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Original article

Assesment of heterotic hybrid frequency with respect to combining ability in forage sorghum [*Sorghum bicolor* (L.) Moench].

Payal Chaudhary[1], Y.A. Viradiya[2] and Jitali Vaghasiya[1]

[1]Department of Genetics and Plant Breeding, CPCA, SDAU, Sardarkrushinagar

[2]Centre For Forage Research, SDAU, Sardarkrushinagar

**Corresponding Author: payalbencha80@gmail.com*

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ABSTRACT

Combining ability analysis helps in the evaluation of inbreds in terms of their genetic value and the selection of suitable parents for hybridization. It also helps in the identification of superior cross combinations. In the present study, the general combining ability of the 8 parents and the specific combining ability of 15 crosses were estimated through combining ability analysis for qualitative and quantitative characters in forage sorghum using a line × tester mating design. Each parent's overall gca status (high or low), as well as each hybrid's overall sca and heterotic status (high or low) across nine attributes, were ascertained. The lines SRF-414, SRF-420 and tester Malwan registered as good general combiners and The crosses SRF-421 × Gundari, SRF-420 × Malwan, GFS-6 × CSV 46F and SRF-414 × CSV 46F recorded high mean green fodder yield heterotic effect along with positive significant sca effect for green fodder yield per plant and its component characters. The perusal of per se performance as well as the heterotic effect of crosses revealed that the cross SRF-421 × Gundari was best for green fodder yield per plant and its component traits. Among hybrids, eight and seven crosses were classified as having high (H) overall sca and heterotic status, respectively and the remaining were classified as having low (L) overall sca and heterotic status. Furthermore, no inferences could be established regarding the frequency of heterotic hybrids based on gca effects because heterotic hybrids for productivity per se traits might be produced by parents with high, low, or contrasting gca effects in forage sorghum.

Keywords: Forage sorghum, overall gca status, overall sca status, Heterosis.

INTRODUCTION

Sorghum [*Sorghum bicolor* (L.) Moench] is the world's fifth-largest and most important cereal grain crop after wheat, maize, rice, and barley (Assefa *et al*., 2020). Sorghum is a C4 plant that has better photosynthetic efficiency and is more resistant to abiotic stress (Reddy *et al*., 2009). Sorghum's origin and early domestication occurred around 5000 years ago in North-East Africa (Mann, 1983). Ethiopia is the origin and diversity center for sorghum, with a wide range of wild and cultivated varieties available (Doggett, 1988). Sorghum bicolor commonly called sorghum and also referred to as durra or jowari, with a chromosome number 2n = 20. It is an often cross-pollinated crop, having average six percent natural cross pollination and belongs to the grass family Poaceae, subfamily Panicoidae, tribe Andropogonae, and therefore the subtribe Sorghastrae (Price *et al*., 2005). Sorghum ranks first among the cereal fodder crops because of its growing ability in low fertile soil, faster growth habit, higher fodder yield, palatability and nutritious quality. It gives almost uniform green fodder yield throughout the year.

Globally sorghum is grown in an area of 40.76 million hectares with a production of 57.58 million tonnes and productivity 1412.60 kg/ha, (Anonymous, 2022). In India, sorghum is having 3.65 million hectare area, 4.03 million tonnes production and 1106 kg/ha productivity (Anonymous, 2023-24).

In order to make forage sorghum an enterprising and remunerative crop, there is a need to develop varieties and hybrids having early maturity, faster growth and high forage yield coupled with high protein content and low HCN content at the flowering stage. To create such forage varieties/hybrids, knowledge and information on breeding strategies for the genetic improvement of sorghum as a forage crop is necessary. A genetic analysis of quantitative characters for forage is necessary before any breeding methodology can be effectively applied for the improvement of sorghum material.

