



GENETIC ANALYSIS ON AGRONOMIC AND QUALITY TRAITS OF SORGHUM HYBRIDS IN INDONESIA

E.P. RINI¹, D. WIRNAS^{2*}, TRIKOESOEMANINGTYAS² and D. SOPANDIE³

¹Major of Plant Breeding and Biotechnology, Department of Agronomy and Horticulture, Faculty of Agriculture, Bogor Agricultural University, Bogor, 16680, Indonesia

²Plant Genetics and Breeding Division, Department of Agronomy and Horticulture, Faculty of Agriculture, Bogor Agricultural University, Bogor, 16680, Indonesia

³Division of Ecophysiology, Department of Agronomy and Horticulture, Faculty of Agriculture, Bogor Agricultural University, Bogor 16680, Indonesia

Corresponding author's email: trikadytia@gmail.com

E-mail addresses of co-authors: erinpuspitarini@gmail.com, dwirnas@gmail.com, didysopandie@gmail.com

SUMMARY

The genetic parameters of 14 sorghum hybrids developed by crossing between seven lines and two testers were analyzed by line \times tester analysis. The analysis of variance revealed significant differences among genotypes, parents, and F_1 hybrids. The presence of non-additive gene effects was realized by higher values of specific combining ability (SCA) compared to general combining ability (GCA), a ratio of variance of SCA to GCA, and the average degree of non-additive. The proportional contribution of testers was observed to be lower than that of line \times tester interaction resulted in higher estimates of SCA variances. The estimates of GCA effects indicates that male parent 'Numbu' and female parent 'B-69' were found to be good general combiners for grain yield. The specific cross combination i.e., 'B-69 \times Numbu' was found to be the best cross combination to have a desirable SCA effects for grain yield which could be further utilized in developing a hybrid variety.

Key words: Combining ability, gene action, genetic parameters

Key findings: Breeding material evaluated had adequate genetic variability which may be exploited further in breeding programs. Among the lines, B-69 and among testers the Numbu were considered to be good combiners and the best cross combinations for grain yield traits. The three studied traits were under the control of additive gene action and the six traits were managed by non-additive gene action.

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INTRODUCTION

Sorghum (*Sorghum bicolor* (L.) Moench) is one of the alternative potential crops to be developed in Indonesia. Sorghum is used not only for food, but also for fodder and animal feed, sugar, and

bio-energy sources (Dahlberg *et al.*, 2011). Sorghum has high carbohydrate content (73 g in 100 g material) and protein, calcium, and vitamin B1 content are higher than rice and maize (Ratnavathi and Patil, 2013). From the environmental aspects, sorghum is one of the

crops that can be adapted to the extreme agro-climatic conditions such as drought and flood (Reddy *et al.*, 2007).

Sorghum productivity in Indonesia only reached to one ton ha⁻¹ because of the growing of local variety with minimum fertilizer use (Sirappa, 2003). Meanwhile, sorghum productivity in America and Canada has achieved the target of seven tons ha⁻¹ with the use of hybrid varieties (FAO, 2011). Therefore, improving the productivity of sorghum in Indonesia through genetic approaches like hybrid sorghum varieties is necessary. Hybrid sorghum technology will offer an opportunity to boost the yield of sorghum and make sorghum more attractive for farmers to grow. Besides the high yield performance, hybrids were found stable under a wide range of environmental conditions (Hausmann *et al.*, 1999).

In hybrid breeding programs, the knowledge of combining ability of the parents and the inheritance of the traits is important (Hochholdinger and Hoecker, 2007). Combining ability is the measure of a parental genotype to transmit their genetic superiority to its offspring when crossed with other individuals. Combining ability always used as a key basis for parent selection and the foundation for generating elite hybrid combinations in breeding works (Falconer and Mackay, 1996).

The knowledge of combining ability is useful to assess nicking ability among genotypes and to elucidate the nature and magnitude of gene action involved in the inheritance of various traits. Its role is important to choose parental genotypes, crosses, and appropriate breeding procedures to be followed to select desirable segregants (Salgotra *et al.*, 2009). The general combining ability could identify superior parental genotypes whereas specific combining ability helps in identification of good specific hybrid combinations which may ultimately lead to the development of hybrids (Indhubala *et al.*, 2010; Saleem *et al.*, 2008). The presence of non-additive genetic variance is the primary justification for initiating the hybrid program (Siles *et al.*, 2004). Line × tester analysis provides information about general and specific combining ability effects of parents and their F₁ hybrids, respectively and is helpful in estimating various types of genes action.

