



## Genetic components of variation of forage yield and attributing traits in sorghum [*Sorghum bicolor* (L.)]

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### ABSTRACT

The investigation was performed using six parental genotypes and resultant 15 half-diallel crosses in sorghum. 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 leaves number plant<sup>-1</sup>. The unit slope of the regression line and non-significant  $t^2$  value asserted the validity of the model of additive-dominance for flowering-maturity days, plant height, leaves number plant<sup>-1</sup>, stem girth, leaf width, green fodder yield plant<sup>-1</sup>, dry fodder yield plant<sup>-1</sup> and brix value. The value of  $H_1$  was superior to  $H_2$  for most of the characters representing that gene sharing frequency in the parent genotypes was not equal and that was also supported by the ratio of  $H_1/4H_2$  (i.e., less than 0.25). The estimations of F element was positive and non-significant, while of KD/KR components value was greater than one among most of the traits except for plant height and leaf width showed that parents had more dominant genes compared to recessive genes frequency. In Hayman graphical investigation, the regression line interrupted Wr axis underneath the origin demonstrating over-dominance for flowering days, height of plant, leaves number plant<sup>-1</sup>, girth of stem, leaf width, green fodder yield plant<sup>-1</sup>, dry fodder yield plant<sup>-1</sup> and brix value.

**Keywords:** Forage traits, gene distribution, genetic components, graphical analysis and sorghum

Sorghum (*Sorghum bicolor* L. Moench) is one of the major cereal crops in the world. It is an essential cereal crop that serves as a human staple food as well as livestock feed in intensive production systems. Both grain and green biomasses (i.e., leaves and stalks) of sorghum are importantly used for animal feed. Sorghum economically substitutes maize, since it needs less water to produce similar yields due to adaptableness to dry conditions. Fodder sorghum cultivation practices are similar to grain sorghum, with an exception of grazing management and green matter harvesting for hay or silage production.

The global production and area under sorghum cultivation is 58.70 million tonnes and 40.25 million hectares, respectively in the year 2020. India stands forth globally for the sorghum production in the year 2020. In India, production and area under sorghum cultivation is 4.77 million tonnes and 5.50 million hectares, respectively in the year 2020 (Anonymous, 2020).

While breeding superior varieties of crops, the breeder is frequently met through the issue of parental lines collection. However, eradication of deprived combinations based on their appearance in the initial age group has been proposed; nonetheless, evidence on the genetic structure of forage yield and its components would support to categories the better combinations further proficiently. 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) 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) 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 (1954b) 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 (1954a) 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 overdominant type of gene action were involved for yield and components in sorghum reported (Ravindrababu, 1998; Nair and Ghorade (2016).

## MATERIALS AND METHODS

The present research comprised six parental genotypes and resultant 15 diallel crosses in half-diallel fashion. The half diallel  $F_1$  were generated during summer-2019 at Sorghum Research Station, Sardarkrushinagar Dantiwada Agril. Univ., Deesa by hand emasculation and crossing technique. The pure seeds of parental lines were preserved by self-pollination. A set of 22 entries comprising of six parental lines, 15  $F_1$  hybrids with one check CSV 32F were raised in *kharif*-2019 in Randomized Block Design (RBD) replicated thrice. Each line was grown in two rows of 3.0 m length, with inter and intra row spacing of 45cm and 15 cm, respectively. Appropriate agronomical operations were adopted to obtain a good crop.

The observations were recorded on five randomly selected plants from each genotype in each replication for all the mentioned traits except days to flowering and days to maturity which were recorded on plot basis. The data were recorded for all the entries in each replication. The mean values were worked out and used to statistical analysis.

The average values of each replication in each entry for the twelve characters were evaluated using Randomized Block Design (Panse and Sukhatme, 1985). The various genetic elements of variance were calculated based on diallel-cross technique proposed (Hayman 1954a) 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 1954a). Whereas the graphical study was performed based on Hayman (1954b).

### Estimation of genetic components:

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

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, and

$h^2$  = Overall dominance effects of heterozygous loci

## RESULTS AND DISCUSSION

A result of variance analysis discovered extremely important differences due to genotypes for utmost studied characters. Additionally, segmentation of the mean sum of squares owing to genotypes revealed variances among parents which were important for most of the characters exclusive of height of the plant, leaf length and grain yield plant<sup>-1</sup> (Table 1). The parental diversity was proved due to significant differences among parental lines.

