was tested by sowing the seeds in four replications each of 50 seeds in cement pots (45 cm diameter) filled with soil. After 10 days, the seedlings with leaves above the soil surface were considered as emerged and noted in percentage. The traits germination of fresh seeds (G-FS) and accelerated aged seeds (G-AS), field emergence of fresh seeds (FE-FS) and accelerated aged seeds (FE-AS), and seedling vigour index of fresh seeds (SVI-FS) and accelerated aged seeds (SVI-AS) were used to analyze and interpret the combining abilities of the parental lines for initial seed quality (fresh seeds) and storability (accelerated aged seeds).

Data analysis

In the present study, GGE biplot was adopted to analyze the L x T data and interpret the combining abilities of the parental lines. GGE concept is originated for analysis of multi-environment trials of crop varieties. Performance of a cultivar in an environment is considered as mixed effect of genotype main effect (G), environmental main effect (E) and genotype × environment interaction (GEI). In GGE biplot analysis E is removed from the model, while G is integrated with the GE interaction effect (Yan *et al*. 2000). Towards a generalized application of GGE biplot to any two-way data with similar data structure, the cultivars are treated as entries and environments as testers (Yan, 2001). In using the GGE biplot for line × tester data, the average yield and stability of genotypes corresponded to respectively GCA and SCA of parents. Contrary to conventional numerical line × tester analysis where SCA relates to a cross, in GGE biplot SCA represents that of parental lines. Mathematical model for GGE biplot analysis of line × tester data has been elaborated by Ruswandi et al. (2015) as follows:

$$Y_{ij}-b_j = a_1e_{i1}h_{j1}+a_2e_{i2}h_{j2}+e_{ij}$$

where, Y_{ij} is genotypic values of the combination (pure inbred lines or F_1 hybrids) between inbred i and tester j for a given trait; b_j average value of all combinations with tester j, a_1 and a_2 are singular values for PC1 and PC2. e_{i1} and e_{i2} are PC1 and PC2 eigenvectors for inbred i (entry), respectively; h_{j1} and h_{j2} are PC1 and PC2 eigenvectors for tester j, respectively; e_{ij} is the residual of model for inbred i and tester j. Data were analyzed using GGE biplot software ver. 7.9 (Yan, 2001) without scaling (Tranform = 0; Scaling = 0; Centring = 2).

Results and discussion

GGE biplot has extensively been used to study complex GEI in multilocation testing data in various crops including sorghum (Rao et al. 2011; Rakshit et al. 2012, Rakshit et al. 2014a, Aruna et al. 2015, Rakshit et al. 2016). The general and interaction effects in a two-way table as come out in GGE biplot can be extended in viewing the GCA and SCA in a cross and identifying best cross combinations both in diallel (Anido et al. 2004; Yi et al. 2006; Bertoia et al. 2006; Vivek et al. 2009; Darvishzadeh et al. 2009; Malla et al. 2009) and line × tester data (Fotokian and Agahi 2014; Ruswandi et al. 2015; Kahriman et al. 2016). Such graphical display of relationship between lines and/or testers helps easy visualization of their combining ability. Use of such an approach in sorghum is lacking.

GCA effects of lines and testers based on GGE biplot model

ANOVA of GGE biplot is presented in Table 2. All the three traits (seed germination, field emergence and seedling vigour index of fresh and aged seeds) showed significant effects of lines, testers and their interaction. Proportion of total variation explained by lines ranged from 23.6% (SVI-FS) to 46.8% (FE-AS). Testers explained variation in the range of 7.4% for SVI-FS to 12.9% for G-AS. Interaction explained variation to the extent of 25.6% for G-AS to 43.1% for FE-FS. Average

Table 2. ANOVA of GGE biplot analysis of different traits

Source	DF	G-FS		G-AS		SVI-FS		SVI-AS		FE-FS		FE-AS	
		MS	%SS	MS	%SS	MS	%SS	MS	%SS	MS	%SS	MS	%SS
Line	5	1485.7**	39.6	1256.0**	42.8	1008096**	23.6	1101463**	29.9	763.6**	34.6	1375.8**	46.8
Tester	8	273.2**	11.7	237.4**	12.9	196489**	7.4	265456**	11.5	118.9**	8.6	148.9**	8.1
Line x tester	40	151.9**	32.4	94.1**	25.6	200192**	37.5	149861**	32.6	118.9**	43.1	134.5**	36.6

