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Research Article

Genetic analysis in sorghum for yield and shoot fly resistance attributes

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Abstract

An experiment was conducted at the Centre for Millets Research, Sardarkrushinagar Dantiwada Agricultural University, Deesa during *kharif*,2022 to estimate general and specific combining ability effects and components of genetic variance for yield and shoot fly resistance attributing traits in sorghum. The mean sum of squares due to general and specific combining ability was found highly significant for all the studied characters. The estimates of σ^2*gca*/σ^2*sca* revealed preponderance of non-additive type of gene action in the expression of yield and shoot fly resistance associated characters. Considering *gca* effect the parents SWARNA, GJ 43 and GNJ 1 revealed significantly superior gca value and were identified as a good general combiner for yield contributing characters. The parents IS 18551 and IS 2205 were good general combiners for shoot fly resistance attributes. The crosses IS 18551 × SWARNA, GJ 43 × GNJ 1 and IS 2205 × SWARNA for grain yield per plant recorded the highest *sca* effects which involved poor × good; good × good and poor × good combination, respectively. The cross, IS 18551 × IS 2205 showed significant desirable *sca* effects for almost all the characters related to shoot fly resistance, *viz.,* seedling vigour, seedling glossiness and shoot fly dead heart at 14th, 21st and 28th days after emergence (DAE).The regression of Wr on Vr was desirable and near unity for seedling vigour, seedling glossiness, days to flowering, total plant height, shoot fly dead heart at 14 DAE, shoot fly dead heart at 21 and 28 DAE, hydrocyanic acid content, grain yield per plant, protein content and total phenol content. The regression line intercepted Wr axis below the origin indicating over dominance for total plant height, shoot fly dead heart at 14 DAE, hydrocyanic acid content and total phenol content. The component D was significant for all the traits suggesting predominance of additive gene effects. The estimates H_1 and H_2 were significant for all the traits except days to flowering. The magnitude of non-additive (H_1) component was higher than additive (D) component for all the traits except seedling vigour which showed more important role of over dominance. In Wr-Vr graph scattering of parental array point along the regression line for the traits hydrocyanic acid content, crude protein content and total phenol content revealed significant genetic diversity among the parents for the above traits.

Keywords: Sorghum, shoot fly, GCA, SCA

INTRODUCTION

Sorghum bicolor (L.) is a C_4 cereal crop that is also known as sorghum, great millet or jowar. It is a true diploid species (2n = 2x = 20) with a genome size of 730 Mb. It belongs to the family *Poaceae*, tribe *Andropogoneae* and subtribe *Sorghastrae* (Price *et al*., 2005). It is an often-cross pollinated crop with high genetic variability that can be successfully exploited through heterosis breeding (Tomar *et al*., 2012; Amare *et al*., 2015; Yaqoob Muhammad, 2015). Shoot fly is a major pest in sorghum which causes major damage during late sowing in *kharif* season (Sukhani and Jotwani, 1980). In India yield losses due to shoot fly damage is estimated to be up to 90 % in case of grain and 45 % in case of fodder sorghum. For breeders, it is essential to understand the nature of gene action and the pattern of inheritance of attributing traits for shoot fly resistance in sorghum.

The diallel mating design is an important tool used by plant breeding programs to obtain information on trait inheritance (Griffing, 1956[a] and Hayman, 1954[a]). Studies on combining ability estimates are useful to understand the nature of genetic variance and to predict the relative performance of different lines in hybrid combinations. Heritability of a trait approaches its maximum in successive generations following hybridization. Information on the nature and magnitude of gene action is important in understanding the genetic potential of a population, and deciding the breeding procedure to be adopted in a given population (Prabhakar and Raut, 2010). Jinks and Hayman (1953) and Hayman (1954[a]) developed methods for estimation of genetic components of variance in diallel crosses. They also proposed a graphical approach, using second order statistics for interpretation of results. 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. In the present study, efforts were made to investigate the combining ability and component of genetic variation and graphical analysis in sorghum to identify superior hybrids and parents for yield and shoot fly resistance contributing traits.

MATERIALS AND METHODS

The experimental material consisted of six parents *viz,* IS 18551, IS 2205, DJ 6514, SWARNA, GNJ 1 and GJ 43 (check) and their 15 half-diallel crosses (**Table 1**). Generated during summer, 202.1 at Centre for Millets Research, S. D. Agricultural University, Deesa (Gujarat). The experimental site is situated at 24°15' 39'' N latitude and 72°12'03'' E longitude and at an elevation of 146 M above the mean sea level. The experiment was conducted during *kharif*, 2022 in a Randomised Block Design (RBD) with three replications to evaluate a set of 21 genotypes comprising of six parents (including the check GJ 43) and 15 F_1 hybrids. Each genotype was planted in rows of 2.0 m length, with 45cm and 15 cm inter and intra-row spacing. All the recommended agronomic practises and plant protection measures were followed for a good stand. The observations on days to flowering were recorded based on visual assessment and while for the traits seedling vigour, seedling glossiness, total plant height, shoot fly dead heart at 14 days after emergence (DAE), shoot fly dead heart at 21 DAE, shoot fly dead heart at 28 DAE, hydrocyanic acid content, 1000-grain weight, grain yield per plant, crude protein content and total phenol content, observations were recorded on randomly selected five competitive individual plants. The significance of difference in mean value from each replication in each genotype for the 12 characters were examined as suggested by Panse and Sukhatme, (1985). The Analysis of Variance (ANOVA) for combining ability was performed as per the method suggested by Griffing (1956[b]) for Model-I and Method-2. The diallel analysis proposed by Jinks and Hayman (1953) and Hayman (1954[a]) was employed to find out the genetic constitution of the parents with respect to various traits . This analysis is based on simple additive-dominance model of gene effects with certain assumptions. The validity of hypothesis of additive-dominance model was tested by confirming unit slope of regressions of Wr and Vr and by non-significant value of t^2 as prescribed by Hayman (1954[b]). Statistical analysis was carried out based on the replicated mean data using SPAR 1.0 software.

RESULTS AND DISCUSSION

Analysis of variance for combining ability suggested that the mean squares due to general (GCA) and specific combining ability (SCA) variance were significant for all the 12 traits, demonstrating the influence of both additive and non-additive genetic variance in their inheritance.

