Estimation of combining ability, gene action and components of genetic variation in forage sorghum [*Sorghum bicolor* (L.)]

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ABSTRACT

Aims: To Study the combining ability effects and evaluate the genetics of the parents for fodder yield and its component traits in sorghum.

Study design: Randomized block design.

Place and Duration of Study: The seeds of F_1 hybrids were produced during summer 2022 at Center for Millets Research, S. D. Agricultural University, Deesa.

Methodology: Six parental genotypes were used in the experiment, which produced 15 half-diallel crosses in sorghum.

Results: The analysis of variance for combining-ability (CA) studies revealed that mean sum of squares due to general combining ability (GCA) were extremely important for most of the characters except the leaf length of blade. Based on the *gca* effect, the parents CSV 46, IS 3338 and Malwan were good general combiners for green and dry fodder yield per plant. The unit slope of regression line and non- significant t^2 value asserted the validity of the additive-dominance model for total plant height, number of leaf per plant, stem diameter, leaf length of blade, leaf width of blade, dry fodder yield per plant and crude protein content in dry fodder. The value of H_1 was superior to H_2 for most of the characters representing that gene distribution frequency in the parent genotypes was asymmetry and that was supported by the ratio of $H_2/4H_1$ (i.e., less than 0.25). The KD/KR components value was greater than one among most of the traits except for number of leaf per plant and crude protein content in dry fodder showed that parents had more dominant genes compared to recessive genes frequency.

Conclusion: The ratio of $\sigma^2_{gca}/\sigma^2_{sca}$ being more than unity, which suggested greater role of additive genetic variance in the inheritance of these traits. The genetic components of variance andgraphical analysis revealed that different type of gene action were involved for forage yield and components traits in sorghum.

***Keywords:** Combining ability, gene distribution, genetic components and graphical analysis*

1. INTRODUCTION

One of the most important cereal crops in the world is sorghum (*Sorghum bicolor* L. Moench). It is a crucial cereal crop that is used in intensive production systems as both a human staple diet and as livestock feed. Both grain and green biomasses (*i.e.*, leaves and stalks) of sorghum are importantly used for animal feed. Due to its ability to grow in dry conditions, sorghum economically replaces maize because it requires less water to provide equivalent yields Chudasama *et al.* (2022). Fodder sorghum cultivation practices are similar to grain sorghum, with an exception of grazing management and green matter harvesting for hay or silage production. Livestock plays an important role in Indian economy. Livestock sector contributes 4.11 per cent GDP and 25.6 per cent of total Agriculture GDP. India is World's highest livestock owner at about 535.78 million. India is number one milk producer in the world. It is producing about 198 million tonnes of milk in a year (2020-21). The area under this crop in the country is about 5.13 million hectares with an annual production of 4.37 million tonnes and productivity of 852 kg/ha (Anonymous, 2021).

The evaluation of breeding material for general combining ability and specific combing ability through diallel mating design for forage yield and contributing characters are prerequisites for any breeding programme aimed in the development of hybrids. Combining ability studies provide useful information regarding the selection of suitable parents for effective hybridization programmes and indicate the nature and magnitude of various types of gene action involved in the expression of quantitative characters. Sprague and Tatum (1942) provided the concept of general and specific combining ability.

The issue of collecting parental lines comes up frequently when creating superior crop types. Although it has been suggested to eliminate deficient combinations based on how they manifested themselves in the earliest age group, information regarding the genetic makeup of forage yield and its components would help to classify the better combinations more accurately. Numerous information in earlier specifies that diallel analysis method is the fastest approach of concerned the genetic basis of polygenic characters and to determine the predominance of parental lines. Kearsey (1965) described that diallel analysis by Hayman and Jink's give more indication than other approaches, however, it has more necessary norms. The report of Griffing (1956^b) is unable to provide any test to notice non-allelic interaction or linkage. Hayman and Jink's approach detects the epistasis or linkage which is absent in Griffing's (1956^b) method. According to Pooni *et al*. (1984) and Wright (1985) the combination of Griffing's approach has been used to evaluate variance components with Hayman's (1954^b) method for Wr-Vr assessment that detects the presence of linkage disequilibrium and/or epistasis. The diallel studied as per Jinks and Hayman (1953) and Hayman (1954^a) was used to reveal the genomic make-up of the parental lines in different fodder characters in sorghum. The regression of array covariance (Wr) on array variance (Vr) provides geometric representation of the degree of dominance free from spurious dominance caused by non-allelic interactions. The slope of the regression line is independent of the degree of dominance, but the position of lines shifts with change in dominance. Position of the array points on the regression line depicts the dominance order of the parents and the distance between points provides a measure of diversity of parents. The parents occupying position near the origin possess most of the dominant genes and those far away from the origin, the recessive genes. The genetic components of variance and graphical analysis revealed that over dominant type of gene action were involved for forage yield and components in sorghum reported by Patel *et al.* (2022).

2. MATERIAL AND METHODS

The present research comprised six parents (*viz*., IS 3265, CSV 46F, IS 3338, IS 3314, IS 3284, Malwan, including the check variety CSV 46F) and their 15 half-diallel crosses. The seeds of 15 F_1 hybrids were produced during summer 2022 at Center for Millets Research, S. D. Agricultural University, Deesa, India by manual emasculation and pollination. The seeds of parental lines were maintained through selfing. A set of 21 genotypes comprising of six parents (including check CSV 46F) and their 15 F_1 hybrids were sown in Randomized Block Design (RBD) with three replications, during Kharif 2022. Each entry was sown in 2.0 m length with 30 cm spacing. The recommended agronomical practices and plant protection measures were adopted for raising a good crop.