DF: Degrees of freedom; MS: Mean sum of square; TSS: Total sum of square; * p <0.05 and ** p<0.01, respectively; G-FS: Germination of fresh seeds; G-AS: Germination of accelerated aged seeds; SVI-FS: Seedling vigour index of fresh seeds; SVI-AS: Seedling vigour index of accelerated aged seeds; FE-FS: Field emergence of fresh seeds; FE-AS: Field emergence of accelerated aged seeds.

tester coordination (ATC) views for each trait are presented in Fig. 1 (a, b) and (c, d). Cumulative explanation of total variation by PC1 and PC2 was maximum (85.5%) in case of SVI-AS and minimum (76.9%) for G-FS. A GGE biplot is said to adequately approximate the variability in the two way data when the first two PCs explain more than 60% of the variability in the data, and the combined interaction effect account for more than 10% of the total variability (Yang et al. 2009; Yan et al. 2010; Rakshit et al. 2012). Thus, it may be said that all the biplots of the line x tester data as presented in Fig. 1 (a, b) and (c, d) have succinctly explained the inherent complexity in data. The small circle on the average tester axis represents the average tester, which is defined by the average PC1 and PC2 values of all testers (Yan and Kang 2003). The line passing through the biplot origin and the average tester is referred to as average tester axis or ATC abscissa. The perpendicular line to the ATC passing through the origin of biplots shown with both side arrow heads in Fig. 1 (a, b) and (c, d) is referred to as ATC ordinate. Akinwale et al. (2014) explained that the length of the average tester vector measures the relative importance of the GCA versus line x tester interaction. In all the cases, the distances are quite pronounced indicating GCA effects to be sufficiently important (Ruswandi et al. 2015). Projection of the entries onto the ATC abscissa denotes GCA effects of the entries. The arrow head indicates the highest GCA effects. Thus, for germination of fresh seeds (G-FS) L1 displayed highest GCA effects, and the relationship among the lines was L1>L3>L5>L6>L4≅L2 for GCA effects (Fig. 1a). The relation almost retained under accelerated aging for the trait (G-AS) as well (L1>L3>L6>L5>L4>L2) (Fig. 1b). For seedling vigour index (SVI-FS) the relation was L6>T5>T4≅L1≅L3>L2, and under accelerated aging (SVI-AS) the relation turned to be T6>L3≅L1≅L5≅L4>L2. For field emergence (FE-FS) the GCA effects were similar to G-FS. Observed relationship was comparable according to conventional GCA analysis (data not shown) which brought out the line L1 with significant and positive *gca* effects for G-FS (12.11**), G-AS (8.71**), SVI-FS (18.36), SVI-AS (14.29), FE-FS (7.33**) and FE-AS (9.58**). Whereas, line L2 showed significantly negative *gca* effects for G-FS (-4.68*), G-AS (-8.01**), SVI-FS (-289.45**), SVI-AS (-301.54**), FE-FS) (-6.16**) and FE-AS (-9.45) followed by L4. The mean performance values also indicated the superiority of the line L1 for all initial seed quality (G-FS, SVI-FS, FE-FS) and storability (G-AS, SVI-AS, FE-AS) traits (Table 3). The study clearly brought out L2 to be a poor combiner for all the traits both under normal and accelerated aging, while L1 to be best G-FS and FE-FS and L6 for SVI-FS. Similarly GCA for the testers was also visualized by switching the role of lines and testers, and conducting mean-versus-stability analysis. For G-FS the GCA relationship among testers was T3>T1>T7>T4>T8>T5>T2>T9>T6 (Fig. 1c). Under accelerated ageing again for this trait (G-AS) the GCA relationship among testers turned out to be T3>T1>T4>T8>T7≅T2>T6>T5>T9 (Fig. 1d). For seedling vigour index of fresh seeds (SVI-FS) the relationship was T8>T4≅T1≅T3≅T2>T6>T7>T9>T5 and for aged seeds (SVI-AS) it turned out to be T8>T3>T4≅T5>T1≅T2≅T9>T7. When compared these results to the conventional GCA analysis (data not shown) which revealed the testers T8 and T4 with positive *gca* effects for G-FS (1.14 and 1.71), SVI-FS (213.36** and 66.07) and FE-FS (2.32 and 0.09). Whereas, tester T9, T6, T5 and T2 showed negative *gca* effects for G-FS, SVI-FS and FE-FS traits. Under accelerated ageing, the testers T3, T1 and T8 showed positive *gca* effects for G-AS (4.7*, 3.65 and 1.12), SVI-AS (44.25, 1.83 and 206.88) and FE-AS (4.22**, 2.89* and 1.26), whereas the testers T6, T5, T7 and T9 showed negative *gca* effects for G-AS, SVI-AS and FE-AS traits. Following similar approach in line x tester dataset, Futokian and Agahi (2014) identified in rice lines with better cooking quality