This research was aimed to obtain information on the combining ability of the parental lines and explored the genetic rule and heritability of main agronomic and quality traits, aiming at providing genetic information as a basis for hybrid sorghum breeding.

MATERIALS AND METHODS

Experimental site and year

This study was conducted at Leuwikopo Field Research and Plant Breeding Laboratory, Bogor Agricultural University, West Java, Indonesia. The seven lines and two testers were crossed through line × tester mating design during 2013, and the evaluation of the F₁ hybrids with parental genotypes was carried out during crop season 2014.

Methodology

A total of 23 genotypes were used in this study consisted of seven lines (N/UP-17-10, N/UP-89-3, N/UP-32-8, PI-150-20-A, PI-10-90-A, PI-150-21-A, B-69), two testers (Numbu, Kawali), and 14 F₁ hybrids. The experiment was laid out in a completely randomized design with three replications. Each plot consisted of three rows; 2.1 m long with 70 cm spacing between rows. All the rows were thinned to 10 cm between hills and to keep one plant per hill. Standard cultural practices for optimum sorghum production were carried out. A dose of fertilizer (23 kg ha⁻¹ for N, 36 kg ha⁻¹ for P and 60 kg ha⁻¹ for K) was applied as a basal dose, with a further 46 kg ha⁻¹ of N top dressed 4 weeks after planting and then incorporated into the soil.

All the recommended agronomic and plant protection practices were uniform by following the crop growth period for raising ideal crop stand.

Statistical analysis

Each row consisted of 10 plants and 5 plants were taken randomly from each row as sample. Agronomic observations were recorded on the plant height, stem diameter, leaf number, panicle length, panicle diameter, panicle weight, grain

weight per panicle, and 1000-grain weight. The grains were carried out also for a quality test (protein and tannin content) at Saraswanti Indo Genetech laboratory, Indonesia. Protein content (%) was tested by Foss Tecator Kjeltac 8400 method and tannin content (%) was tested by spectrophotometric method.

The data analysis includes variance analysis (ANOVA) at $\alpha = 5\%$ and line \times tester analysis to estimate combining ability, genetic variance (genotype, phenotype, lines, testers, additive, dominance, GCA), degree of dominance, variance ratio, narrow sense and broad sense heritability based by using Ms. Excel, SAS programme and R studio (Kempthorne, 1957; Singh and Chaudary, 1979).

RESULTS

The analysis of variance revealed highly significant differences among the genotypes, parents, crosses and parent vs. crosses for all traits studied, except tannin content in crosses component and 1000 grain weight and protein content in parent vs. crosses component (Table 1). In analysis of variance, the lines component revealed significant differences for traits i.e., plant height, stem diameter, leaf number, panicle length, and 1000-grain weight. Meanwhile, the tester component revealed nonsignificant differences for all traits except grain weight per panicle. The line \times tester interactions revealed significant differences for plant height, leaf number, panicle diameter, panicle weight, and grain weight per panicle (Table 1).

The proportional contribution of lines, testers and their interaction to the total variance showed that lines showed greater contribution than tester for all traits (Table 2). Line \times tester interactions revealed greater contribution than the testers for all the traits except 1000-grain weight.

Genetic parameters

The results revealed that plant height, panicle weight, and tannin content have higher GCA variance than SCA resulted higher additive variance than dominance variance with variance ratio of more than one and degree of dominance

less than one (Table 3). Meanwhile, stem diameter, leaf number, stem diameter, panicle weight, grain weight per panicle, and protein content revealed higher SCA variance than GCA resulted in higher dominance variance than additive variance, with variance ratio less than one and degree of dominance higher than one.

Broad sense heritability (h^2_{bs}) of all traits was higher than narrow sense heritability (h^2_{ns}) (Table 3). There was medium broad sense heritability ($0.2 \leq h^2_{bs} \leq 0.5$) for all traits except protein content because protein content showed the low narrow sense heritability ($h^2_{ns} \leq 0.2$) (Stanfield, 1983). The narrow sense heritability of these agronomic and quality traits was in ranking order i.e., plant height > panicle length > stem diameter > leaf number > 1,000 grain weight > protein content > panicle diameter > tannin content > weight grain per panicle > grain weight.