Table 1 List of parents and their sources

S. No.	Name of genotypes	Particular about genotype	Source
1	IS 18551	Resistant to shoot fly	Indian Institute of Millets Research, Hyderabad, Telangana, India.
2	IS 2205		
3	DJ 6514	Susceptible to shoot fly	
4	SWARNA		
5	GNJ 1	Released varieties	Centre for Millets Research, S. D. Agricultural University, Deesa, Gujarat, India.
6	GJ 43 (Check)		

For all traits assessed, the estimates of σ^2sca were greater than σ^2gca. The ratio of σ^2gca/σ^2sca showed the predominance of non-additive type of gene action in the expression of yield and shoot fly resistance associated characters (**Table 2**). Similar findings have been reported by Sayed and Said (2016), Akata *et al*. (2017), Kumari *et al*. (2018) and Mengistu *et al*. (2020). The general combining ability effects of six parents for 12 parameters is furnished in **Table 3**. The *gca* effects of parents explicated that none of the parents was consistently good general combiner for all the characters under investigation. The parent IS 18551 was good general combiner for seedling vigour, seedling glossiness, total plant height, shoot fly dead heart at 14, 21 and 28 DAE, hydrocyanic acid content and total phenol content. The parent IS 2205 was good general combiner for seedling glossiness, total plant height, shoot fly dead heart at 14, 21 and 28 DAE and hydrocyanic acid content. The parent SWARNA was good general combiner for days to flowering, 1000-grain weight and grain yield per plant. The parent DJ 6514 was good general combiner for days to flowering. The parent GJ 43 was good general combiner for total plant height, 1000-grain weight, grain yield per plant and crude protein content. The parent GNJ 1 was good general combiner for 1000-grain weight, grain yield per plant and crude protein content. These good general combiners of yield and its contributing characters can be utilized in intensive crossing programme for generation of superior segregants for desired characters. In the case of shoot fly resistance characters, two parents *viz.,* IS 18551 and IS 2205 were categorized as good general combiners as they found good combiners for various shoot fly resistance attributes *viz.,* seedling vigour, seedling glossiness, shoot fly dead heart at 14, 21 and 28 DAE.

A perusal of data (**Table 4**) 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 were accompanied by high-ranking mean performance, suggesting predominant role of non-additive gene effects in expression of grain yield per plant and component characters. The crosses IS 18551 × SWARNA, GJ 43 × GNJ 1 and IS 2205 × SWARNA for grain yield per plant recorded the highest *sca* effects which involved poor × good; good × good and poor × good combination, respectively. Furthermore, these crosses also exhibited a positive significant *sca* effect for other contributing characters *viz.,* seedling glossiness, days to flowering, total plant height and 1000-grain weight. It could be concluded that, two specific combinations *viz.,* IS 18551 × IS 2205 and IS 18551 × SWARNA were observed in desirable direction, since it had significant *sca* effects for shoot fly resistance characters. These cross combinations are promising for selecting good homozygous lines for future exploitation. Since high general combining effects correspond with additive and additive × additive gene interaction and represents the fixable genetic component of variation, these parents appear to be worthy of exploitation in recombination breeding programme for shoot fly resistance. The present results are analogous with reports of Wagaw and Tadesse, (2020), Patel *et al.* (2021), Vinoth *et al.* (2021) and Joshi *et al.* (2022) for grain yield per plant; Ravindrababu (1998) and Ravindrababu *et al.* (2003) for

Table 2. Analysis of variance for combining ability in 12 characters of sorghum

Sources of variation	d.f.	Seedling vigour	Seedling glossiness	Days to flowering	Total plant height	Shoot fly dead heart at 14 DAE	Shoot fly dead heart at 21 DAE
GCA	5	0.41**	2.00**	87.08**	829.49**	299.52**	707.57**
SCA	15	0.02*	0.32**	6.00*	167.47**	66.40**	114.90**
Error	40	0.49	0.02	2.98	37.72	8.80	10.11
δ^2GCA		0.01	0.25	10.51	98.97	36.34	87.18
δ^2SCA		0.46	0.30	13.02	29.75	57.61	104.78
δ^2GCA / δ^2SCA		0.02	0.83	0.81	0.76	0.63	0.83

Sources of variation	d.f.	Shoot fly dead heart at 28 DAE	Hydrocyanic acid content	1000–grain weight	Grain yield per plant	Crude protein content	Total phenol content
GCA	5	897.61**	393.48**	40.75**	1500.25**	6.48**	2.00**
SCA	15	160.05**	305.66**	9.75**	291.10**	0.86**	1.03**
Error	40	13.43	10.45	0.76	15.67	0.06	0.02
δ^2GCA		110.52	47.87	5.00	185.57	0.80	0.24
δ^2SCA		146.61	295.20	8.98	275.43	0.98	1.01
δ^2GCA / δ^2SCA		0.75	0.16	0.55	0.67	0.82	0.24

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

Table 3. Estimation of general combining ability effect of parents for the 12 characters in sorghum

Parents	Seedling vigour	Seedling glossiness	Days to flowering	Total plant height	Shoot fly dead heart at 14 DAE	Shoot fly dead heart at 21 DAE	Shoot fly dead heart at 28 DAE	Hydrocyanic acid content	1000 – grain weight	Grain yield per plant	Crude protein content	Total phenol content
IS 18551	0.39** (G)	0.66** (G)	1.68** (P)	4.89* (G)	-8.99** (G)	-12.44** (G)	-13.02* (G)	-3.52* (G)	-2.34* (P)	-18.59** (P)	-1.24* (P)	0.55** (G)
IS 2205	0.26 (A)	0.58** (G)	2.76** (P)	7.87** (G)	-6.47* (G)	-11.46* (G)	-13.49** (G)	-9.67** (G)	-2.45* (P)	-9.15* (P)	-0.47* (P)	-0.01 (A)
SWARNA	-0.19 (A)	-0.53** (P)	-5.98** (G)	-13.92** (P)	5.57* (P)	7.41* (P)	10.42** (P)	0.50 (A)	2.49* (G)	15.76** (G)	0.27* (G)	-0.72* (P)
DJ 6514	-0.15 (A)	-0.34** (P)	-1.69** (G)	-10.24** (P)	4.01* (P)	3.45* (P)	4.13* (P)	11.50** (P)	-1.21* (P)	-7.51* (P)	-0.50* (P)	-0.45* (P)
GJ 43 (C)	-0.11 (A)	-0.10 (A)	1.72** (P)	11.56** (G)	2.92* (P)	7.92** (P)	6.38** (P)	2.40* (P)	1.50* (G)	7.18* (G)	1.14** (G)	0.31* (G)
GNJ 1	-0.14 (A)	-0.27** (P)	1.51** (P)	-0.14 (A)	2.94* (P)	5.11* (P)	4.56* (P)	-1.22 (A)	2.00* (G)	12.30** (G)	0.79** (G)	0.33* (G)
S.E.(g_i) (±)	0.21	0.05	0.56	2.03	0.96	1.03	1.18	1.04	0.28	1.28	0.08	0.04
Range	-0.19 to 0.39	-0.53 to 0.66	-5.98 to 2.76	-13.92 to 11.56	-8.99 to 5.57	-12.44 to 7.92	-13.49 to 10.42	-9.67 to 11.50	-2.45 to 2.49	-18.59 to 15.76	-1.24 to 1.14	-0.72 to 0.55

* $P \leq 0.05$, ** $P \leq 0.01$
Where
G = Good combiner; A = Average combiner; P = Poor combiner.

seedling vigour, seedling glossiness and shoot fly dead heart at 14 DAE, 21 and 28 DAE.