The observations were recorded on five randomly selected plants from each genotype in each replication for all the mentioned characters except days to flowering were recorded on a plot basis. The data were recorded for all the entries in each replication.

The average values of each replication in each entry for the eleven characters were evaluated using Randomized Block Design (Panse and Sukhatme, 1985). The mean value of 21 entries (parent and their F_1 hybrids) were entered in computer and combining ability analysis was carried out according to the procedure given by Griffing (1956^a) as per Method II (in which parents and a set of F_1's without reciprocals are included) and Model I [which assumes that the genotypes and block effects are constant (fixed), but environmental effect is variable].The statistical analysis performed using INDOSTAT statistical software as per Singh and Chaudhary (1977). The various genetic elements of variance were calculated based on diallel-cross technique proposed (Hayman1954^a) for the characters in which model of additive – dominance could be suitable. Appropriateness of the model of additive dominance was verified with the provision of ' t^2 ' test (Hayman 1954^a). Whereas the graphical study was performed based on Hayman (1954^b).

2.1 Estimation of genetic components:

Following genetic components of variance were estimated according to Hayman (1954^a).

D = Component of genetic variance due to additive effects of the genes,
H_1 = Component of genetic variance due to dominant effects of the genes,
H_2 = Component of genetic variance due to dominance effects corrected for the genes distribution,
F = The mean of Fr over the arrays, where Fr is the dominance effects in single array,
h^2 = Overall dominance effects of heterozygous loci and
E = Environmental components.

3. RESULTS AND DISCUSSION

3.1 Combining ability

The analysis of variance components (mean sum of square) for combining ability showed in Table 1. It is estimated by partitioning the total genetic variance into general combining ability representing additive genetic variance and specific combining ability as a measure of non-additive genetic variance was carried out for eleven characters. The results revealed that mean sum of squares due to general and specific combining ability were found highly significant for all the characters *viz*., days to flowering, total plant height, number of leaf per plant, stem diameter, leaf width of blade, leaf: stem ratio, green fodder yield per plant, dry fodder yield per plant, total soluble solids and crude protein content in dry fodder except the leaf length of blade.

The ratio of σ^2gca/σ^2sca being more than unity was found for stem diameter, leaf width of blade and crude protein content in dry fodder which suggested greater role of additive genetic variance in the inheritance of these traits (Table 1). These traits can be improved further as a source of favorable genes for minimum stem diameter and fodder yield contributing traits through selection of desired transgressive segregants from segregating generations. The predominant role of additive gene action was reported earlier by Chaudhary *et al.* (2020) for stem diameter; Chaudhary *et al.* (2020), Rathod *et al.* (2020) for leaf width of blade; Sen *et al*. (2018) for crude protein content in dry fodder.

Table 1. Analysis of variance components (mean sum of squares) for combining ability of eleven traits in forage sorghum

Source of Variation	**d.f.**	**Days to flowering**	**Total plant height (cm)**	**Number of leaf per plant**	**Stem diameter (mm)**	**Leaf length of blade (cm)**	**Leaf width of blade (cm)**	**Leaf: stem ratio**	**Green fodder yield per plant (g)**	**Dry fodder yield per plant (g)**	**Total soluble Solids (%)**	**Crude protein content in dry fodder**

GCA	5	326.12**	2743.20**	12.28**	24.70**	31.28	6.07**	0.002**	90930.32**	7025.85**	3.16**	11.07**
SCA	15	45.50**	1021.92**	6.38**	4.44*	54.60**	0.44*	0.002**	29262.30**	3740.40**	3.00**	1.46*
Error	40	2.29	158.37	1.40	1.65	19.44	0.19	0.00004	670.62	80.48	0.76	0.13
σ^2GCA		40.48	323.11	1.36	2.88	1.48	0.73	0.0002	11282.46	868.17	0.30	1.37
σ^2SCA		43.22	863.55	4.98	2.79	35.15	0.25	0.002	28591.60	3659.92	2.24	1.32
σ^2GCA/ σ^2SCA		0.94	0.37	0.27	1.03	0.04	2.92	0.086	0.39	0.24	0.13	1.03

*** $P \leq 0.05$, ** $P \leq 0.01$**

The magnitude of specific combining ability variance was higher than general combining ability variance for majority of the traits *viz*., days to flowering, total plant height, number of leaf per plant, leaf length of blade, leaf: stem ratio, green fodder yield per plant, dry fodder yield per plant, total soluble solids which evincing that non-additive genetic effects were played a more important role than additive effects. The predominant role of non-additive gene action in the inheritance of green fodder yield per plant, dry fodder yield per plant and contributing characters in sorghum was in accordance with the results reported earlier by various workers in different characters *viz.,* for green fodder yield per plant [Patel *et al*. (2021) and Chudasama *et al*. (2022)], for dry fodder yield per plant [Patel *et al.* (2021), Chudasama *et al*. (2022) and Joshi *et al*. (2022)].