The application of heterosis is a preferred approach to enhance the productivity potential of crop species where the development of an F_1 hybrid is technically and economically feasible. However, the F_1 hybrid has been the major cultivar option for enhancing sorghum production. Genetic diversity has always been estimated by sorghum breeders to identify suitable parents for the development of the best hybrid combinations. The hypothetical concerns also implied that genetic diversity among prospective parents is important for the success of a hybrid breeding program as it determines the magnitude of heterosis in F_1 hybrid to a large extent (Teklewold and Becker, 2006). However, a strong correlation between heterosis and parental genetic distance has been rarely observed (Melchinger, 1999; Singh and Singh, 2004). The heterotic F1s are helpful in generating a high frequency of productive inbred lines as compared to non-heterotic F1s as observed in Brassica campestris (Arunachalam and Bandopadhyay, 1984). Therefore, the identification of heterotic hybrids is relevant not only for commercial purposes but also for deriving superior inbred lines. In this context, the choice of a parent for developing a high frequency heterotic hybrid is another issue often debate by plant breeders. Considering theoretical analysis of single gene systems with two or multiple alleles (Falconer and Mackay, 1996) and two gene system (Arunachalam and Qwen, 1971), phenotypic/ genetic diversity has been very commonly used criterion for choosing parents for developing heterotic hybrids (Durga Prasad et al., 1985; Arunachalam and Bandopadhyay, 1984). However, when diverse parents are crossed, heterosis is not always found to occur (Cress, 1966). Combining ability (CA) is another criteria that has been used as one of the criteria for choosing the parents for producing a higher frequency of heterotic hybrids. The practical utility of CA lies in the performance prediction of hybrids (Griffing, 1956). Apart from providing an objective criterion for choosing parents, CA also provides useful clues about the mode of action of genes controlling economically important traits. Being used on first degree statistics, the greatest advantage of the

CA approach for genetic analysis is that it is statistically robust and genetically neutral and hence applicable to crops irrespective of their mode of reproduction (Arunachalam and Reddy, 1981). Under these premises, an attempt was made to arrive at a simple and rational criteria for choosing the parents for developing high frequency of heterotic hybrids using experimental data from sorghum.

MATERIAL AND METHODS

Experimental material and design

The present study was carried out in the summer of 2023 and the Kharif of 2023 at the Centre for Forage Research, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar, Gujarat, India. The experimental material chosen for this study consisted of the five genotypes designated as lines (GFS-6, GFS-8, SRF-414, SRF-420 and SRF-421) crossed with three testers (CSV 46F, Gundari and Malwan) during the 2023 summer season following Line × Tester mating design (Kempthorne, 1957). Fifteen F1 and eight parents (Table 1) were evaluated in randomized block design with three replications during the 2023 Kharif season. Each entry was sown in a single row of 2 m in length with a spacing of 45 cm between rows and 15 cm between plants within a row. Recommended agronomic and plant protection practices were followed during the crop growth period to raise a healthy crop.

Collection of data and Statistical analysis

Data were recorded on five randomly selected plants in each of the 15 F_1 and 8 parents and in each replication on thirteen characters viz., days to flowering, plant height, number of leaf per plant, stem girth, leaf length of blade, leaf width of blade, panicle length, grain yield per plant, green fodder yield per plant, dry fodder yield per plant, protein content, Brix content and HCN content. The data were compiled for analysis of the variance of different traits and combining ability was analyzed as a method suggested by Kempthorne (1957) using TNAUSTAT software (Manivannan, 2014). The traits mean of three replications were used for statistical analysis. General combining ability (gca) effects of 3 testers and 5 lines and specific combining ability (sca) effects of 15 F1 hybrids and variances due to gca and sca effects were estimated (Kempthorne, 1957). For each of the thirteen traits, the better parent heterosis (BPH) and standard heterosis (SH) of 15 F1 hybrids were assessed. Given that quantitative and qualitative features might have positive or negative correlations, it is common to find that, for a given parent and hybrid, gca effects, sca effects, BPH and SH respectively, point in the desired direction. Hence, the overall status of parents with respect to their gca effects and the hybrids with respect to their sca effects BPH and SH across traits were determined. Crosses were divided into three categories based on the overall gca status of the parents: HH (both parents in a cross with high overall gca status), HL/LH (one parent with high and the other parent with low overall gca status), and LL (both parents with low overall gca status).