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 grain yield plant<sup>-1</sup>, and leaf: stem ratio. 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-important value of  $t^2$  in sorghum diallel analysis for yield and component characters in sorghum was also reported by Ravindrababu (1998).

The additive effects of genes are measured by the D component. In the present study it was important for most of the characters excluding plant height, leaf length and leaf width (Table 2). It advocates that such traits can be simply fixed in the initial age group. The results were in concord with those conveyed by Ravindrababu (1998) and Ravindrababu *et al.* (2003) for forage yield and its various attributes in sorghum.

The estimates ( $H_1$  and  $H_2$ ) were important for days to maturity, days to flowering, plant height and brix value, while traits *viz.*, green fodder yield plant<sup>-1</sup> and leaves number plant<sup>-1</sup> where only  $H_1$  component established significant effects (Table 2). The significant  $H_1$  and  $H_2$  components signify that the gene effect was non-additive (dominance or epistatic), that acts a key role in the transmission of such characters. These results were in treaty with the results described by Ravindrababu (1998) and Ravindrababu *et al.* (2003) for forage yield and its various attributes, while Nair and Ghorade (2016) for grain yield plant<sup>-1</sup> in sorghum. The extent of  $H_1$  (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. The higher magnitude of the component dominance was also reported for flowering days and dry fodder yield plant<sup>-1</sup> by Ravindrababu *et al.* (2003), while for grain yield plant<sup>-1</sup> by Nair and Ghorade (2016) in sorghum.

**Table 1: Analysis of variance (mean summation of squares) for experimental design of twelve traits in sorghum**

Sources of variation	d.f.	Flowering days	Maturity days	Height of plant	Leaves number plant <sup>-1</sup>	Girth of stem	Leaf length
Replication .	2	3.68	2.61	217.90	2.28	4.86	92.50
Total genotypes	21	162.40**	167.59**	5316.82**	2.10*	5.42*	119.95*
Parental line	5	294.13**	304.40**	2284.43	4.11**	9.99**	127.11
Crosses	14	136.66**	140.95**	5413.89**	1.35	3.92	133.88*
Parental line Vs Crosses	1	26.53**	24.21**	24436.63*	4.58*	9.09	9.22
Error	42	2.19	2.51	1162.30	1.08	2.51	60.90

\* P ≤ 0.05, \*\* P ≤ 0.01

Sources of variation	d.f.	Leaf width	Leaf : stem ratio	Grain yield plant <sup>-1</sup>	Green fodder yield plant <sup>-1</sup>	Dry fodder yield plant <sup>-1</sup>	Brix value
Replication	2	0.12	0.0001	5.27	6340.69	797.58	0.04
Total genotypes	21	1.40**	0.002**	17.37**	24443.01**	2633.81**	9.79**
Parental line	5	2.69**	0.002**	3.64	36802.30**	3811.97**	8.83**
Crosses	14	0.64	0.004**	24.19**	18817.82**	1939.26**	9.87**
Parental line Vs Crosses	1	6.95**	0.001	6.32	65842.20**	9100.51**	23.30**
Error	42	0.46	0.0004	1.68	3355.38	350.48	0.72

\* P ≤ 0.05, \*\* P ≤ 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 (1998) and Ravindrababu *et al.* (2003) for forage yield and components, while Nair and Ghorade (2016) for grain yield plant<sup>-1</sup> in sorghum.

The estimates of positive and non-significant F component for most characters excluding height of plant and leaf width 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 (1998) and Ravindrababu *et al.* (2003) for forage yield and one or more components, while, Nair and Ghorade (2016) for grain yield plant<sup>-1</sup> in sorghum.

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 dry fodder yield and components characters *viz.*, number of leaves plant<sup>-1</sup>, plant height and green fodder yield plant<sup>-1</sup> (Table 2). These results are in analogue with result reported by Ravindrababu (1998) and Ravindrababu *et al.* (2003) for forage yield and its various attributes,

while Nair and Ghorade (2016) for grain yield plant<sup>-1</sup> in sorghum.