Nature and magnitude of combining ability effects helps in identifying the best parents for crossing and their utilization in the plant breeding programme. The result based on *gca* effect revealed that none of the parents was found good combiner for all the traits studied. Based on the estimates of general combining ability effects, the parents were classified as good, average and poor combiners for eleven traits (Table 2). Among them the parent IS 3265 was good general combiner for days to flowering. The parent CSV 46F was good general combiner for leaf width of blade, green fodder yield per plant and dry fodder yield per plant. The parent IS 3338 was good general combiner for days to flowering, total plant height, leaf length of blade, leaf width of blade, green fodder yield per plant, dry fodder yield per plant and crude protein content in dry fodder. The parent IS 3314 was good general combiner for days to flowering, stem diameter, leaf: stem ratio, total soluble solids and crude protein content in dry fodder. The parent IS 3284 was good general combiner for stem diameter, leaf : stem ratio and crude protein content in dry fodder. The parent Malwan was good general combiner for total plant height, number of leaf per plant, leaf width of blade, green fodder yield per plant and dry fodder yield per plant. Looking to the overall scenario of *gca* the parent Malwan, CSV 46F and IS 3338 were found good general combiners for green fodder yield per plant and dry fodder yield per plant. These good general combiners of fodder yield and its contributing characters can be utilized in intensive crossing programmes and subsequently select transgressive segregants for desired characters in segregating generations to develop superior parental material.

Table 2: Estimation of general combining ability effect associated with each parent for eleven characters in forage sorghum

Parents	Days to flowering		Total plant height (cm)		Number of leaf per plant		Stem diameter (mm)		Leaf length of blade (cm)		Leaf width of blade (cm)	
IS 3265	-4.25**	(G)	-0.95	(A)	-0.37	(A)	-0.42	(A)	1.11	(A)	-0.22	(A)
CSV 46F	2.54**	(P)	-2.24	(A)	0.75	(A)	0.17	(A)	-1.76	(A)	0.38**	(G)
IS 3338	-2.17**	(G)	22.59**	(G)	-0.56	(A)	1.31**	(P)	3.50*	(G)	0.45**	(G)
IS 3314	-6.92**	(G)	-11.79**	(P)	-1.02*	(P)	-2.07**	(G)	-1.20	(A)	-1.01**	(P)

IS 3284	-0.46	(A)	-26.49**	(P)	-0.96*	(P)	-1.58**	(G)	-1.06	(A)	-0.87**	(P)
Malwan	11.25**	(P)	18.89**	(G)	2.16**	(G)	2.59**	(P)	-0.59	(A)	1.27**	(G)
S.E. (g_i)	0.49		4.06		0.38		0.42		1.42		0.14	
Range	-6.92 to 11.25		-26.49 to 22.59		-1.02 to 2.16		-2.07 to 2.59		-1.76 to 3.50		-1.01 to 1.27	

Table 2 conti….

Parents	Leaf: stem ratio		Green fodder yield per plant (g)		Dry fodder yield per plant (g)		Total soluble Solids (%)		Crude protein content in dry fodder (%)	
IS 3265	0.004	(A)	-61.51**	(P)	-12.69**	(P)	-0.55	(A)	-0.79**	(P)
CSV 46F	-0.001	(A)	44.94**	(G)	17.97**	(G)	0.38	(A)	-1.44**	(P)
IS 3338	-0.016**	(P)	55.82**	(G)	12.94**	(G)	-0.24	(A)	0.66**	(G)
IS 3314	0.021**	(G)	-124.12**	(P)	-36.54**	(P)	1.03**	(G)	1.60**	(G)
IS 3284	0.006**	(G)	-77.78**	(P)	-24.28**	(P)	0.003	(A)	0.74**	(G)
Malwan	-0.014**	(P)	162.65**	(G)	42.60**	(G)	-0.63*	(P)	-0.79**	(P)
S.E. (g_i)	0.0022		8.36		2.89		0.28		0.12	
Range	-0.001 to 0.021		-124.12 to 162.65		-36.54 to 42.60		-6.02 to 1.03		-1.44 to 1.60	

*** P ≤ 0.05, ** P ≤ 0.01.** The letter on parenthesis indicates the status of parent, *i.e.*, G = Good Combiner; A = Average Combiner; P = Poor combiner.

The top three crosses selected on the basis of *sca* effects for various characters are presented in Table 3. A perusal of data implied that none of the crosses had high-ranking *sca* effects for all the characters. The data revealed that the high ranking *sca* for most of the characters where accompanied by high ranking mean performance, which proving predominant role of non-additive gene effects in expression of green fodder yield per plant, dry fodder yield per plant and component characters. The crosses CSV 46F × IS 3338, CSV 46F × IS 3284 and IS 3265 × Malwan for green fodder yield per plant, while CSV 46F × IS 3338, IS 3265 × Malwan and CSV 46F × IS 3284 for dry fodder yield per plant recorded the highest *sca* effects which involved good × good; good × poor; poor × good for green fodder yield per plant and good × poor; good × good; poor × good for dry fodder yield plant^{-1} parent combinations, respectively. Further more, these crosses also exhibited a positive significant *sca* effects for other contributing characters *viz.,* total plant height, number of leaf per plant, leaf width of blade and leaf length of blade.

The top three cross combinations for green and dry fodder yield per plant were CSV 46F × IS 3338, CSV 46F × IS 3284 and IS 3265 × Malwan involving either one or both parent having high *gca* effects. The cross IS 3314 × Malwan for total plant height and number of leaf per plant, IS 3265 × CSV 46F for leaf length of blade, CSV 46F × IS 3284 for leaf width of blade, IS 3265 × IS 3338 for leaf: stem ratio, IS 3265 × IS 3338 for total soluble solids and IS 3314 × IS 3284 for crude protein content in dry fodder manifested high *sca* effects. These crosses are hopeful for selecting of good homozygous lines for amelioration of respective characters in forage sorghum and it can also use directly in varietal breeding programme.