Combining ability

Among lines, PI-150-20-A was a good general combiner for short plant stature with general combining ability value of -44.72. The line N/UP 17-10 was the best general combiner for larger stem diameter and leaf number with GCA values of 6.37 and 2.58, respectively. The line B-69 as the female parent could be used to improve the yield characters because it had the best GCA effects for panicle length, diameter and panicle weight traits with values 5.85, 8.68, and 7.78, respectively. The line PI-150-21-A was the best combiner for grain weight per panicle traits and 1000 grains weight with GCA values of 8.98 and 5.24, respectively. The line PI-10-90-A had the best general combining ability for protein content with a value 0.59, while N/UP 32-8 was the best combiner for tannin content with a value of -0.12 (Table 4).

Among testers, Numbu was a good general combiner for leaf number (0.23), panicle diameter (0.94), panicle weight (6.33), grain weight per panicle (7.27), and 1000-grain weight (1.51). These result revealed that Numbu as a male parent could be better used for yield improvement as compared to Kawali. Male parent Kawali would be good to shorten plant height and widen the stem diameter with GCA values of 0.57 and 0.13, respectively.

Table 1. Analysis of variance for various agronomic and quality traits in sorghum.

Source of variation	d.f.	Plant height	Stem diameter	Leaf number	Panicle length	Panicle diameter	Grain weight	Grain weight panicle ⁻¹	1000-grain weight	Protein content	Tannin content
Genotypes	22	6898.6**	43.53**	8.37**	52.50**	448.29**	1825.7**	1544.3**	84.9**	1.49**	0.22**
Parent	8	7677.1**	14.65**	9.92**	36.36**	201.45**	1424.2**	1046.8**	153.9**	2.29*	0.47**
Parent vs. crosses	1	3176.9**	486.84**	30.00**	193.54**	6201.95**	19873.4**	16144.5**	0.024 ^{NS}	1.29 ^{NS}	0.36**
Crosses	13	6705.9**	27.20**	5.76**	51.59**	157.61**	684.5*	727.5**	48.9**	1.02*	0.07 ^{NS}
Lines	6	13151.4**	52.00**	10.36 ^c	103.75**	175.14 ^{NS}	379.1 ^{NS}	396.7 ^{NS}	81.1**	1.47 ^{NS}	0.07 ^{NS}
Testers	1	3450.2 ^{NS}	0.65 ^{NS}	2.27 ^{NS}	13.83 ^{NS}	36.77 ^{NS}	1680.4 ^{NS}	2222.1 ^{NS}	96.3*	0.75 ^{NS}	0.16 ^{NS}
Line x Tester	6	802.95**	6.83 ^{NS}	1.74*	5.72 ^{NS}	160.22**	823.82*	809.1**	8.8 ^{NS}	0.62 ^{NS}	0.0 ^{NS}

*, ** – significant at 5% and 1% level of probability, NS – Non-significant, d.f. – degree of freedom

Table 2. Percent contribution of different component (lines, testers and line × tester) towards the hybrid sum of squares for various agronomic and quality traits in sorghum.

Traits	Contribution (%)		
	Lines	Testers	Line × Tester
Plant height	90.52	3.96	5.53
Stem diameter	88.22	0.18	11.59
Leaf number	83.03	3.03	13.94
Panicle length	92.82	2.06	5.11
Panicle diameter	51.29	1.79	46.92
Panicle weight	25.56	18.89	55.55
Grain weight per panicle	25.17	23.50	51.34
1,000-grain weight	76.58	15.15	8.27
Protein content	66.30	5.68	28.03
Tannin content	49.15	18.67	32.18

As shown in Table 4, different cross combinations were found highly varied in specific combining ability which indicated that the genetic interaction was complex and diverse. For instance, the specific combining ability of plant height was found highest in cross combination PI-150-21-A × Kawali (-19.85), followed by F₁ hybrids PI-10-90-A × Numbu (-14.20) and PI-150-21-A × Numbu (19.85) (Table 5). The specific combining ability of

panicle weight varied from -20.08 (B-69 × Kawali) to 20.08 (B-69 × Numbu). The specific combining ability of leaf number, panicle length, 1000-grain weight, protein, and tannin content, were relatively less, indicating that these traits do not have advantage. During selection of parental genotypes and cross combinations, the specific combining ability should be considered rather than general combining ability.

Table 3. Estimates of genetic components of variance, degree of dominance and heritability for various agronomic and quality traits in sorghum.