The parents comprised in the study were homozygous and diverse in their origin. The maternal effects are presumed to be absent in the present material. For testing other assumptions, two general tests *i.e.,* t^2 test and regression of Wr on Vr were used. The characters under study *viz.,* seedling vigour, seedling glossiness, days to flowering, total plant height, shoot fly dead heart at 14 DAE, 21 DAE and 28 DAE, hydrocyanic acid content, grain yield per plant, crude protein content and total phenol content revealed non-significant t^2 value which specified the fulfillment of assumptions required under diallel analysis. While rest of the traits showed significant t^2 value indicated that nonfulfillment of assumption in these traits shows the unjustifiability of the hypothesis of simple additive-dominance model of gene action and involvement of epistasis and for linkage disequilibrium hence Hayman diallel analysis was not valid. Non-significant t^2 values in sorghum diallel analysis have been reported by Ravindrababu (1998) and Ravindrababu *et al.* (2003) for seedling vigour, days to flowering, plant height, 1000-grain weight and grain yield per plant; Patel *et al.* (2022) for days to flowering, plant height and protein content.

The significant value of additive (D) and non-additive components (H_1 and H_2) clearly indicates the predominance of role of both fixable and non-fixable components. The component D measures the additive effects of genes and it was observed to be significant for all the traits under study (**Table 5**). It implies that these traits can be easily fixed in early generation. These results were in harmony with those reported 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 significant for all the characters except days to flowering. The significant H_1 and H_2 components 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 results reported by Ravindrababu (1998), Ravindrababu *et al.* (2003) for seedling vigour, days to flowering, plant height, grain yield per plant and 1000-grain weight; Nair and Ghorade (2016) for grain yield per plant; Patel *et al.* (2022) for days to flowering, plant height and protein content in sorghum. Further, the magnitude of non-additive (H_1) component was higher than additive (D) component for all the traits except seedling vigour suggesting the important role of over dominance for these traits. This result is according with Patel *et al.* (2022). This was also evident from the mean degree of dominance (> 1) for

Table 4. Estimates of specific combining ability effects associated with sorghum hybrids

S.No.	Hybrids (F_1)	Seedling vigour	Seedling glossiness	Days to flowering	Total plant height	Shoot fly dead heart at 14 DAE	Shoot fly dead heart at 21 DAE	Shoot fly dead heart at 28 DAE	Hydro-cyanic acid content	1000-grain weight	Grain yield per plant	Crude protein content	Total phenol content
1	IS 18551 × IS 2205	0.33*	0.52**	2.90*	15.67**	-8.10**	-12.91**	-15.69**	4.21	1.27	4.30	1.32**	0.09
2	IS 18551 × SWARNA	0.11	0.55**	-3.01*	6.80	2.43	3.53	4.32	-6.54**	0.58	28.75**	0.00	0.08
3	IS 18551 × DJ 6514	0.01	-0.68**	-0.64	-4.62	10.89**	16.62**	15.27**	3.46	0.85	15.70**	0.76**	0.88**
4	IS 18551 × GJ 43	-0.18	-0.36**	-1.72	-18.17**	7.36**	5.75*	10.18**	4.67	-0.80	0.74	-1.13**	-0.21*
5	IS 18551 × GNJ 1	-0.18	-0.67**	-1.51	-12.05*	-9.77**	10.89**	18.24**	-4.40	2.19**	13.85**	-0.31	-2.48**
6	IS 2205 × SWARNA	-0.13	-0.37**	-3.43**	16.53**	2.75	7.00**	6.73	4.97*	-2.00**	17.11**	0.09	-1.04**
7	IS 2205 × DJ 6514	0.02	-0.35**	0.95	-6.28	12.31**	13.65**	15.67**	-24.64**	-0.63	1.08	-0.06	-1.75**
8	IS 2205 × GJ 43	-0.21	-0.24	-0.80	-2.89	7.86**	8.48**	9.27**	16.01**	3.29**	12.79**	0.15	-0.30**
9	IS 2205 × GNJ 1	-0.13	-0.23	-1.93	6.82	6.40**	11.55**	14.44**	-11.47**	-1.25	-6.83*	0.56**	1.00**
10	SWARNA × DJ 6514	0.03	-0.17	-1.97	5.52	-3.90	-5.64*	-5.94	-29.31**	-1.35*	-1.08	-1.69**	0.25
11	SWARNA × GJ 43	-0.06	-0.31**	2.28	9.77	-2.38	-4.69	-2.59	23.16**	-2.73**	-13.38**	-0.01	0.36**
12	SWARNA × GNJ 1	0.13	-0.27	5.49**	2.75	-3.00	-6.85**	-8.23**	-13.99**	-0.43	4.85	-0.30	0.90**
13	DJ 6514 × GJ 43	-0.02	0.36**	-0.01	-12.31**	1.23	-3.78	-1.52	-16.67**	7.05**	8.40**	1.72**	0.58**
14	DJ 6514 × GNJ 1	0.10	-0.31**	1.53	11.87*	-1.14	-7.73**	-11.50**	29.65**	-1.70*	-5.60	0.48*	-0.06
15	GJ 43 × GNJ 1	0.13	0.08	-0.22	-4.94	6.31**	5.74*	-0.03	-10.24**	3.64**	18.09**	0.28	0.21*
S.Ed.(±)		0.18	0.20	1.53	5.60	2.63	2.82	3.25	2.87	0.78	3.51	0.22	0.12
Range		-0.21 to 0.33	-0.68 to 0.55	-3.43 to 5.49	-18.17 to 16.53	-9.77 to 12.31	-12.91 to 16.62	-15.69 to 18.24	-29.31 to 29.65	-2.73 to 7.05	-13.38 to 28.75	-1.69 to 1.72	-2.48 to 1.00
No. of positive significant		1	3	2	3	6	8	6	4	4	7	5	6
No. of negative significant		0	7	2	3	2	4	3	7	4	2	2	5
Total significant		1	10	4	6	8	12	9	11	8	9	7	11