RESULTS AND DISCUSSION

Analysis of variance

An analysis of variance for combining ability showed that, means squares due to lines highly significant for all the traits except leaf width of blade and due to testers highly significant for all the traits. This indicated a significant contribution of both females and males towards general combining ability variance components for all the characters (Table 2). For every character, The mean sum of squares due to line × tester interaction was significant for all traits, suggesting that the experimental material was very variable and that heterosis breeding may potentially improve the many qualities that were being studied. The results are in agreement with the findings of Dehinwal *et al*. (2017) and Ingle *et al*. (2018). The ratio of σ^2gca/σ^2sca being more than unity was found for leaf width of blade and green fodder yield per plant suggesting a greater role of additive genetic variance in the inheritance of this trait. These traits can be improved further as a source of favourable by selecting desired transgressive segregants from segregating generations. The predominant role of additive gene action observed for the leaf width of blade is analogous with results reported earlier by Singh and Singh (2017), Vekariya *et al*. (2017 and Chaudhary *et al*. (2020).

The magnitude of specific combining ability variance was higher than general combining ability variance for the majority of traits which indicated the importance of non-additive gene effects in the inheritance of these traits, which suggests exploitation of these traits for improvement of yield through heterosis breeding. The results are in fidelity with Dehinwal *et al*. (2017), Kumar and Chand (2015), Jadhav and Deshmukh (2017), Joshi *et al.* (2022) and Chudasama *et al*. (2022).

Trait-wise parental gca effects and hybrid sca and heterosis

Variations in the frequency of genes that are passed down to the progeny with the additive and non additive effects account for the variations in gca effects. Tester Malwan was found good general combiner for all the characters having a high gca effect (Table 3). Line SRF-414 was a good general combiner for days to flowering, plant height, stem girth, leaf length of the blade, panicle length and green fodder yield per plant. Line SRF-421 was good general combiner days to flowering, number of leaf per plant, panicle length, grain yield per plant, dry fodder yield per plant, protein content, and HCN content. Given that gca effects are a result of additive and non additive gene effects, the parents listed above have a good chance of yielding their respective characters and could be used in a multiple crossing programme to create a dynamic population that can accumulate most of the favourable genes.

The hybrids varied greatly for their sca effects, just as they did for lines and testers for gca effects (Table 4). The crosses SRF-421 × Gundari, SRF-420 × Malwan, GFS-6 × CSV 46F and SRF-414 × CSV 46F for green fodder yield per plant recorded the highest *sca* effects which were also highest in per se performance. Thus, the cross combination with high per se performance, high *sca* effects, and at least one parent having high *gca* effects would increase the frequency of favourable alleles. select transgressive segregants for desired characters in segregating generations to develop superior lines. According to Joshi *et al.* (2022) Chudasama *et al.* (2022). Rathod *et al*. (2019) and Patel *et al*. (2021), these results are consistent.

When it came to heterosis, the hybrid SRF-421 × Gundari showed the best parent heterosis for all the traits, with the exception of Days to flowering, Stem girth, leaf width of the blade, Panicle length and Brix content. In terms of Days to flowering, panicle length, and green fodder yield per plant, cross SRF-414 × CSV 46F showed better parent heterosis; in terms of stem girth, leaf width of the blade, dry fodder yield per plant, protein content, brix content and HCN content, cross SRF-420 × Malwan showed the highest better parent heterosis. It was clear, therefore, that not every characteristic that affected fodder production contributed equitably to the heterosis for green fodder yield per plant. This could be because of a circumstance that negatively impacted the development of one component while favouring the development of the other. Thus, to create an efficient selection programme and achieve a good yield, the desired level of each component should be determined. Similar results were also reported earlier by Naik *et al*. (2018), Soujanya *et al*. (2018), Patel *et al*. (2018), Rathod *et al*. (2020), Patel *et al*. (2020) and Chudasama *et al*. (2022).

Parental overall gca status and hybrids overall sca and heterotic status

Three of the 5 lines, SRF-421, SRF-414, GFS-8 and one of the three testers Malwan, displayed high overall gca status and the remaining exhibited low overall gca status (Table 5). Similarly among hybrids, eight and seven crosses were classified as having high (H) overall sca and heterotic status, respectively and remaining were classified as having low (L) overall sca and heterotic status (Table 6 and 7). Similarly, Ramesh *et al*. (2000) and Keerthi *et al*. (2016) classified parents based on gca, sca and heterotic status.