3.2 Components of genetic variation and graphical analysis

The parental lines used in the present research were verified for the accord with norms basic to Hayman diallel study. The effects of maternal are supposed to be vague in the parental genotypes. Two general tests *i.e.,* Wr on Vr regression and t^2 test were used to other norms. Outcomes of test of t^2 stated the satisfaction of norms essential under diallel examination for all the characters studied except days to flowering. Non-sufficient of supposition in these characters displays the undistinguishable of the modest additive dominance model of gene action and participation of epistasis by linkage-disequilibrium. The non-significant value of t^2 in sorghum diallel analysis for forage yield and component characters in sorghum was also reported by Patel *et al.* (2022).

The component D measures the additive effects of genes, it was significant for all the traits except number of leaf per plant, leaf: stem ratio, total soluble solids and crude protein content in dry fodder (Table 4). It implies that these traits can be fixed in early generation. These results were in harmony with those reported by Ravindrababu *et al.* (2003) and Patel *et al.* (2022) for forage yield and its various attributes in sorghum *viz*., plant height, leaf length and leaf width.

The estimates H_1 and H_2 were significant for the traits *viz*, total plant height, number of leaf per plant, stem diameter, leaf length of blade, leaf width of blade, leaf: stem ratio, green fodder yield per plant, dry fodder yield per plant and crude protein content in dry fodder, while in case of total soluble solids in where only H_1 component confirmed significant effects. The significant H_1 and H_2 component denotes non-additive (dominance or epistatic) genetic effects, which plays a major role in the inheritance of these traits. These findings were in agreement with the result reported by Ravindrababu *et al.* (2003) and Patel *et al.* (2022) for forage yield and its various attributes *viz.*, plant height, number of leaves per plant, green fodder yield per plant and total soluble solids (brix value). The extent of H (non additive) element was more than additive (D) element for all the characters which revealed the role of over dominance for these traits. This was also apparent from the average dominance degree (*i.e*.,>1) for most characters representing over-dominance for all traits except for stem diameter and leaf width of blade. The higher magnitude of the component dominance was also reported for days to flowering and dry fodder yield per plant by Ravindrababu *et al.* (2003) and Patel *et al.* (2022) for traits *viz.*, plant height, number of leaves per plant, stem girth, leaf length, leaf width, green fodder yield per plant, dry fodder yield per plant and total soluble solids.

Table 3: The top three ranking parents based on mean performance, combining ability and heterosis over better parent and standard check CSV46F

Characters	Best performing parents	Best general combiners	Best performing hybrids	Hybrid with high *sca* effect	*gca* of parents	*sca* effects	Heterosis over	
							Better Parent	Standard Check
Days to flowering	IS 3314 (57.00)	IS 3314	IS 3265 × IS 3338 (57.00)	IS 3265 × IS 3338	G × G	-10.73**	-17.39**	-29.33**
	IS 3265 (69.00)	IS 3265	IS 3265 × IS 3314 (57.00)	IS 3338 × IS 3284	G × A	-9.18**	-15.00**	-22.73**
	IS 3338 (73.33)	IS 3338	IS 3338 × IS 3284(62.33)	IS 3265 × CSV46F	G × P	-7.10**	-5.31*	-19.01**
Total plant height	IS 3338 (296.50)	IS 3338	IS 3314 × Malwan(306.66)	IS 3314 × Malwan	P × G	43.11**	9.85*	48.75**
	Malwan (279.16)	Malwan	IS 3265 × Malwan (296.66)	IS 3265 × CSV46F	A × A	40.80**	41.96**	42.77**
	IS 3265 (207.33)	-	CSV46F × IS 3338 (295.16)	CSV46F × IS 3284	A × P	29.17**	24.73**	24.74**
Number of leaf per Plant	Malwan (15.83)	Malwan	IS 3314 × Malwan (21.16)	IS 3314 × Malwan	P × G	4.61**	33.67**	49.42**
	CSV 46F (14.16)	-	IS 3265 × Malwan (19.33)	CSV 46F × IS 3284	A × P	3.97**	34.18**	34.12**
	IS 3265 (14.00)	-	IS 3338 × Malwan (18.66)	IS 3265 × Malwan	A × G	2.30**	22.10*	36.48**
Stem diameter	IS 3314 (4.31)	IS 3314	IS 3265 × IS 3284 (6.85)	IS 3265 × IS 3284	A × G	-1.84	14.74	-7.10
	IS 3284 (5.97)	IS 3284	IS 3265 × IS 3314 (8.42)	CSV 46F × Malwan	A × P	-1.39	63.41**	63.44**
Leaf length of blade	IS 3338 (85.60)	IS 3338	IS 3265 × CSV 46F (89.58)	IS 3265 × CSV 46F	A × A	11.65**	14.97*	50.61**
	IS 3265 (77.91)	-	CSV 46F × IS 3284 (86.73)	CSV 46F × IS 3284	A × A	10.97**	21.65**	45.82**
	IS 3314 (71.40)	-	IS 3314 × IS 3284 (85.46)	IS 3314 × IS 3284	A × A	9.15**	18.89**	43.69**
Leaf width of blade	Malwan (8.36)	CSV 46F	IS 3338 × Malwan (8.45)	CSV 46F × IS 3314	G × P	1.29**	14.57*	14.58*
	CSV 46F (5.83)	IS 3338	IS 3265 × Malwan (7.66)	IS 3338 × Malwan	G × G	0.70*	1.07	44.86**
	IS 3265 (4.93)	Malwan	CSV 46F × IS 3338 (6.81)	IS 3314 × IS 3284	P × P	0.65*	31.50**	-17.72*
Leaf : stem ratio	IS 3284 (0.272)	IS 3314	IS 3265 × IS 3338 (0.247)	IS 3265 × IS 3338	A × P	0.06**	10.59*	-4.00
	CSV 46F (0.257)	IS 3284	CSV 46F × IS 3314 (0.225)	IS 3265 × IS 3314	A × G	0.04**	13.92**	4.94
	IS 3314 (0.237)	-	IS 3314 × IS 3284 (0.219)	IS 3338 × IS 3284	P × G	0.02**	-21.55**	-17.07**
Green fodder yield per plant	Malwan (678.00)	CSV 46F	CSV 46F × IS 3338 (866.33)	CSV 46F × IS 3338	G × G	315.07**	74.08**	208.13**
	IS 3338 (497.66)	IS 3338	IS 3265 × Malwan (742.00)	CSV 46F × IS 3284	G × P	292.01**	152.40**	152.41**
	IS 3265 (357.83)	Malwan	CSV 46F × IS 3284 (709.66)	IS 3265 × Malwan	P × G	190.36**	9.44*	163.91**