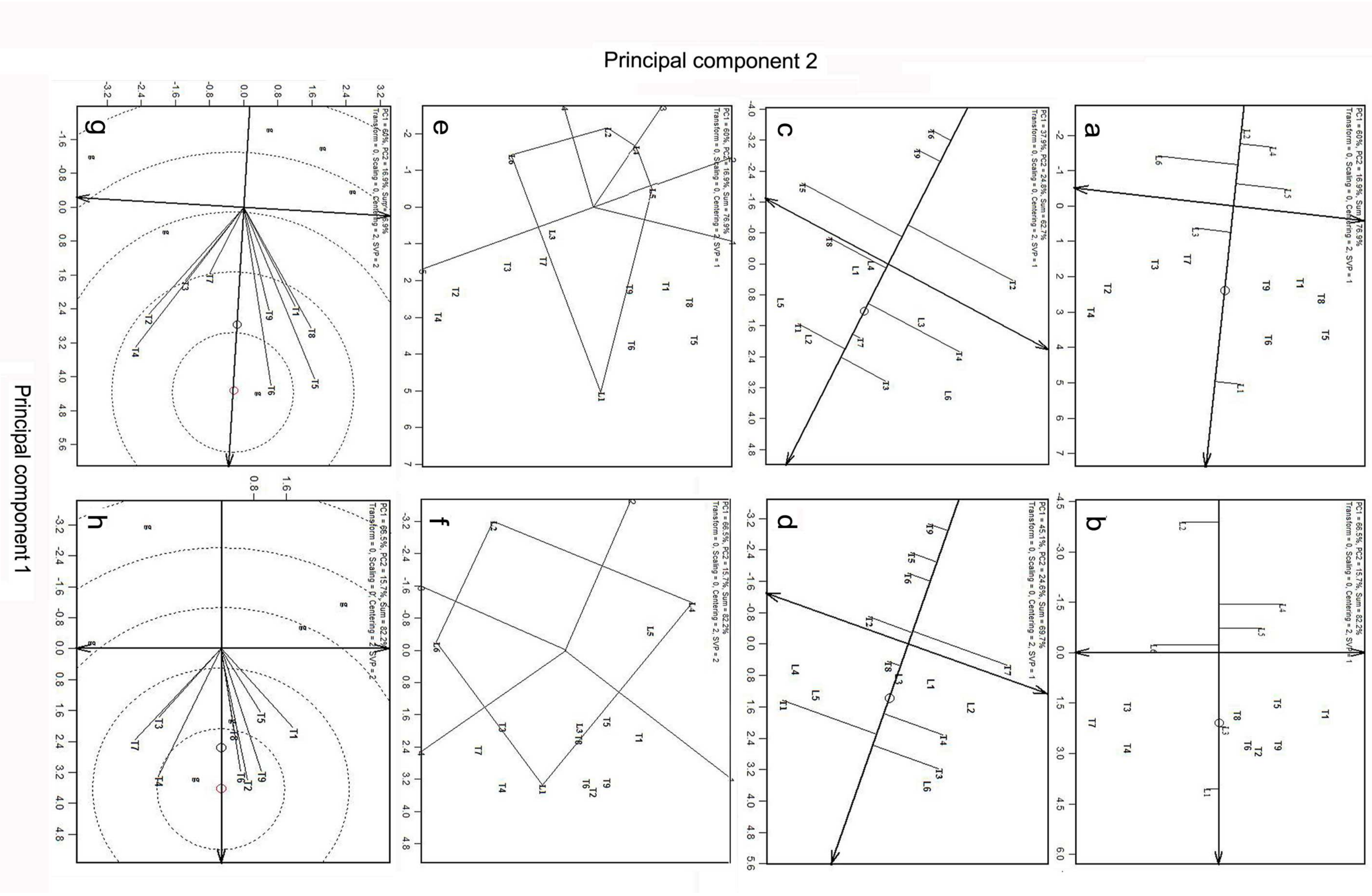

Fig. 1. (a, b). Mean-versus-stability view of lines for G-FS (a), G-AS (b). Genotype code as in Table 1; (c, d). Mean-versus-stability view of testers for G-FS (c), G-AS (d). Genotype code as in Table 1; (e, f). Which-won-where plot for G-FS (e), G-AS (f). Genotype code as in Table 1; (g, h). Mean-versus-stability view of GGE biplot for G-FS (g), G-AS (h). Genotype code as in Table 1

and Ruswandi et al. (2015) identified maize mutants with better GCA for days to tasseling, days to maturity and per plant grain yield. Recently Kahriman et al. (2016) effectively deployed similar system in maize to identify better combining genotypes for oil content and other oil quality traits.