Relationship of overall parental gca status with hybrids overall sca and heterotic status

Distribution of crosses with high overall sca and heterotic status in relation to overall parental gca status across qualitative and quantitative traits in forage sorghum is presented in Table 8. Furthermore, hybrids with HH, LH, or HL parental combination types frequently generated hybrids exhibiting a high heterotic status, demonstrating the significance of both additive and non-additive gene actions. The genetic transmission of forage yield and other parameters assessed in sorghum was dominated by both additive and non-additive gene actions (BaduApraku et al., 2021). The relevance of employing parents with diverse GCA effects to generate hybrids with overall high SCA and heterotic status was underlined by these findings (Boraiah et al., 2019). The supremacy of HL or LH crosses was previously noted in sweet sorghum (Sandeep *et al*., 2010), sesame (Ramesh *et al*., 2000), tobacco (Lohitha *et al*., 2010), and dolichos bean (Keerthi *et al*., 2016). For the purpose of optimally utilizing resources; it is worthwhile to begin performing HH, LH, or HL crossing combinations. The theoretical reports supported the use of parents with differing gene frequencies attributed to the diverse combining ability of parents resulting in hybrids with high heterotic status (Cress, 1966; Falconer & Mackay, 1996). The current investigation suggested the unique superiority of HH crosses followed by HL and LH crosses highlighting the importance of choosing parent in realizing superior heterotic hybrids. Thus, using parents with contrasting GCA status can be a suitable strategy to optimize resources and achieve rapid genetic improvement in forage sorghum. The utility of heterotic crosses resulting from divergent genotypes has been amply demonstrated in grain sorghum and finger millet. By utilizing exotic (and temperate) × Indian (and tropical) and dwarf × tall crosses, several grain sorghum varieties and hybrids were developed (Rao, 1972; Rao and Rana, 1982).

CONCLUSION

The efficiency of the breeding programme depends on the predictive power of parental gca effects on hybrid heterosis which would save substantial resources and time. The line SRF-414, SRF-421 and tester Malwan registered as good general combiners for most of the characters. The crosses SRF-421 × Gundari, SRF-420 × Malwan, GFS-6 × CSV 46F and SRF-414 × CSV 46F recorded high mean green fodder yield heterotic effect along with positive significant sca effect for green fodder yield per plant and its component characters. Hence, these crosses were identified as potential for getting good transgressive segregants for green fodder yield per plant and its component traits and suggested for further evaluation in future breeding programme. As in our study, heterotic hybrids for productivity per se traits were created by parents with high, low, or contrasting gca effects, no definite association could be established about the frequency of heterotic hybrids based on gca effects.

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Table 1: **List of genotypes used as parents**

Sr no	Name of Genotype	Source	Sr no	Name of Genotype	Source
Lines			Testers		
1.	GFS-6	CMR, Deesa	1.	CSV 46F	MSRS, Surat
2.	GFS-8	CMR, Deesa	2.	Gundari	CMR, Deesa
3.	SRF-414	MSRS, Surat	3.	Malwan	CMR, Deesa
4.	SRF-420	MSRS, Surat			
5.	SRF-421	MSRS, Surat			
CHECK		CSV 46F			

CMR: Centre for Millet Research

MSRS: Main Sorghum Research Station

Table 2: Analysis of variance (Mean square) for combining ability and estimates of component of variance for different characters in forage sorghum

		Mean sum of square						
Source of variation	**d.f**	**Days to flowering**	**Plant height**	**Number of leaves per plant**	**Stem girth**	**Leaf length of blade**	**Leaf width of blade**	**Panicle length**
Replications	2	3.20	488.86	2.05	3.86	8.84	0.17	1.37
Crosses	22	70.64**	7124.92**	10.90**	27.52**	64.56**	1.81**	94.98**
Testers	2	61.80**	15154.32**	48.10**	76.6**	78.64*	14.63**	314.35**
Lines	4	166.53**	11323.70**	10.78**	44.67**	88.65*	0.43	143.87**
Lines × Testers	8	95.55**	10143.11**	12.57**	34.2**	113.56**	1.10**	110.68**
Error	58	2.62	732.54	2.34	2.74	24.84	0.34	1.89
σ^2 Lines		7.89	131.18	-0.20	1.16	-2.77	-0.07	3.69
σ^2 Testers		-2.25	334.08	2.37*	2.83**	-2.33	0.90**	13.58
σ^2 gca		1.55	257.99*	1.41*	2.20**	-2.49	0.53**	9.91*
σ^2 sca		30.98**	3136.86**	3.41*	10.49**	29.57**	0.21*	35.99**
σ^2 gca/ σ^2 sca		0.05	0.08	0.41	0.21	-0.08	2.13	0.27