A component value of environment (E) significant for characters like leaves number plant<sup>-1</sup>, girth of stem and leaf length (Table 2) indicated the extensive environmental role for the expression of such characters. The low to medium levels of narrow-sense heritability was documented for 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 ( $Y_p$ ) 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 (1998) and Ravindrababu *et al.* (2003) also described the role of dominance genes for forage yield and its various attributes in sorghum.

The  $Wr$  on  $Vr$  regression was suitable and close to one for characters like flowering days (Fig 1), maturity days (Fig. 2), height of plant (Fig. 3), leaves number plant<sup>-1</sup> (Fig. 4), girth of stem (Fig. 5), leaf width (Fig. 6), green fodder yield plant<sup>-1</sup> (Fig 7), dry fodder yield plant<sup>-1</sup> (Fig 8) and brix value (Fig 9). 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 flowering days (Fig. 1), height of plant (Fig. 3), leaves number plant<sup>-1</sup> (Fig. 4), girth of stem (Fig. 5), leaf width (Fig. 6), green fodder yield plant<sup>-1</sup> (Fig. 7),

Table 2: Assessment of genetic elements of difference and other parameters for twelve traits in sorghum

Parameters	Flowering	Maturity days	Height of days	Leaves number plant <sup>-1</sup>	Girth of stem	Leaf length	Leaf width	Leaf:stem ratio	Grain yield plant <sup>-1</sup>	Green fodder yield plant <sup>-1</sup>	Dry fodder yield plant <sup>-1</sup>	Brix value
<b>b (Wr, Vr)</b>	0.76	0.71	0.42	0.73	0.60	0.05	0.94	0.27	17.00	0.60	0.61	0.77
<b>t<sub>b-0</sub></b>	4.66**	4.93**	1.10	1.99	2.29	0.19	5.60**	2.72	3.91*	2.17	2.18	4.32*
<b>t<sub>1-b</sub></b>	1.48	2.05	2.72	0.73	1.50	3.50*	0.38	-7.37**	19.67**	1.45	1.42	-1.28
<b>t<sup>2</sup></b>	1.93	4.26	4.57	0.02	0.91	3.37	0.00	40.17**	259.25**	0.74	0.70	1.20
<b>D</b>	97.31**	100.63**	374.04	1.01**	2.49**	22.07	0.05	-	-	11148.97*	1153.78**	2.70**
<b>H<sub>1</sub></b>	146.32*	140.91*	5596.92*	1.98*	4.68	91.64	1.18	-	-	24320.65*	2492.16	10.11**
<b>H<sub>2</sub></b>	123.43*	119.6*	4578.03*	1.52	2.92	80.19	1.09	-	-	18051.67	1848.07	8.14**
<b>F</b>	65.13	61.33	-21.24	1.31	3.23	3.25	-0.30	-	-	11548.56	1188.68	1.93
<b>h<sup>2</sup></b>	-0.01	-0.40	4762.32**	0.76	-0.05	11.15	-0.04	-	-	4282.79	425.53	-0.04
<b>E</b>	0.73	0.84	387.44	0.36*	0.84*	20.30*	0.15	-	-	1118.46	116.83	0.24
<b>(H1/D)<sup>0.5</sup></b>	1.23	1.18	3.87	1.40	1.37	2.04	5.04	-	-	1.48	1.47	1.93
<b>H<sub>2</sub>/4H<sub>1</sub></b>	0.21	0.21	0.20	0.19	0.16	0.22	0.23	-	-	0.19	0.19	0.20
<b>KD/KR</b>	1.25	3.12	0.97	26.16	36.17	1.16	-0.11	-	-	5.70	425.53	2.17
<b>h<sup>2</sup>/H<sub>2</sub></b>	0.00	0.00	1.04	0.50	-0.02	-0.14	-0.04	-	-	0.24	1848.07	0.00
<b>r(P, Wr + Vf)</b>	-0.41	-0.48	-0.71	-0.87	-0.58	0.47	0.27	-	-	-0.90	-0.90	-0.82
<b>Heritability</b>	53.64	54.82	4.96	32.43	34.19	11.52	2.17	-	-	39.26	39.45	22.83