*P ≤ 0.05, **P ≤ 0.01

Table 5. Estimation of genetic components of variance as per Hayman diallel in sorghum

Parameters	Seedling vigour	Seedling glossiness	Days to flowering	Total plant height	Shoot fly dead heart at 14 DAE	Shoot fly dead heart at 21 DAE	Shoot fly dead heart at 28 DAE	Hydrocyanic acid content	1000-grain weight	Grain yield per plant	Crude protein content	Total phenol content
b (Wr,Vr)	1.01	0.79	0.99	1.08	0.97	1.00	1.01	0.59	-0.33	0.95	0.50	0.65
t_{b-0}	12.51**	4.25*	4.07*	4.67**	5.70**	9.63**	8.67**	2.09	-0.56	6.40**	1.73	1.67
t_{1-b}	-0.01	1.17	0.04	-0.35	0.17	-0.04	-0.04	1.45	2.21**	0.29	1.72	0.91
t^2	0.06	0.45	0.20	0.69	0.03	0.06	0.05	0.34	0.23	0.01	0.52	0.01
D	1.86*	1.37*	43.97*	817.45*	241.45*	559.75*	758.78*	389.54*	30.98*	1004.15*	4.10*	1.75*
H_1	0.71*	3.14*	69.39	2585.66*	995.58*	1643.10*	2330.41*	4994.20*	166.82*	3706.60*	14.37*	17.17*
H_2	0.65*	2.53*	66.55	1558.56*	772.54*	1422.95*	2024.33*	4399.01*	118.10*	3294.01*	11.37*	15.07*
F	0.62*	0.74	5.17	1445.28*	337.13*	645.29*	956.19*	747.33	47.31*	847.71*	3.49	2.80
h^2	-0.01	0.25	-3.91	68.26	531.99*	1017.17*	1396.91*	563.85	36.98	5868.26*	1.86	1.35
E	0.04*	0.05	2.96	40.48	8.98*	13.49	14.82	10.01	0.75	15.58	0.06	0.02
$\sqrt{H_1/D}$	0.31	0.76	0.63	0.88	1.01	0.86	0.88	1.79	1.16	0.97	0.94	1.57
$H_2/4H_1$	0.23	0.20	0.24	0.15	0.19	0.22	0.22	0.22	0.18	0.22	0.20	0.22
KD/KR	3.33	2.12	1.20	3.38	5.40	5.11	6.13	3.30	4.85	2.56	2.67	3.08
h^2/H_2	-0.01	0.10	-0.05	0.04	0.69	0.72	0.69	0.13	0.31	1.78	0.16	0.09
r (P, Wr +Vr)	-0.11	0.01	0.11	-0.43	-0.76	-0.92*	-0.89*	0.77	0.46	-0.88	0.39	0.14
Heritability	0.76	0.47	0.51	0.31	0.24	0.15	0.01	0.09	0.35	0.25	0.38	0.12

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

traits *viz.,* shoot fly dead heart at 14 DAE, hydrocyanic acid content, 1000-grain weight and total phenol content demonstrating over dominance effect for the traits. Mather and Jinks (1971) while discussing the short comings of numerical component analysis suggested that ($\sqrt{H_1/D}$) at each locus is true for major degree of dominance only, where the distribution of dominance and recessive genes are symmetrical. Asymmetrical distribution of genes influences of over estimation of the mean degree of dominance. The higher magnitude of dominance component was also reported by various workers for different characters *viz.,* Ravindrababu (1998) and Ravindrababu *et al.* (2003) for days to flowering and dry yield per plant; Nair and Ghorade (2016) for grain yield per plant; Patel *et al.* (2022) for plant height. However, the over-dominance observed may not be considered as index for true over-dominance. Since the degree of dominance could be biased due to linkage, epistasis or both (Comstock and Robinson, 1952).

The equal distribution of positive and negative alleles in the parents aids the breeder in choosing precise desirable traits without losing any other desirable traits. The value of H_1 was greater than H_2 for all the traits indicating that frequency of gene distribution in the parental lines was unequal and that was also proved by the ratio of $H_2/4H_1$ (< 0.25) which confirmed the unbalanced distribution of negative and positive effects of gene at the loci in the parents entailing dominance for all the traits. The results are in accordance with those of Ravindrababu (1998) and Ravindrababu *et al.* (2003) for forage yield and components, Nair and Ghorade (2016) for grain yield per plant and Patel *et al.* (2022) for green and dry fodder yield per plant in sorghum.

The values of estimate of F component was positive and significant (> 0) for the traits *viz.,* seedling vigour, total plant height, shoot fly dead heart at 14 DAE, shoot fly dead heart at 21 DAE, shoot fly dead heart at 28 DAE, 1000-grain weight and grain yield per plant explicating the presence of unequal proportion of dominant and recessive gene but the proportion of dominant genes were higher and it was also confirmed by greater than one value of KD/KR components for all the traits divulging higher frequency of dominant genes than recessive genes in the parents. The present findings are in accordance with those of Ravindrababu *et al.* (2003) for seedling vigour, days to flowering, grain yield per plant and 1000-grain weight; Nair and Ghorade (2016) for grain yield per plant and Patel *et al.* (2022) for days to flowering, grain yield per plant and protein content in sorghum.

The information on number of genes / group of gene responsible for particular traits is vital for the genetic progress through selection. The value h^2/H_2 indicating at least one group of gene operates for yield attributes traits *viz.,* seedling glossiness, days to flowering, total plant height, shoot fly dead heart at 14 DAE, shoot fly dead heart at 21 DAE, shoot fly dead heart at 28 DAE, hydrocyanic acid content, 1000-grain weight, grain yield per plant, protein content and total phenol content. These results are analogue with results reported by Ravindrababu (1998) and Ravindrababu *et al.* (2003) for seedling vigour, days to flowering, plant height, grain yield per plant, 1000-grain weight and dead heart; Nair and Ghorade (2016) for grain yield per plant; Patel *et al.* (2022) for plant height, green fodder yield per plant and protein content in sorghum. While the trait seedling vigour and days to flowering, the negative value of h^2/H_2 did not provide any valid interpretation about the group of gene exhibiting dominance. The ratio could be underestimated when the dominance effects of all the genes concerned are not equal in size and distribution, when the distribution of genes are correlated (Jinks and Hayman, (1953) or when complementary gene interaction occur (Liang *et al.,* 1968 and Marlatt *et al.,* 1996).