Mean sum of square							
Source of variation	**d.f**	**Grain yield per plant**	**Green fodder yield per plant**	**Dry fodder yield per plant**	**Protein content**	**Brix**	**HCN content**
Replications	2	4.78	774.6	114.15	0.05	1.22	4.41
Crosses	22	273.35**	37548.75**	23343.49**	7.76**	9.29**	1009.61**
Testers	2	306.32**	249824.96**	131557.39**	13.13**	35.53**	777.57**
Lines	4	260.76**	26197.08**	16338.54**	8.85**	14.87**	2539.17**
Lines × Testers	8	544.75**	27704.28**	23135.97**	13.63**	9.22**	1312.45**
Error	58	3.49	1991.79	115.16	0.20	1.75	6.57
σ^2 Lines		-31.55	-167.47	-755.26	-0.52	0.62	136.29
σ^2 Testers		-15.90	14808.05**	7228.09*	-0.03	1.75	-35.65
σ^2 gca		-21.77	9192.34**	4234.33*	-0.21	1.33*	28.82
σ^2 sca		180.42**	8612.45**	7636.15**	4.44**	2.44**	435.38**
σ^2 gca/ σ^2 sca		-0.12	1.07	0.55	-0.05	0.54	0.07
***and** indicate significant at 5 *per cent* and 1 *per cent* levels of significance, respectively**							
Where, '-' indicates -ve estimates							

Table 3: Desirable general combiners for qualitative and quantitative traits in forage sorghum

Traits	Parents	gca effect
Days to flowering	SRF-414(L)	-2.49**
	SRF-421(L)	-1.60**
	GFS-8(L)	-2.93**
	Malwan(T)	-2.20**
Plant height	SRF-414(L)	43.13**
	Malwan(T)	14.28*
	Gundari(T)	22.14**
Number of leaves per plant	SRF-421(L)	1.05*
	Malwan(T)	1.27**
Stem girth	SRF-414(L)	-1.64**
	GFS-8(L)	-1.32*
	CSV 46F(T)	-1.59**
	Malwan(T)	-1.00*
Leaf length of blade	SRF-414(L)	3.64*
Leaf width of blade	Malwan(T)	0.94**
Panicle length	SRF-420(L)	0.95*
	SRF-414(L)	2.92**
	SRF-421(L)	4.18**
	CSV 46F(T)	4.08**
	Malwan(T)	0.88*
Grain yield per plant	SRF-421(L)	4.80**
	GFS-8(L)	4.77**
	Malwan(T)	5.22**
Green fodder yield per plant	SRF-414(L)	78.79**
	Malwan(T)	110.96**
	Gundari(T)	30.66*
Dry fodder yield per plant	SRF-420(L)	15.38**
	SRF-421(L)	44.24**
	GFS-8(L)	7.69*
	Malwan(T)	94.75**
Protein content	SRF-421(L)	1.49**
	Malwan(T)	1.08**
Brix	GFS-8(L)	2.22**
	Malwan(T)	1.76**
HCN content	SRF-421(L)	-18.17**
	GFS-8(L)	-18.01**
	Gundari(T)	-7.44**

*, **, Significant at 5% and 1% level, respectively. L- Line; T-Tester

Table 4: Desirable specific combinations based on sca effect and better parent heterosis (BPH) for qualitative and quantitative traits in forage sorghum