\* P ≤ 0.05, \*\* P ≤ 0.01

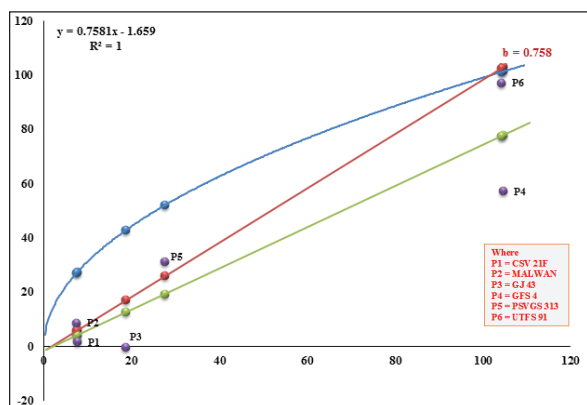


Fig. 1: Graph of Vr-Wr for flowering days in sorghum

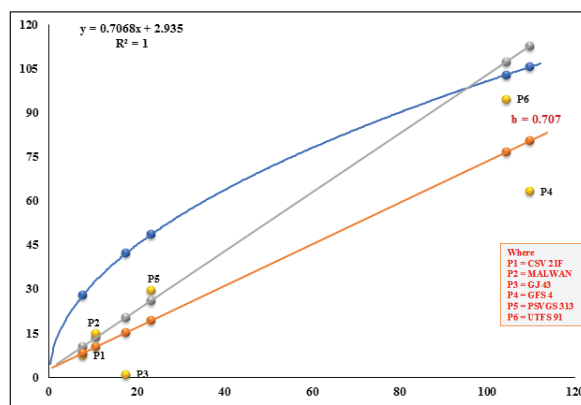


Fig. 2: Graph of Vr-Wr for maturity days in sorghum

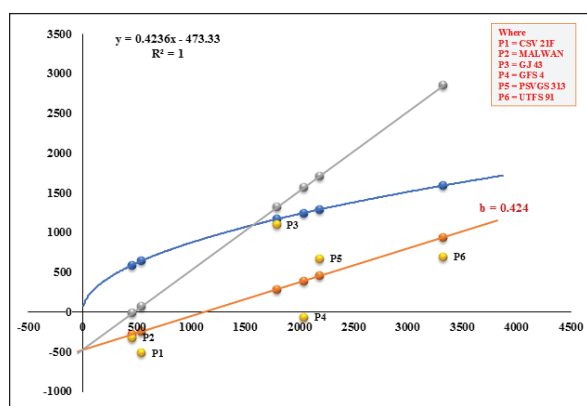


Fig. 3: Graph of Vr-Wr for height of plant in sorghum

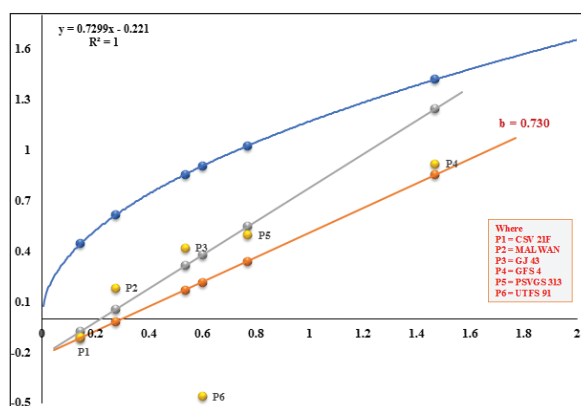


Fig. 4: Graph of Vr-Wr for leaves number plant<sup>-1</sup> in sorghum

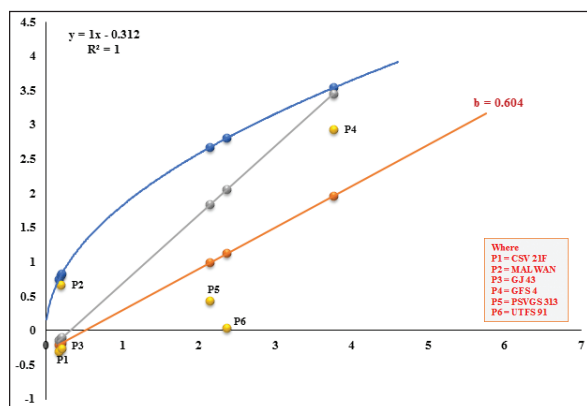


Fig. 5: Graph of Vr-Wr for girth of stem in sorghum

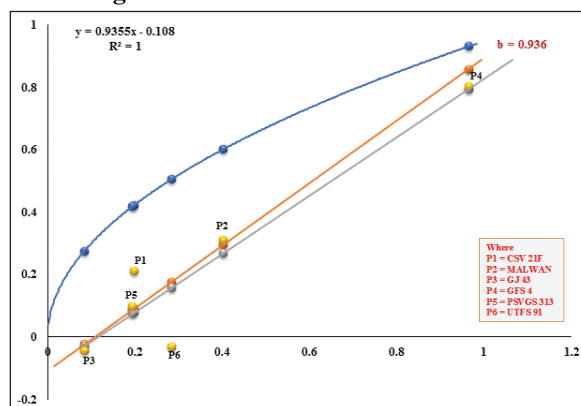


Fig. 6: Graph of Vr-Wr for leaf width in sorghum

dry fodder yield plant<sup>-1</sup> (Fig. 8) and brix value (Fig. 9). The line of regression interrupted the positive adjacent the axis of Wr for a maturity day suggested partial dominance role. The widespread parental range points laterally the regression line in the Vr-Wr graph for number of leaves plant<sup>-1</sup> and stem girth which displayed significant genetic range among the parents. The parent UTFS 91 had extreme recessive genes for early flowering and