Genetic components	Plant height	Stem diameter	Leaf number	Panicle length	Panicle diameter	Grain weight	Grain weight panicle ⁻¹	1000 grain weight	Protein content	Tannin content
σ^2 lines	2058.07	7.53	1.44	16.34	2.49	-74.12	-68.74	12.06	0.14	0.004
σ^2 testers	126.06	-0.29	0.03	0.39	-5.88	40.79	67.28	4.17	0.01	0.01
σ^2 GCA	192.33	0.66	0.13	1.49	-0.08	-4.54	-2.66	1.31	0.01	0.0006
σ^2 SCA	141.11	0.98	0.26	0.53	28.93	134.68	161.19	0.51	0.04	0.00
Variance ratio (σ^2 GCA/ σ^2 SCA)	1.36	0.68	0.51	2.81	-0.002	-0.03	-0.02	2.56	0.31	0.00
σ^2 Additive (σ^2_A)	384.65	1.33	0.26	2.99	-0.17	-9.08	-5.32	2.61	0.03	0.0013
σ^2 Non-additive (σ^2_D)	192.81	1.27	0.35	0.65	38.15	178.66	213.38	0.64	0.05	0.0005
Degree of dominance (σ^2_D/σ^2_A) ^{1/2}	0.71	0.98	1.16	0.47	14.98	4.44	6.33	0.49	1.29	0.62
Broad-sense heritability (h^2_{bs})	0.31	0.29	0.28	0.29	0.27	0.24	0.27	0.28	0.18	0.22
Narrow-sense heritability (h^2_{ns})	0.05	0.03	0.03	0.05	0.00	0.00	0.00	0.03	0.02	0.00

Table 4. General combining ability effects of lines and testers for various agronomic and quality traits in sorghum.

Parents	Plant height	Stem diameter	Leaf number	Panicle length	Panicle diameter	Grain weight	Grain weight panicle ⁻¹	1000 grain weight	Protein content	Tannin content
Lines										
N/UP 17-10	-29.64	6.37	2.58	-5.10	0.66	-13.72	-11.13	-4.22	0.03	-0.03
N/UP 89-3	-26.08	-0.73	0.18	-2.61	-3.49	-6.84	-8.23	1.56	-0.18	-0.10
N/UP 32-8	26.11	0.63	0.58	-4.68	3.67	4.43	6.65	4.11	0.13	-0.12
PI-150-20-A	-44.72	-2.28	-1.20	2.66	-6.53	-2.42	-5.82	-2.45	-0.76	-0.07
PI-10-90-A	66.35	-1.33	-0.21	1.59	-5.15	5.75	4.18	-1.25	0.59	0.12
PI-150-21-A	51.31	-1.29	-0.93	2.29	2.16	5.02	8.98	5.24	0.58	0.13
B-69	-43.31	-1.37	-1.00	5.85	8.68	7.78	5.38	-2.99	-0.39	0.08
S.E(gi)	6.30	0.70	0.34	0.77	2.72	6.89	5.23	1.06	0.27	0.09
S.E(gi - gj)	8.92	0.98	0.49	1.09	3.85	9.75	7.40	1.50	0.39	0.12
Testers										
Numbu	9.06	-0.12	0.23	-0.57	0.94	6.33	7.27	1.51	-0.13	-0.06
Kawali	-9.06	0.12	-0.23	0.57	-0.94	-6.33	-7.27	-1.51	0.13	0.06
S.E(gi)	3.37	0.37	0.18	0.41	1.46	3.68	2.80	0.57	0.15	0.05
S.E(gi - gj)	4.77	0.53	0.26	0.58	2.06	5.21	3.96	0.80	0.21	0.07

Table 5. Specific combining ability effects of lines and testers for various agronomic and quality traits in sorghum.