Table: 3 contin…

Characters	Best performing parents	Best general combiners	Best performing hybrids	Hybrid with high *sca* effect	*gca* of parents	*sca* effects	Heterosis over	
							Better Parent	Standard Check
Dry fodder yield per plant	Malwan (226.43)	CSV 46F	CSV 46F × IS 3338 (278.13)	CSV 46F × IS 3284	G × P	97.47**	144.10**	144.11**
	IS 3338 (151.93)	IS 3338	IS 3265 × Malwan (250.16)	CSV 46F × IS 3338	G × G	95.49**	83.06**	179.54**
	IS 3265 (113.18)	Malwan	CSV 46F × IS 3284 (242.88)	IS 3265 × Malwan	P × G	68.53**	10.48*	151.43**
Total soluble solids	CSV46F (14.18)	IS 3314	IS 3265 × IS 3314 (15.95)	IS 3265 × IS 3338	A × A	3.19**	31.86**	8.94
	IS 3284 (14.05)	-	IS 3265× IS 3338 (15.45)	IS 3265 × IS 3314	A ×G	2.38**	24.35**	12.23
	Malwan (13.15)	-	CSV 46F × IS 3314(14.36)	IS 3338 × IS 3314	A × G	1.75**	21.88**	9.99
Crude protein content in dry fodder	IS 3314 (11.41)	IS 3314	IS 3314 × IS 3284 (13.34)	IS 3314 × IS 3284	G × G	1.92**	16.94**	78.20**
	IS 3284 (9.98)	IS 3284	IS 3338 × IS 3314 (12.86)	IS 3338 × IS 3314	A × G	1.52**	12.73**	71.79**
	IS 3338 (9.26)	-	IS 3338 × IS 3284 (10.73)	CSV 46F × Malwan	P × P	1.23**	7.79	7.79

* P ≤ 0.05; ** P ≤ 0.01. Figure in parenthesis indicates mean data and letter indicates the status of parent, i.*e.*, G = Good combiner; A = Average combiner and P = Poor combiner.

Table 4: Estimation of genetic components of variance and other parameters for eleven traits in sorghum

Parameters	Days to flowering	Total plant height	Numbers of leaf per Plant	Stem diameter	Leaf length of balde	Leaf width of balde	Leaf : stem ratio	Green fodder yield per plant	Dry fodder yield per plant	Total soluble solids	Crude protein content in dry fodder
b (Wr, Vr)	0.50	0.91	0.70	0.77	0.73	1.30	-0.73	0.05	-0.05	-0.05	0.67
t_{b-0}	-4.09*	-3.80*	-2.84*	-1.94	-2.48	-4.60**	-1.61	-0.24	-0.11	-0.22	3.94*
t_{1-b}	4.08*	0.37	1.18	0.58	0.89	-1.07	4.07*	3.88*	2.27	4.07*	1.88
t^2	7.93*	0.016	0.25	0.077	0.032	3.24	0.0021	2.45	0.022	1.97	1.51
D	-	2295.90**	2.91	13.97**	56.92*	3.35**	0.001	47215.40*	4331.40*	1.90	2.86**
H_1	-	3157.00**	19.74*	10.64*	157.49*	1.05*	0.01*	112620.60*	13277.20*	12.03*	6.02**
H_2	-	2511.90**	17.62*	9.72*	120.75*	1.05*	0.01*	96734.90*	11881.40*	8.12	4.17*
F	-	1795.40*	-2.01	3.68	92.31	0.50	0.001	14583.30	2177.50	3.74	-2.11
h^2	-	5066.70**	20.14**	20.88**	186.91**	1.75**	0.01*	62665.70*	6970.30*	0.56	0.17
E	-	158.37	1.40*	1.65*	19.44*	0.17*	0.00005	670.62	80.31	0.76	0.14
$\sqrt{H_1/D}$	-	1.17	2.61	0.87	1.66	0.56	2.88	1.54	1.75	2.52	1.45
$H_2/4H_1$	-	0.20	0.22	0.23	0.19	0.25	0.21	0.21	0.22	0.17	0.17
KD/KR	-	1.99	0.74	1.35	2.89	1.30	1.68	1.22	1.34	2.28	0.59
h^2/H_2	-	2.02	1.14	2.15	1.55	1.67	0.88	0.65	0.59	0.07	0.04
r(P, Wr+Vr)	-	-0.50	-0.82	-0.35	-0.81	0.09	0.62	-0.46	-0.21	-0.72	0.91*
Heritability	-	53.50	9.60	50.72	28.47	72.99	12.34	31.91	27.49	14.34	24.82

*** $P \leq 0.05$; ** $P \leq 0.01$.**

The identical spreading of positive (+) and negative (-) alleles in the parental lines helps the crop scientist to choose exact required characters. In present study the H_1 value was higher than H_2 for most of the characters signifying that gene distribution frequency was unequal in the parental genotypes. These could be also proved by the $H_2/4H_1$ (< 0.25) ratio. The results are in congruence with those of Ravindrababu *et al.* (2003) and Patel *et al.* (2022) for forage yield and components.