early maturity. Likewise, the parent MALWAN had extreme dominant genes for increasing plant height and number of leaves plant<sup>-1</sup>. The parent CSV 21F had high frequency of dominant gene for green fodder yield plant<sup>-1</sup> and dry fodder yield plant<sup>-1</sup> and late flowering and maturity, while GJ 43 possessed maximum dominant genes for leaf width, Parent GFS 4 had maximum recessive gene for reducing stem girth.

Genetic components of variation of forage yield

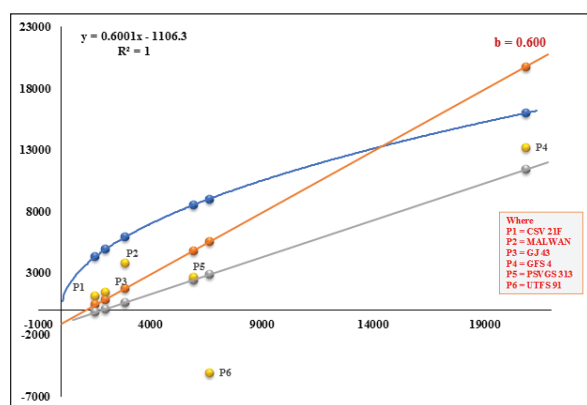


Fig.7: Graph of Vr-Wr for green fodder yield plant<sup>-1</sup> in sorghum

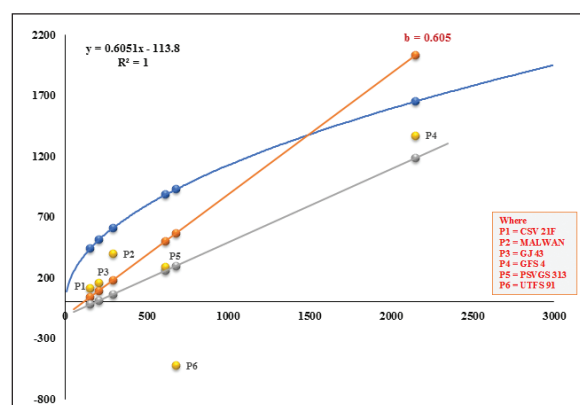


Fig. 8: Graph of Vr-Wr for dry fodder yield plant<sup>-1</sup> in sorghum

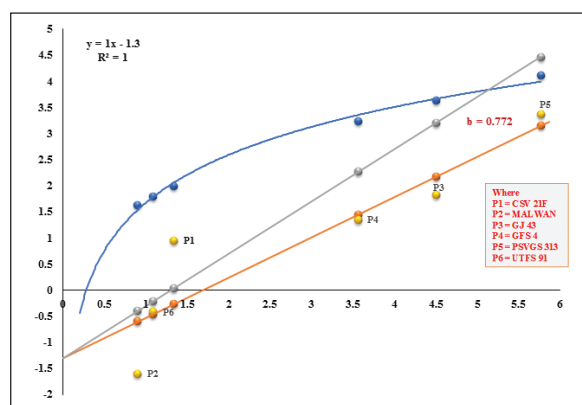


Fig. 9: Graph of Vr-Wr for brix value in sorghum

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