Environment component (E) was significant for seedling vigour and shoot fly dead heart at 14 DAE. This signifies that considerable role of environmental factor in the expression of these traits. Estimated narrow sense heritability was low to moderate levels for yield and its most of the traits indicating that all the traits could be controlled by additive and non-additive genes with a preponderance of non-additive genes. This also shows that selection should be rewarding in late generations. The correlation between parental order of dominance (Vr + Wr) and parental mean (Y_i) was negative for seedling vigour, total plant height, shoot fly dead heart at 14 DAE, shoot fly dead heart at 21 DAE, shoot fly dead heart at 28 DAE and grain yield per plant indicates more role of dominant as compared to recessive genes for increasing mean values. Ravindrababu (1998), Ravindrababu *et al.* (2003) and Patel *et al.* (2022) also reported role of dominance genes for days to flowering, plant height and grain yield per plant in sorghum. The regression of Wr on Vr was desirable and near unity for seedling vigour, seedling glossiness, days to flowering, total plant height, shoot fly dead heart at 14 DAE, shoot fly dead heart at 21 DAE, shoot fly dead heart at 28 DAE, hydrocyanic acid content, grain yield per plant, protein content and total phenol content. Thus, graphical analysis was performed for these traits only. For the remaining trait, 1000-grain weight, the Wr-Vr graph was much distorted and failed to provide much information. In graphical analysis, the regression line intercepted Wr axis below the origin revealed that over dominance for total plant height (**Fig. 4**), shoot fly dead heart at 14 DAE (**Fig. 5**), hydrocyanic acid content (**Fig. 8**) and total phenol content (**Fig. 11**). The regression line intercepted the positive side of Wr axis for seedling vigour (**Fig. 1**), seedling glossiness (**Fig. 2**), days to flowering (**Fig. 3**), shoot fly dead heart at 21 DAE (**Fig. 6**), shoot fly dead heart at 28 DAE (**Fig. 7**), grain yield per plant (**Fig. 9**) and crude protein content (**Fig. 10**) implies the presence of partial dominance. The wide scattering of parental array points along the