SCA effects of lines and testers identified using GGE biplot

The projections of the lines onto the ATC ordinate indicate their SCA effects (Yan and Hunt 2002; Akinwale et al. 2014). Yan and Hunt (2002) pointed out that in conventional analyses, SCA is associated with crosses rather the parents. However, GGE biplot of such crosses bring out this additional advantage. Observed SCA indicates the tendency of the lines to produce superior hybrids with specific testers. In the current study L6 followed by L5 showed highest SCA for G-FS, while L5 and L4 for G-AS (Fig. 1a,b). L4 both for seedling vigour index of fresh seeds (SVI-FS) and aged seeds (SVI-AS) demonstrated highest SCA, respectively. Among testers highest SCA effect for G-FS was noticed in T2 followed by T5 and T4 (Fig.1c), while that for G-AS was in T7, T1, T3 and T4 in decreasing order (Fig. 1d). In case of SVI-FS, T9 followed by T8, T7 and T4 recorded high SCA. For SVI-AS, testers with high SCA were T7 followed by T2 and T9. However, identified genotypes with highest SCA not necessarily indicate always SCA towards positive direction but bring out only higher numerical values without the sign of it. Akinwale et al. (2014) with GGE biplot analysis of a line ´ tester data set of Singh and Choudhury (1977) successfully identified lines with better SCA.

Best crosses between lines and testers and identified heterotic relationships among lines

It may be observed in Fig. 1 that in all cases nearly equal numbers of testers were positioned on the same side of the ATC ordination axis. These suggest that GCA was significantly large enough in each case, and the testers could classify the lines into distinct heterotic groups (Akinwale et al. 2014). Lines closer to ATC axis may not show heterosis, while the distant ones will be. For example for G-FS, L1 will be heterotic with L2 and L4 but L3 with L5 and L6 may not be heterotic (Fig. 1a). For SVI-FS and SVI-AS, L6 will be heterotic with L2 but not other combinations, and for FE-FS and FE-AS, L1 and L2 will be heterotic.

The polygon view of ‘Which-won-where’ analysis of GGE biplot provides us opportunity to visualize which tester combines well with which line (Yan and Hunt 2002, Akinwale et al. 2014). The entries located on the vortex of the polygon are the best mating partners with the testers in the same sector and the poorest-mating partners with the testers in other sector. Similarly, lines at the vortex of opposite sector will be poorest with the testers in facing section. Further, entries located near the biplot origin are less responsive to the changes of testers (Ruswandi et al. 2015). For G-FS, L1 combines well with all testers, as all of them fall in the same sector at vortex of which L1 was placed (Fig. 1e). All other lines were poor combiners with the testers. This is true for germination of accelerated aged seeds (G-AS) as well except for L3 (Fig. 1f). For SVI-FS, L6 combines best with T4, T6, T3 followed by other testers except T8 and T9, with which L4 combined well. In case of SVI-AS, L4 combined well with T2 and T9, while L6 with the other testers, best being with T4. L1, L3 and L5 being placed at the origin of the biplot found to be nonresponsive. Yan and Hunt (2002) were first to indicate possibility to identify best combiners using GGE biplot approach in diallele crosses. Subsequently, GGE approach has been deployed in identifying best combiners in diallel crosses across crops (Anido et al. 2004 in squash; Yi et al. 2006 in Brassica; Bertoia et al. 2006 in maize, Vivek et al. 2009 in maize; Darvishzadeh et al. 2009 in sunflower; Malla et al. 2009 in wheat). Employing GGE biplot in line x tester data set best combiners have been identified in rice (Futokian and Agahi 2014) and maize (Ruswandi et al. 2015, Kahriman et al. 2016) for quality and yield attributing traits. Observed combination pattern clearly indicated why L1 was best combiner for G-FS and G-AS, FE-FS and FE-AS. It may be observed that it was at the vortex of the sector covering all for G-FS and G-AS, or majority of testers for FE-FS and FE-AS. Similarly, L6 combined well with majority of testers for SVI-FS and SVI-AS making it best general combiner for the said traits. It may be noted that though L6 has come out to be best with highest SCA for G–FS (Fig. 1a), it failed to combine well with any tester (Fig. 1e). This is because it is placed at the opposite side of the ATC ordinate. This holds true in other cases as well. Hence, the SCAs effect of lines which may come out in mean-versus-stability pattern may not necessarily identify lines with desirable SCA. Polygon view always gives a better visualization of the heterotic pattern.