Traits	Crosses	*sca* effect	Crosses	Estimates of BPH
Days to flowering	SRF-421 × Gundari	-7.47**	GFS-8 × Malwan	-9.35**
	GFS-6 × Gundari	-5.58**	SRF-414 × Malwan	-7.88**
	GFS-8 × Malwan	-3.47**	SRF-414 × CSV 46F	-7.51**
Plant height	SRF-421 × Gundari	80.94*	GFS-8 × Malwan	67.91**
	SRF-414 × CSV 46F	59.57*	SRF-421 × Gundari	50.05**
	GFS-8 × Malwan	42.02*	SRF-414 × Malwan	44.41**
Number of leaves per plant	SRF-420 × Malwan	2.34*	SRF-421 × Gundari	35.81**
			GFS-8 × Gundari	27.77**
			SRF-414 × Gundari	25.97**
Stem girth	SRF-421 × Gundari	-4.97**	SRF-414 × Malwan	-19.90*
	SRF-414 × Malwan	-2.35*	SRF-420 × Malwan	-17.42*
	SRF-420 × Malwan	-2.28*		
Leaf length of blade	GFS-6 × CSV 46F	8.35*	GFS-8 × Gundari	13.97*
	GFS-8 × Malwan	7.76*	SRF-421 × Gundari	13.67*
			GFS-8 × Malwan	13.52*
Leaf width of blade	GFS-6 × Gundari	0.77*	SRF-420 × Malwan	39.23**
	SRF-420 × Malwan	0.70*	SRF-414 × Malwan	36.63**
			GFS-8 × Malwan	29.48**
Panicle length	GFS-8 × Malwan	8.26**	GFS-8 × Malwan	93.20**
	SRF-421 × CSV 46F	5.8**	SRF-421 × CSV 46F	47.34**
	SRF-420 × Malwan	5.39**	SRF-414 × CSV 46F	31.49**
Grain yield per plant	SRF-421 × Gundari	19.32**	GFS-8 × Malwan	292.11**
	GFS-8 × Malwan	15.31**	SRF-421 × Gundari	159.12**
	SRF-414 × Malwan	9.85**	SRF-414 × Malwan	110.33**
Green fodder yield per plant	SRF-421 × Gundari	123.3**	SRF-421 × Gundari	62.94**
	SRF-420 × Malwan	121.32**	SRF-414 × CSV 46F	60.99**
	GFS-6 × CSV 46F	77.86**	GFS-8 × Gundari	49.84**

Dry fodder yield per plant	SRF-421 × Gundari	148.7**	SRF-421 × Gundari	184.99**
	GFS-8 × Malwan	68.49**	SRF-420 × Malwan	151.23**
	SRF-420 × Malwan	68.25**	GFS-8 × Malwan	145.94**
Protein content	SRF-414 × CSV 46F	2.62**	SRF-420 × Malwan	23.25**
	SRF-421 × Gundari	1.73**	SRF-421 × Gundari	19.29**
	GFS-6 × Gundari	1.24**	GFS-6 × Malwan	12.43*
Brix	SRF-420 × Malwan	2.26*	SRF-420 × Malwan	25.09**
	GFS-6 × Gundari	2.12*		
HCN content	SRF-420 × Malwan	-38.65**	SRF-421 × Gundari	-63.58**
	SRF-421 × CSV 46F	-15.43**	SRF-420 × Malwan	-62.49**
	SRF-421 × Gundari	-9.64**	SRF-421× CSV 46F	-55.49**

*, **, Significant at 5% and 1% levels, respectively

Table 5: Overall general combining ability status of parents across qualitative and quantitative traits in forage sorghum

Parents	**Total rank**	**Overall status**
Lines		
SRF-420	42	L
SRF-414	34	H
SRF-421	30	H
GFS-8	36	H
GFS-6	53	L
Final norm	**39**	
Testers		
CSV 46F	33	L
Malwan	18	H
Gundari	27	L
Final norm	**26**	

H = High overall gca status; L = Low overall gca status

Table 6: Overall sca status of crosses across qualitative and quantitative traits in forage sorghum

Lines / Testers	CSV 46F (L)		Malwan (H)		Gundari (L)	
	Total score	**Status**	**Total score**	**Status**	**Total score**	**Status**
SRF-420 (L)	146	L	48	H	124	L
SRF-414 (H)	59	H	94	H	154	L
SRF-421 (H)	92	H	176	L	46	H
GFS-8 (H)	127	L	62	H	116	L
GFS-6 (L)	85	H	140	L	84	H
Final norm	**103.53**					

H = High overall sca status L = Low overall sca status

(H) = High overall gca status of parents (L) = Low overall gca status of parents

Table 7: Overall heterotic status of crosses across qualitative and quantitative traits in forage sorghum