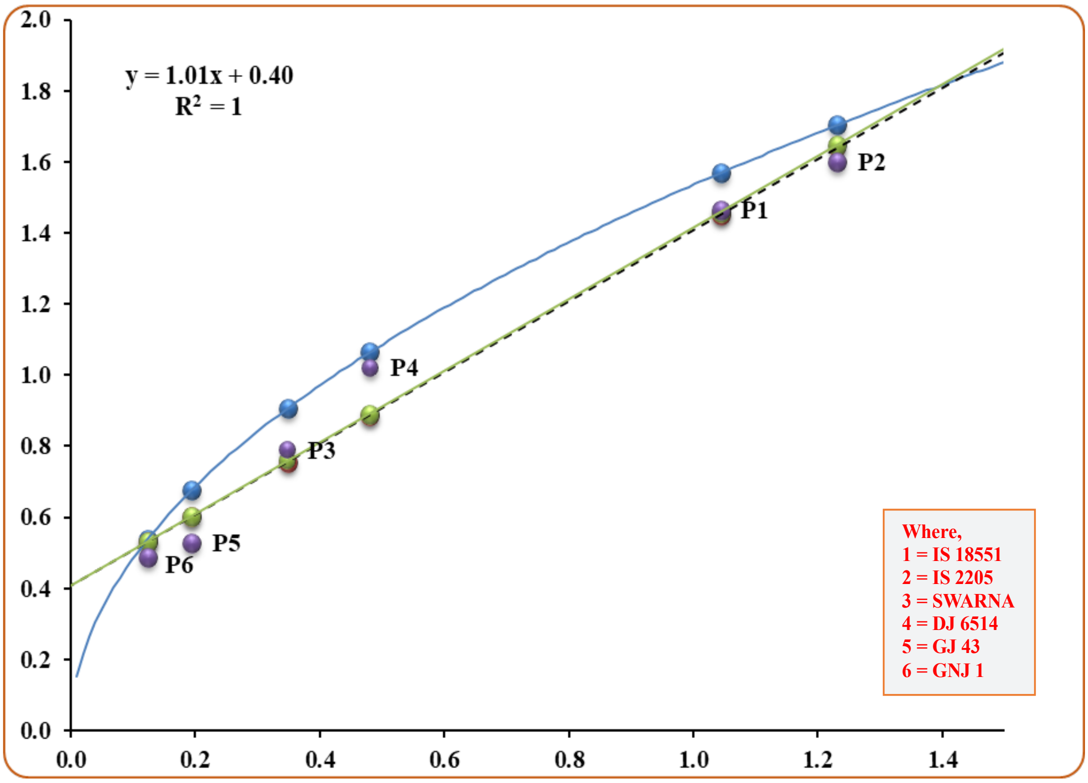

Fig. 1. Wr, Vr graph for seedling vigour

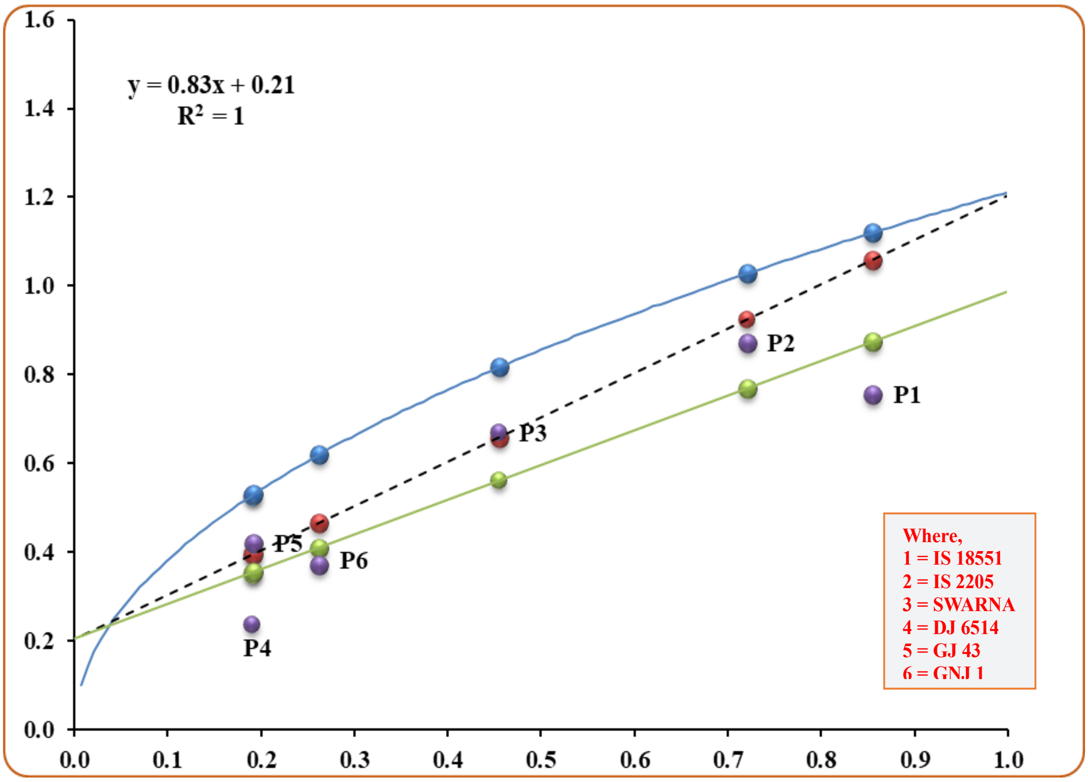

Fig. 2. Wr, Vr graph for seedling glossiness

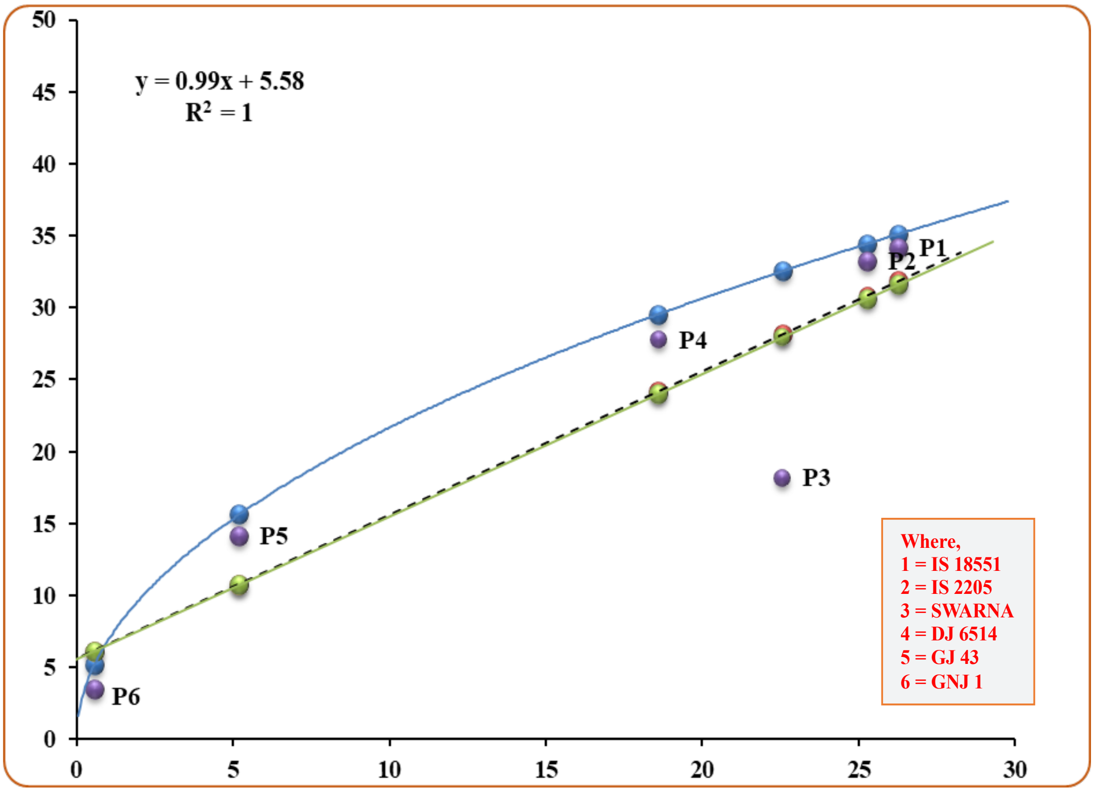

Fig. 3. Wr, Vr graph for days to flowering