The estimates of positive and non-significant F component for most characters excluding total plant height, number of leaf per plant and crude protein content in dry fodder explicating the presence of both recessive and dominant alleles in unequal proportion and these could also prove by more than unity of KD/KR elements. The results are accord with those of Ravindrababu *et al.* (2003) and Patel *et al.* (2022) for forage yield and one or more components.

The evidence of gene per group and number of gene responsible for particular character is dynamic for the genetic improvement by selection. The h^2/H_2 value signifies that minimum one gene group operates for total plant height, leaf number per plant, stem diameter, leaf length of blade and leaf width of blade (Table 4). These results are in analogue with result reported by Ravindrababu *et al.* (2003) and Patel *et al.* (2022) for forage yield and its various attributes *viz.*, plant height and dry fodder yield per plant.

A component value of environment (E) significant for characters like number of leaf per plant, stem diameter, leaf length of blade and leaf width of blade (Table 4) indicated the extensive environmental role for the expression of such characters. The low to medium levels of narrow-sense heritability was documented for forage yield and all of its traits indicating majority by non-additive genes. This also illustrated that assortment should have merits at delay or late generation. The connection between parental mean (Yi) and order of dominance (Vr + Wr) was negative for majority of the characters which showed the role of dominant genes role in increasing mean values. Ravindrababu *et al.* (2003) and Patel *et al.* (2022) also described the role of dominance genes for forage yield and its various attributes in sorghum *viz*., plant height, number of leaves per plant, stem girth, green fodder yield per plant, dry fodder yield per plant and total soluble solids.

The Wr on Vr regression was suitable and close to one for characters like total plant height (Fig 1), number of leaf per plant (Fig. 2), stem diameter (Fig. 3), leaf length of blade (Fig. 4), leaf width of blade (Fig. 5), dry fodder yield per plant (Fig. 6), crude protein content in dry fodder (Fig 7). Consequently, graphical analysis was accomplished only these characters. In graphic investigation, the line of regression interrupted axis of Wr underneath the origin signified over dominance for total plant height (Fig. 1), number of leaf per plant (Fig. 2), leaf length of blade (Fig. 4). The line of regression interrupted the positive adjacent the axis of Wr suggested partial dominance role for stem diameter (Fig. 3), leaf width of blade (Fig. 5) and crude protein content in dry fodder (Fig. 7) while, the regression line that intercepted the Wr axis above to the limiting parabola and touch the limiting parabola which asserted no dominance type of gene action for dry fodder yield per plant (Fig. 6). The widespread parental range points laterally the regression line in the Vr-Wr graph for number of leaf per plant and crude protein content in dry fodder which displayed significant genetic range among the parents. The parent Malwan had extreme dominant genes for increasing total plant height. The parent CSV 46F had high frequency of dominant gene for leaf numbers per plant, stem diameter, leaf width of blade and crude protein content in dry fodder, while IS 3338 possessed maximum dominant genes for leaf length of blade. The parent IS 3314 possessed maximum dominant genes for dry fodder yield per plant and the Parent IS 3265 had maximum recessive gene for reducing stem diameter.