Lines / Testers	CSV 46F (L)		malwan (H)		gundari (L)	
	Total score	**Status**	**Total score**	**Status**	**Total score**	**Status**
SRF-420 (L)	147	L	48	H	132	L
SRF-414 (H)	84	H	59	H	129	L
SRF-421 (H)	106	L	111	L	59	H
GFS-8 (H)	147	L	53	H	92	H
GFS-6 (L)	148	L	122	L	128	L
Final norm	**104.33**					

H = High overall sca status L = Low overall sca status

(H) = High overall gca status of parents (L) = Low overall gca status of parents

Table 8: Distribution of crosses with high overall sca and heterotic status in relation to overall parental gca status across productivity *per se* traits in forage sorghum

	Number of crosses		
Parental gca status of crosses	**Under the category**	**With high (H) overall sca status**	**With high (H) heterotic status**
H × H	3	2	2
H × L / L × H	8	4	1
L × L	4	2	3

HH: Both parents are high in their overall general combining ability.
HL / LH: One parent is high and other one is low in their overall general combining ability.
LL: Both parents are low in their overall general combining ability.

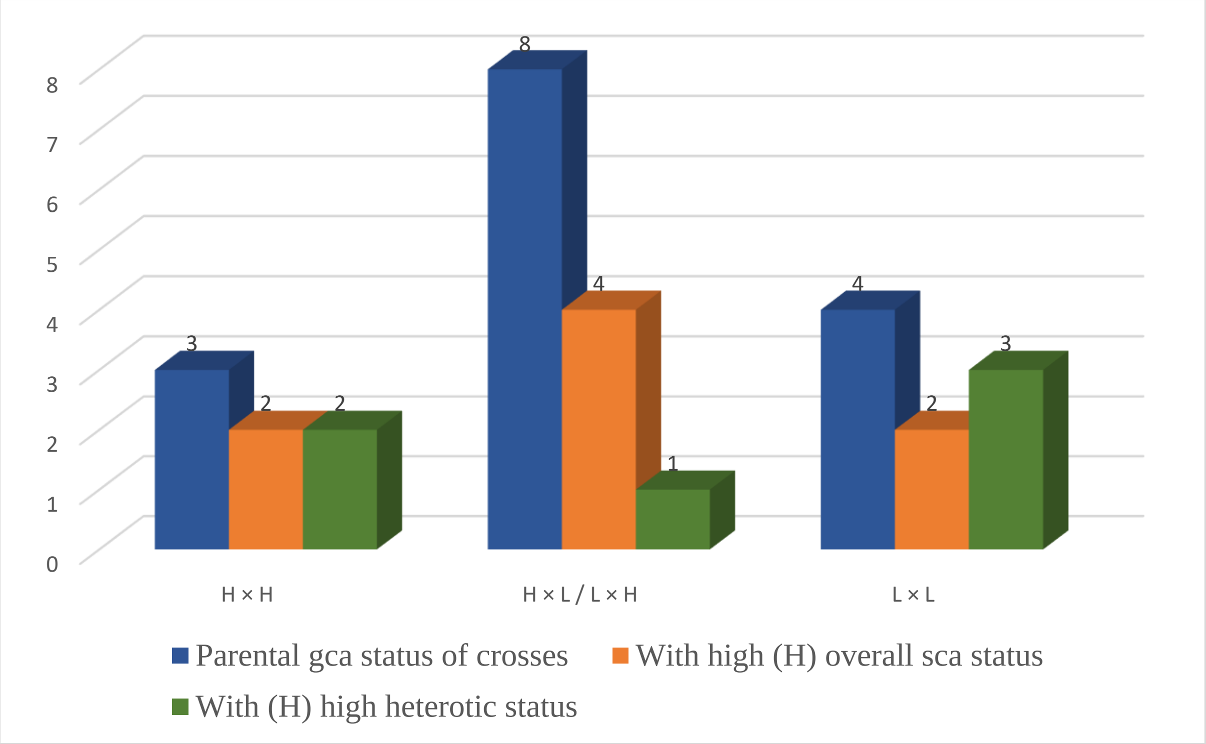

Fig 1: Frequency of heterotic hybrids in relation to gca of parents