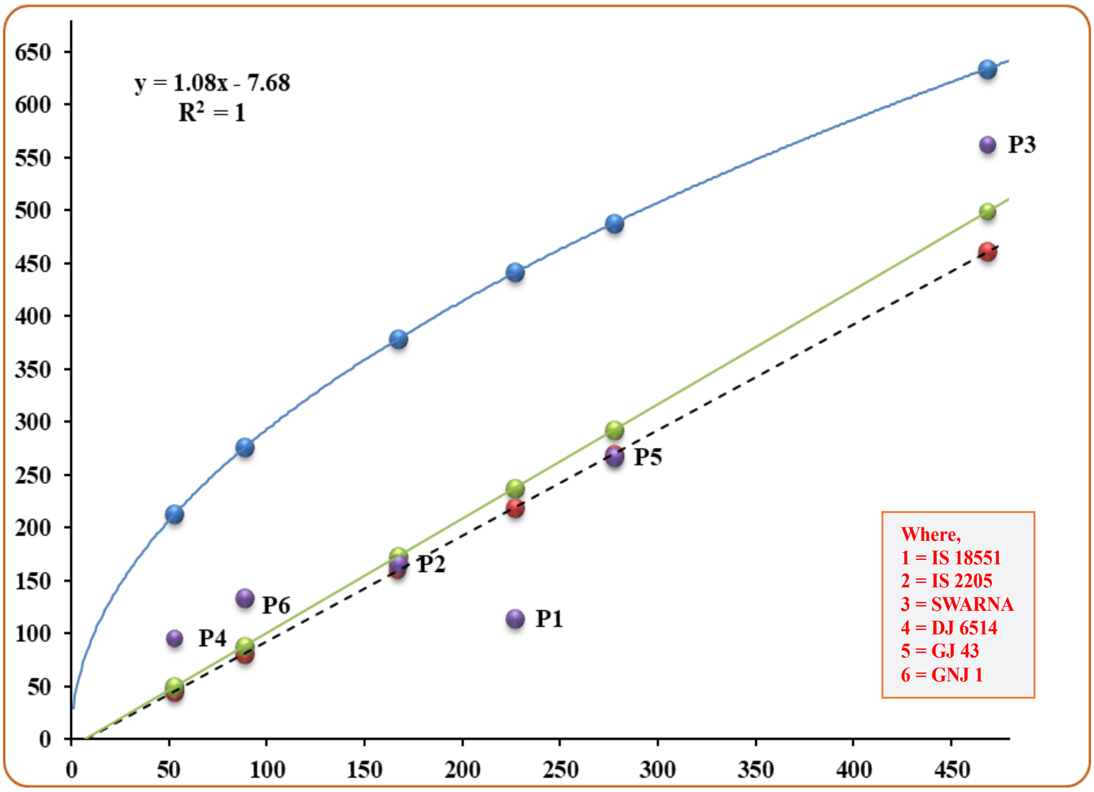

Fig. 4. Wr, Vr graph for total plant height

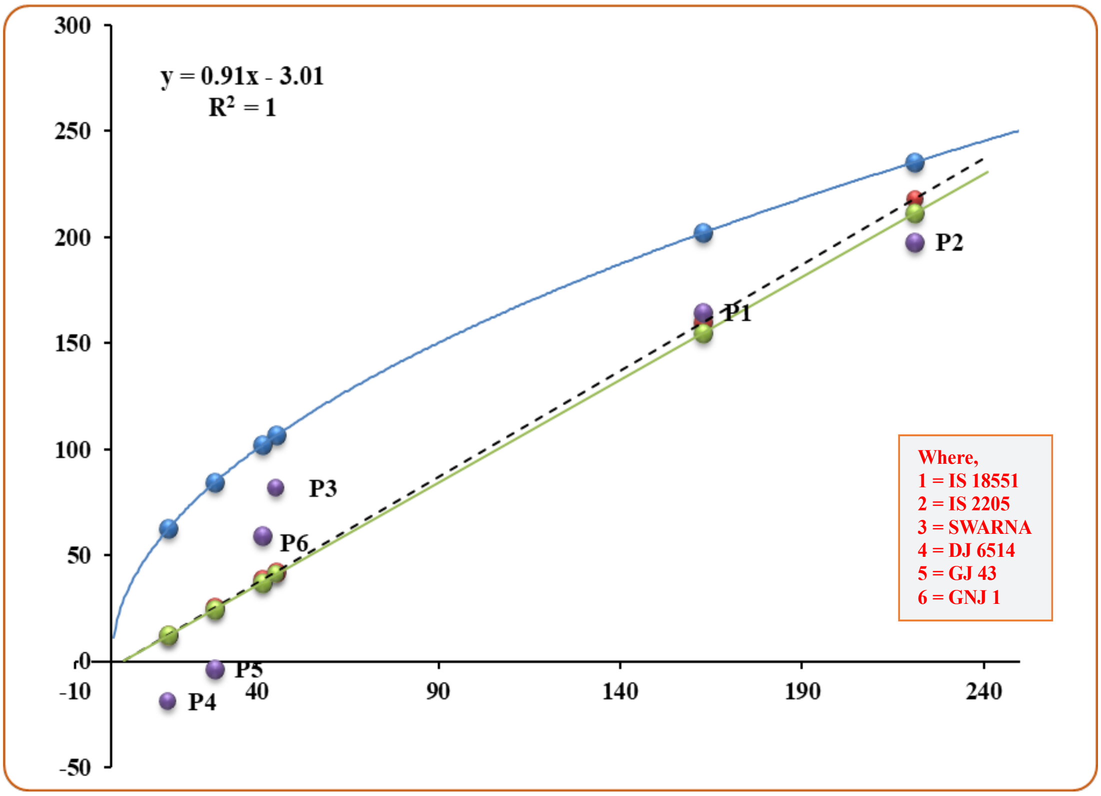

Fig. 5. Wr, Vr graph for shoot fly dead heart at 14 DAE

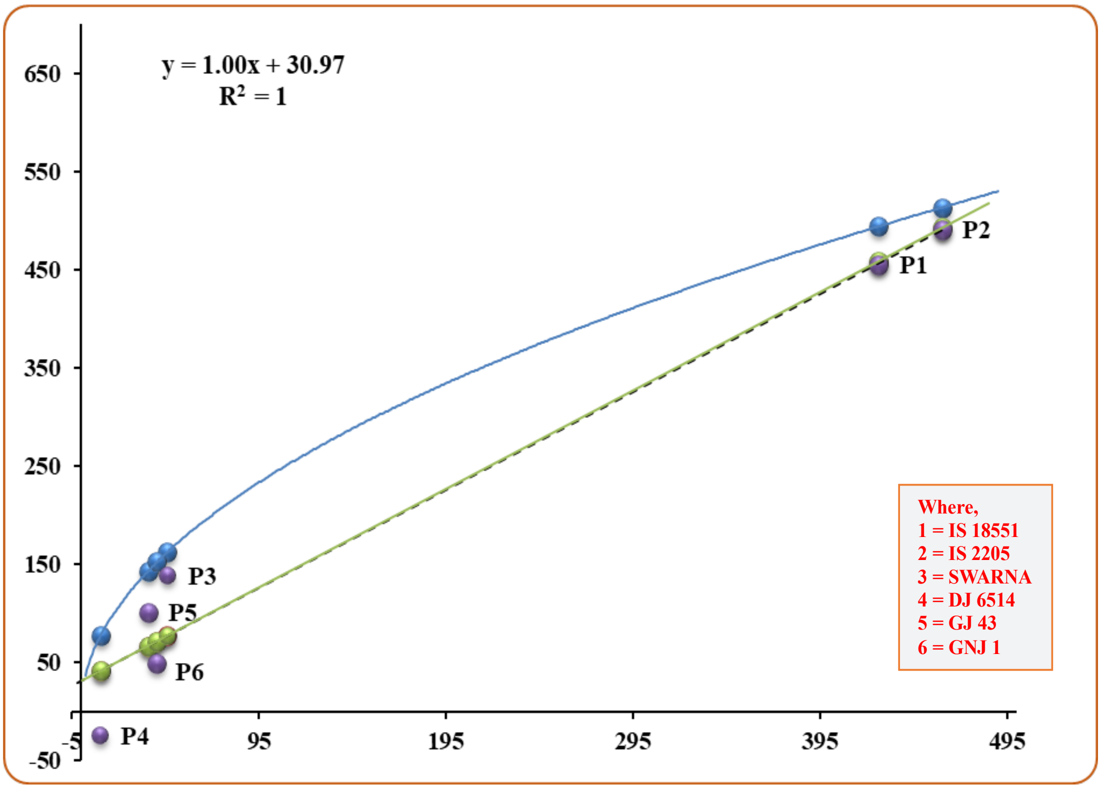