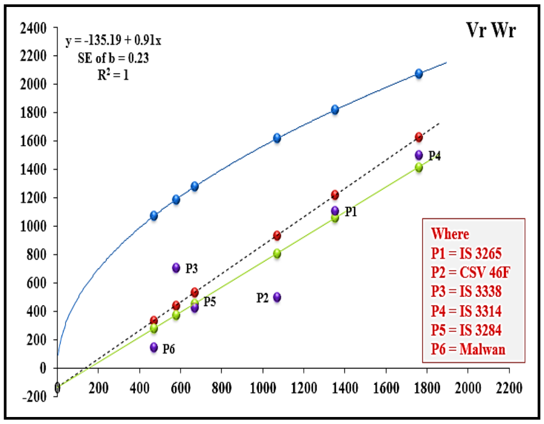

Fig. 1: Graph of Vr-Wr for total plant height in sorghum

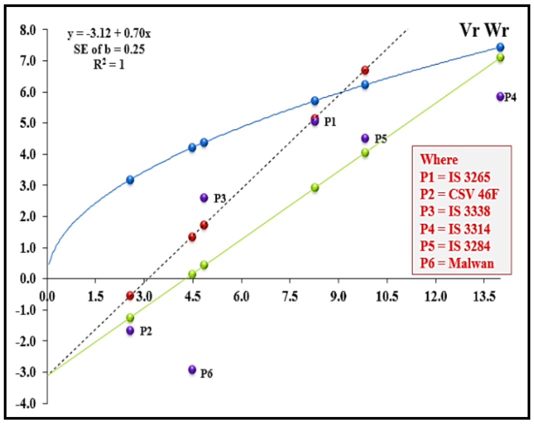

Fig. 2: Graph of Vr-Wr for numbers of leaf per plant in sorghum

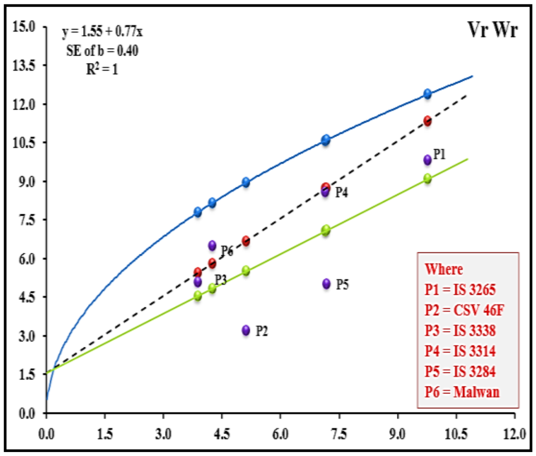

Fig. 3: Graph of Vr-Wr for stem diameter in sorghum

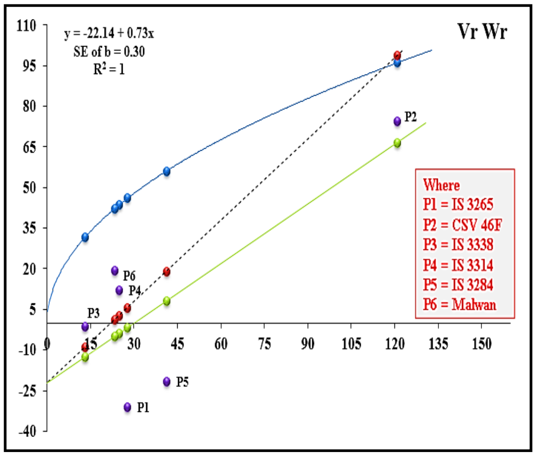

Fig. 4: Graph of Vr-Wr for leaf length of blade in sorghum

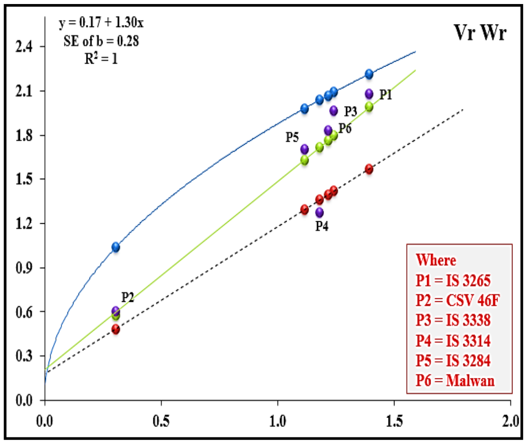

Fig. 5: Graph of Vr-Wr for leaf width of blade in sorghum

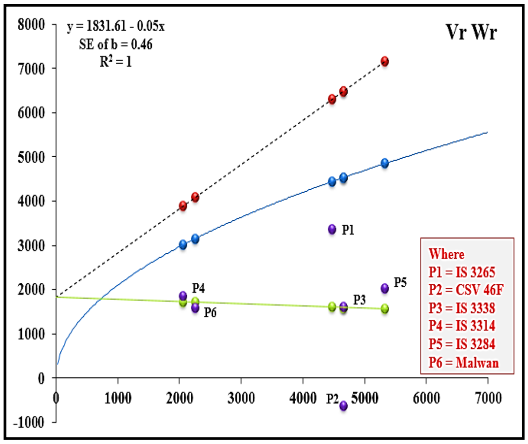

Fig. 6: Graph of Vr-Wr for dry fodder yield per plant in sorghum

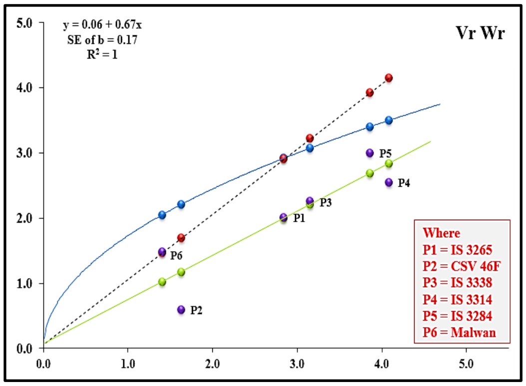

Fig. 7: Graph of Vr-Wr for crude protein content in dry fodder in sorghum

4. CONCLUSION

The ratio of σ^2gca/σ^2sca being more than unity was found for stem diameter, leaf width of blade and crude protein content in dry fodder which suggested greater role of additive genetic variance in the inheritance of these traits. Among them the parent Malwan, CSV 46F and IS 3338 were found good general combiners for green fodder yield per plant and dry fodder yield per plant. These good general combiners of fodder yield and its contributing characters can be utilized in intensive crossing programmes and subsequently select transgressive segregants for desired characters in segregating generations to develop superior parental material. The crosses CSV 46F × IS 3338, CSV 46F × IS 3284 and IS 3265 × Malwan for green fodder yield per plant, while CSV 46F × IS 3338, IS 3265 × Malwan and CSV 46F × IS 3284 for dry fodder yield per plant recorded the highest *sca* effects involving either one or both parent having high *gca* effects. The component D measures the additive effects of genes, it was significant for all the traits except number of leaf per plant, leaf: stem ratio, total soluble solids and crude protein content in dry fodder. It implies that these traits can be fixed in early generation. The significant H_1 and H_2 component denotes non-additive (dominance or epistatic) genetic effects, which plays a major role in the inheritance of the traits. The H_1 value was higher than H_2 for most of the characters signifying that gene distribution frequency was unequal in the parental genotypes. The low to medium levels of narrow-sense heritability was documented for forage yield and all of its traits indicating majority by non-additive genes. The line of regression interrupted axis of Wr underneath the origin signified over dominance for total plant height, number of leaf per plant, leaf length of blade. The line of regression interrupted the positive adjacent the axis of Wr suggested partial dominance role for stem diameter, leaf width of blade and crude protein content in dry fodder while, the regression line that intercepted the Wr axis above to the limiting parabola and touch the limiting parabola which asserted no dominance type of gene action for dry fodder yield per plant. The parent CSV 46F had high frequency of dominant gene for number of leaf per plant, stem diameter, leaf width of blade and crude protein content in dry fodder, while the Parent IS 3265 had maximum recessive gene for reducing stem diameter.