Best testers for assessment of GCA of the lines

In multi-location trial data best environment can be identified using GGE which has maximum

Table 3. Superior sorghum lines, testers and their crosses identified based on mean performance for initial initial seed quality (fresh seeds) and storability (accelerated aged seeds).

S.No.	Trait	Range (among 69 genotypes)	Grand mean	Best lines (2)	Best testers (2)	Best cross combinations (5)
1	Seed germination (%) (G-FS)	48-96	80	2219A (88), 14A (85)	Indore12 (96), RS673 (94)	2219A x AKR150 (96), 2219A x RS585 (96), 2219A x Indore12 (95), 2219A x CS3541 (95), 2219A x C43 (94)
2	Seed germination (%) (G-AS)	38-87	68	2219A (77), 27A (74)	RS673 (86), C43 (78)	2219A x AKR150 (87), 2219A x Indore 12 (86), 2219A x RS29 (82), 14A x RS29 (82), 27A x CS3541 (82)
3	Seedling vigour index (SVI-FS)	594-1842	1222	2219A (1606), 14A (1561)	RS585 (1580), C43 (1484)	IMS9A x AKR150 (1842), 104A x Indore 12(1838), 27A x Indore12 (1756), 104A x R354 (1595), IMS9A x Indore12 (1561)
4	Seedling vigour index (SVI-AS)	334-1522	945	2219A (1433), 27A (1104)	C43 (1134), Indore12 (939)	IMS9AxAKR150 (1522), IMS9A x Indore 12(1378), 27A x Indore12 (1375), IMS9A x RS673 (1359), 104A x Indore12 (1273)
5	Field emergence (%) (FE-FS)	38-90	70	2219A (84), 27A (73)	RS673 (88), Indore12 (86)	2219A x Indore12 (90), 2219A x C43 (86), 2219A x RS673 (83), 2219A x MR750 (82), IMS9A x AKR150 (82)
6	Field emergence (%) (FE-AS)	25-82	58	2219A (70), 27A (65)	RS673 (81), R354 (71)	2219A x C43 (82), 2219A x RS673 (79), 2219A x R354 (79), 2219A x Indore 12 (77), IMS9A x AKR150 (74)

representativeness as well as discrimination ability (Rakshit et al. 2014a; Aruna et al. 2015). This means it must fall on the ATC axis to be representative of all environments and its vector should be longest to be most discriminating. Following same principle ideal tester can also be identified from GGE biplot, which has mentioned two criteria (Yang and Kang 2003). In Fig. 1 (g, h) such ideal testers are indicted by small circle at the center of the concentric rings. It is quite obvious that hardly any tester will be exactly ideal, i.e. will fall on the center of the concentric rings but one or two may be closer to it. For G-FS ideal tester was T6, while that for G-AS also T6 along with T2 and T9 (Fig. 1g, h). T6 was near ideal tester for all other traits except for SVI-FS. For SVI-AS, T1 proved to be better than T6. Among all testers T3 found to be relatively less informative as it mostly remained closer to origin of biplot (non discriminatory) or away from the ATC axis (non representative). Following similar approach Akinwale et al. (2014) identified best tester in an earlier published data of Singh and Choudhary (1977). Futokian and Agahi (2014) successfully identified best tester for cooking quality in rice using similar approach. Ruswandi et al. (2015) also could identify best testers for crop phenology and plant yield using similar approach.

The present GGE biplot analysis indicated that 2219A was the best combiner for G-FS and FE-FS and IMS 9A for SVI-FS. 296A in general proved to be a poor combiner for all the traits both in fresh and aged seeds. C43 found to be the best tester for G-FS and G-AS, and was near ideal tester for all other traits except for SVI-FS. For SVI-AS, CS 3541 was a better tester than C 43.

Authors' contribution

Conceptualization of research (NKB, RMS); Designing of the experiments (NKB, RMS); Contribution of experimental materials (NKB, VAT, IKD, KRN); Execution of field/lab experiments and data collection (NKB, VAT, IKD, KRN); Analysis of data and interpretation (SR, NKB, IKD); Preparation of manuscript (SR, NKB, IKD, RMS).

Declaration

The authors declare no conflict of interest.

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