Cross combination	Plant height	Stem diameter	Leaf number	Panicle length	Panicle diameter	Grain weight	Grain weight panicle ⁻¹	1000 grain weight	Protein content	Tannin content
N/UP 17-10 × Numbu	-9.23	-2.08	0.27	0.12	-1.46	-10.16	-12.98	-1.38	0.03	0.10
N/UP 17-10 × Kawali	9.23	2.08	-0.27	-0.12	1.46	10.16	12.98	1.38	-0.03	-0.10
N/UP 89-3 × Numbu	5.32	-0.30	0.28	-1.19	-3.73	-8.92	-7.30	-0.82	0.21	0.06
N/UP 89-3 × Kawali	-5.32	0.30	-0.28	1.19	3.73	8.92	7.30	0.82	-0.21	-0.06
N/UP 32-8 × Numbu	-6.65	-0.04	0.27	1.45	6.27	4.35	6.58	-0.99	0.10	0.01
N/UP 32-8 × Kawali	6.65	0.04	-0.27	-1.45	-6.27	-4.35	-6.58	0.99	-0.10	-0.01
PI-150-20-A × Numbu	6.81	1.04	0.43	-0.40	0.87	3.52	0.75	0.74	-0.38	0.00
PI-150-20-A × Kawali	-6.81	-1.04	-0.43	0.40	-0.87	-3.52	-0.75	-0.74	0.38	0.00
PI-10-90-A × Numbu	-14.20	-0.20	-1.14	-0.61	-6.19	-13.58	-12.22	1.81	0.23	-0.11
PI-10-90-A × Kawali	14.20	0.20	1.14	0.61	6.19	13.58	12.22	-1.81	-0.23	0.11
PI-150-21-A × Numbu	19.85	0.73	0.04	-0.53	7.44	4.71	6.35	-0.45	0.32	0.07
PI-150-21-A × Kawali	-19.85	-0.73	-0.04	0.53	-7.44	-4.71	-6.35	0.45	-0.32	-0.07
B-69 × Numbu	-1.90	0.87	-0.15	1.17	-3.20	20.08	18.81	1.09	-0.52	-0.13
B-69 × Kawali	1.90	-0.87	0.15	-1.17	3.20	-20.08	-18.81	-1.09	0.52	0.13
S.E.	8.92	0.02	0.49	1.09	3.85	9.75	7.40	1.50	0.39	0.12
SE (sij-skl)	12.61	0.03	0.69	1.55	5.45	13.79	10.47	2.12	0.55	0.17

DISCUSSION

The significant differences of mean squares between parental genotypes and F₁ crosses for most of the traits indicated the data suitability for combining ability studies. Further, significant mean squares of parent vs. crosses revealed good scope for the manifestation of heterosis in all traits except in 1000-grain weight and protein content traits (Table 1). These results coincide with the finding of Rahimi *et al.* (2010) who also found significant differences among parent vs. crosses. The significant differences between line × tester interactions for plant height, leaf number, panicle diameter, panicle weight, and grain weight per panicle indicated that specific combining ability attributed heavily in the expression of these traits and provide the importance of dominance or non-additive variance for the traits.

The significant mean squares of line and tester component revealed the presence of

additive variance, whereas the nonsignificant means square revealed the presence of non-additive or dominance variance. Plant height, stem diameter, leaf number, panicle length and 1000-grain weight traits in lines component were affected by additive variance. Meanwhile, stem diameter, grain weight, grain weight per panicle, protein and tannin content traits in lines component and all traits in tester component except grain weight per panicle affected by non-additive or dominance variance.

The proportional contribution of lines, testers and their interaction to the total variance showed that lines played an important role towards the traits indicating predominant lines influence for traits (Table 2). It also suggested that in the hybrid sorghum breeding more efforts should be paid to the selection of lines. The greater contribution of line × tester interaction than the testers for all the traits except 1,000-grain weight indicated higher estimates of specific combining ability variance effect. These

results are in agreement with the gene action that controlled the trait was very important to thoroughly understand the effect of the parents and their interaction on agronomic and quality traits of hybrid. The presence of non-additive genetic variance is the primary justification for initiating the hybrid program (Siles *et al.*, 2004). Major role of non-additive gene effects in the manifestation of the traits was observed by higher value of specific combining ability variance (σ^2 SCA) than the general combining ability variance (σ^2 GCA), ratio of σ^2 GCA/ σ^2 SCA being less than one, greater value of non-additive variance (σ^2 D) than the additive variance (σ^2 A) and degree of dominance (σ^2 D/ σ^2 A)^{1/2} being higher than one (Table 3).

The results revealed that for plant height, panicle weight, and tannin content, the additive genetic effects were more pronounced than non-additive effects, and the general combining ability variance was higher than specific combining ability. This result suggesting that the inheritance of these traits was mainly controlled by additive genes and selection of parents should be more important in breeding practice.

Meanwhile, stem diameter, leaf number, stem diameter, panicle weight, grain weight per panicle and protein content traits more affected by non-additive/dominance genes thus the interaction of two parents should be more considered. The results indicated the presence of non-additive gene action in the expression of most of all the traits especially in yield traits was a very good prospect for the exploitation of non-additive genetic variation for traits through hybrid breeding. The importance of non-additive genes for expression of yield and its components had also been reported by Thakare *et al.* (2014) and Maarouf (2009).