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Competing interests

Authors have declared that no competing interests exist.

AUTHORS' CONTRIBUTIONS

'Authors 1st and 2nd equally contributed in the research work and manuscript preparation. Authors 3rd , 4th and 5th were helped to performed the statistical analysis and manuscript preparation. All authors read and approved the final manuscript.

CONSENT (WHERE EVER APPLICABLE)

All authors declare that 'written informed consent was obtained from the patient (or other approved parties) for publication of this case report and accompanying images. A copy of the written consent is available for review by the Editorial Board members of this journal.

ETHICAL APPROVAL (WHERE EVER APPLICABLE)

All authors hereby declare that all experiments have been examined and approved by the appropriate ethics committee and have therefore been performed in accordance with the ethical standards.

REFERENCES

1. Anonymous. Ministry of Agriculture and Farmer Welfare, Department of Agriculture, Co-operation and Farmer Welfare Directorate of Economics and Statistics. New Delhi, India. 2021;23-34.
2. Sprague GF and Tatum LA. General vs. specific combining ability in single crosses of corn. Journal American Society of Agronomy. 1942;34:923-32. DOI: 10.2134/agronj1942. 00021962003400100008x.
3. Kearsey MJ. Biometrical analysis of a random mating population, a comparison of five experimental designs. Heredity. 1965;20:205-235.
4. Griffing BA. generalized treatment of the use of diallel crosses in quantitative inheritance. Heredity. 1956[b];10: 31-50. DOI: https://doi.org/10. 1038/hdy.1956.2.
5. Pooni HS, Jinks JL and Singh RK. Methods of analysis and the estimation of the genetic parameters from a diallel set of crosses. Heredity. 1984;52:243-253.
6. Wright AJ. Diallel designs, analysis and reference populations. Heredity. 1985;54: 307-311.
7. Hayman BI. The theory and analysis of diallel crosses. Genetics. 1954[b];39: 789-809. DOI : https://doi.org/10.1093/genetics/39.6.789.
8. Jinks JL and Hayman BI. The analysis of diallel crosses. Maize Genetic News Letter. 1953;27:48-54.
9. Hayman BI. The analysis of variation of Diallel tables. Biometrics. 1954[a];10:235-244. DOI : https://doi.org/10.2307/3001877.
10. Patel PS, Patel, NB, Gami RA, Patel RN, Patel PR. Genetic components of variation of forage yield and attributing traits in sorghum [*Sorghum bicolor* (L.)]. Journal of Crop and Weed. 2022;18(2): 185-190. DOI: https://doi.org/10.22271/09746315.2022.v18.i2.1588.

11. Griffing B. Concept of general and specific combining ability in relation to diallel crossing systems. Australian Journal of Biological Sciences. 1956[a];9(4): 463-493. DOI: https://doi.org/10.1071/BI9560463.
12. Panse VG, Sukhatme PV. Statistical methods for agricultural workers. 4th Ed., ICAR, New Delhi. 1985;97-156.
13. Singh RK, Chaudhary BD. Biometrical methods in quantitative genetics analysis. Kalyani Publishers: New Delhi;1977.
14. Chaudhary M, Singh SK, Kumar M, Chand P. Combining ability and heterosis analysis in forage sorghum [*Sorghum bicolor* (L.) Moench] for yield and yield components. Journal of Pharmacognosy and Phytochemistry. 2020;9(5): 1339-1348.
15. Rathod DP, Gami RA, Chauhan RM, Kugashiya KG, Patel RN. Study of per se performance and heterosis for forage yield and its attributing traits in sorghum [*Sorghum bicolor* (L.) Moench]. Forage Research. 2020;45(4): 258-263.
16. Sen R, Singh SK, Chand P, Kerkhi SA, Singh G, Kumar M. Studies on combining ability in forage sorghum for yield and quality parameters. Journal of Pharmacognosy and Phytochemistry. 2018;7(4): 2182-2188.
17. Patel PS, Patel NB, Gami RA, Kugashiya KG, Patel PR. Elucidation of gene action and combining ability for forage yield and its attributing traits in sorghum [*Sorghum Bicolor* (L.) Moench]. Forage Research. 2021;46(4): 320-324.
18. Chudasama CR, Gami RA, Patel RN, Patel MA. Genetic analysis using Griffing 's approach for forage yield and components in sorghum. Electronic Journal of Plant Breeding. 2022;13(3): 1042-1050. DOI: http://dx.doi.org/10.37992/2022.1303.138.
19. Joshi AH, Gami RA, Patel RN, Arvinth S. Elucidation of gene action and combining ability for grain and fodder yield and contributing traits in sorghum [*Sorghum bicolor* (L.) Moench]. Electronic Journal of Plant Breeding. 2022;13(1): 75-82. DOI: 10.37992 /2022. 1301.007.
20. Ravindrababu Y, Pathak AR, Tank CJ. Genetic components of variation in sorghum [*Sorghum bicolor* (L.) Moench]. Indian Journal of Genetics and Plant Breeding. 2003;63(4): 328.