The low broad sense heritability indicated that environment has larger effect on the expression of the phenotype. Mirarab *et al.* (2011) reported that low narrow sense heritability indicating that non-additive effects play important role in controlling these traits. Therefore, it seems that hybridization must be a choice for utilizing the putative heterosis in special crosses. The important role of non-additive gene action for hybrid breeding also reported by many researchers. Kenga *et al.*

(2004) showed the role of non-additive genes and low narrow heritability in yield traits in sorghum and also found in others crops i.e., rice (Tiwari *et al.*, 2011), pepper (Sitaresmi *et al.*, 2010), and papaya (Sukartini and Budiyanti, 2009).

General combining ability reflects the average performance of a parental genotype to transmit its superiority to offspring and depends on additive gene effects. The higher the general combining ability was the more the related minor genes existed which indicates larger additive genetic effect and more stable heredity (Falconer and Mackay, 1996). The close examination of result revealed that none of the parents showed GCA effects simultaneously in the desired direction for all the traits (Table 3). However, to find the good parent for subsequent hybrid sorghum development, variation in GCA effect was estimated among lines and testers for all the traits. The best general and specific combining ability were chosen by selected genotype in line, tester, and F₁hybrids that had the best values for all traits except plant height and tannin content. Meanwhile, the lowest values of the plant height and tannin content traits were chosen because of the negative selection of these traits (Tables 2 and 3).

For each parent, some agronomic traits showed higher general combining ability, while the others showed lower general combining ability. It was indicated that there was no remarkable differences in general combining ability among various traits of a specific parent, thus it was hard to improve all the traits in hybrids based on one parent. This also suggested that the performance of other traits should be considered when improving a specific trait.

Specific combining ability reflected the non-additive effects of the interaction of two parents in a crossing, i.e., dominant effect, over dominant effect and epistasis effects. It was easily influenced by external environment and does not steadily heritable. While it could be used as a reference for generating combinations (Falconer and Mackay, 1996).

The inheritance of combining ability was relatively complex because the materials with multiple excellent traits usually do not have the best combining ability. Two parents with the strongest heterosis do not necessarily have the

best general combining ability, and the combination with its parents having higher general combining ability do not necessarily have high specific combining ability. For example, B-69 and Kawali had higher general combining ability for plant height traits, but their specific combining ability (B-69 × Kawali) had a higher height and the specific combining ability. Meanwhile, the parent with low GCA may have high SCA. For example, the GCA of plant height in PI-10-90-A and Numbu could make plant higher with the GCA, respectively, but their SCA could shorten the plant height.

Therefore, it was generally thought that to get the combinations with high heterosis, one of the parents must have high GCA. This indicated that GCA of parents did not conform to the SCA in the F₁ cross combinations correspondingly, there is no a necessary correlation. However, the parents with higher GCA harbor more advantageous genes and their combinations usually had higher mean heterosis. Meanwhile, the role of SCA is also not ignorable, determination if which in test lines could provide a reference for the utilization of heterosis, provide the theoretical basis for the design of hybrid combinations.

The selected line indicated that the line was the best female parent because it had a good value than all testers and the selected tester indicated that the tester was the best male parent because it had a good value than all lines. The selected F₁ indicated that the crosses were the best cross combinations for the hybrid. The knowledge of combining ability was useful to assess nicking ability among genotypes and to elucidate the nature and magnitude of gene action involved. Its role is important to decide parents, crosses and appropriate breeding procedures to be followed to select desirable segregants. The general combining ability could identify superior parental genotypes whereas specific combining ability helps in identification of good hybrid combinations which may ultimately lead to the development of hybrids (Hausmann *et al.*, 1999; Sandeep *et al.*, 2010). The other things could be considered in the parent selection is gene action, GCA, SCA, the genetic distance of the parents and the correlation between the traits. According to Xianlin (2012) when the value of GCA is much

larger than the SCA then the trait is controlled by additive gene but if SCA value higher than the GCA then the trait is controlled by non-additive gene action (dominant, dominant over, epistasis). The presence of non-additive genetic variance is the primary justification for initiating the hybrid program.

CONCLUSION

This study highlighted the rewarding parents and crosses of sorghum that can be exploited by sorghum breeders to launch effective breeding strategies. We conclude that breeding material evaluated had adequate genetic variability which may be exploited further in hybrid breeding programs. The result showed that parent 'B-69' as a line and 'Numbu' as a tester were found to be best general combiners for grain yield traits. The crosses between 'B-69' and 'Numbu' was the best specific combination for grain yield traits. The higher value of specific combining ability variance than general combining ability and low narrow sense heritability value make sense that hybrid technique can be used for increasing sorghum productivity.

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