Fig. 6. Wr, Vr graph for shoot fly dead heart at 21 DAE

https://doi.org/10.37992/2023.1404.151

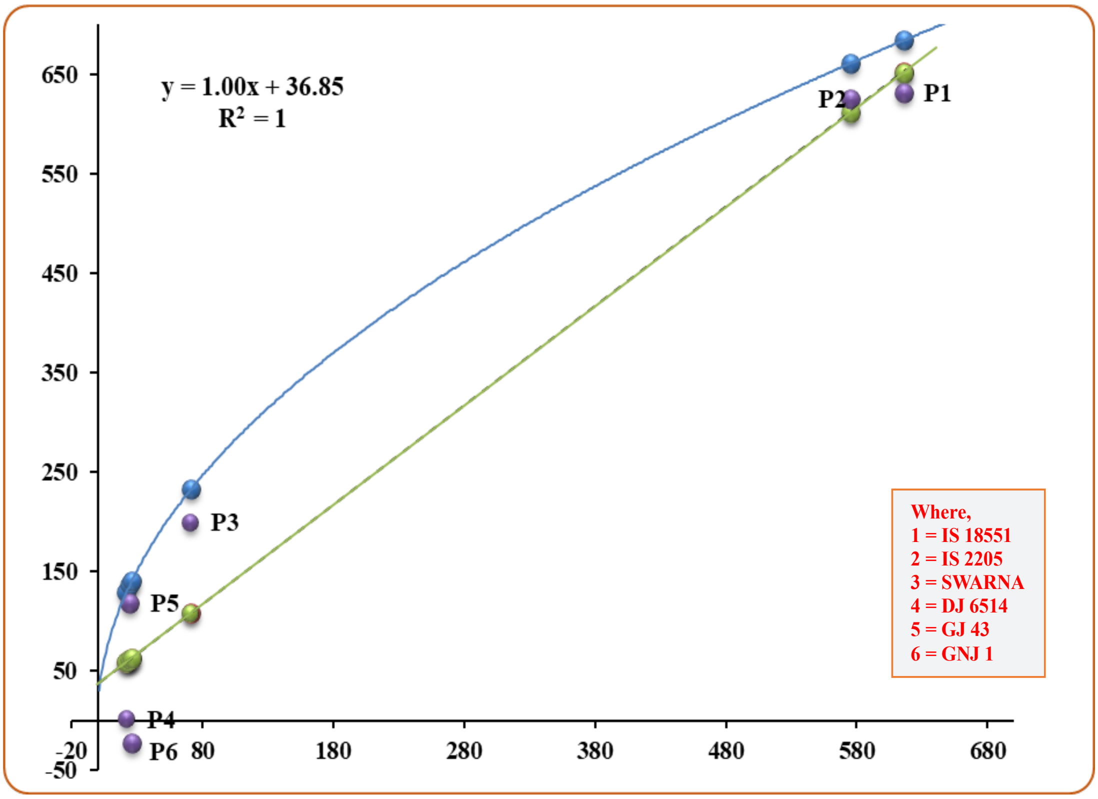

Fig. 7. Wr, Vr graph for shoot fly dead heart 28 DAE

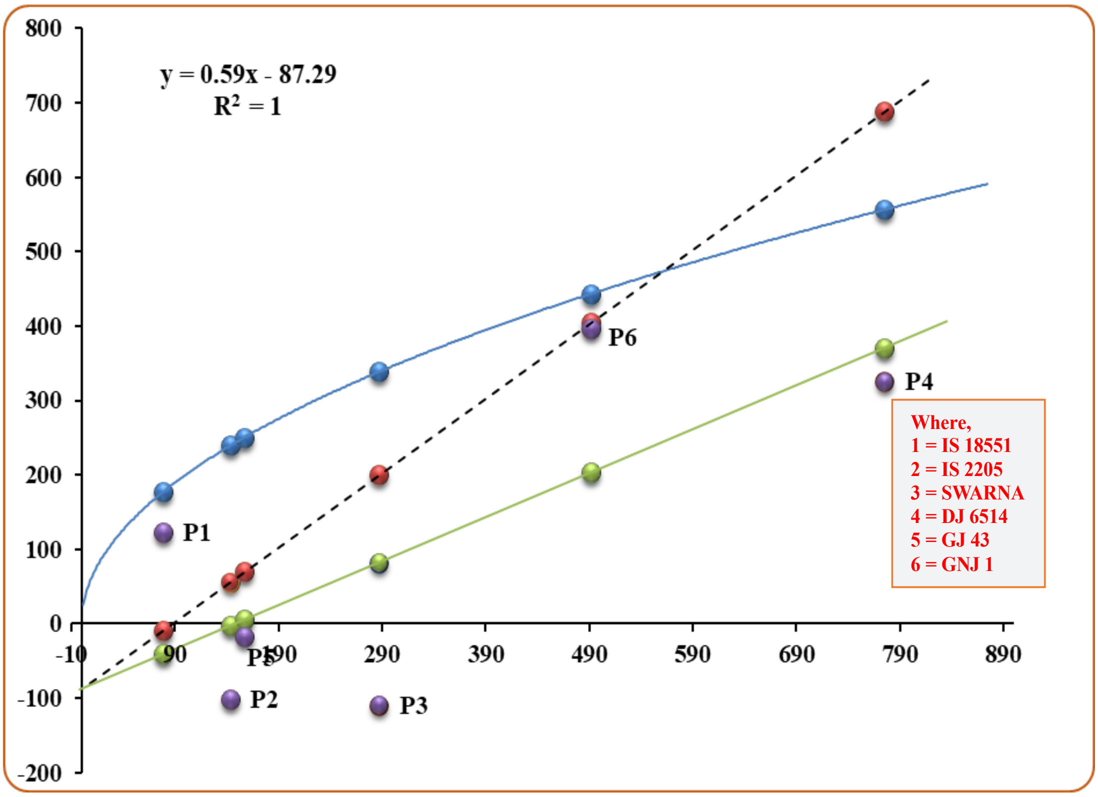

Fig. 8. Wr, Vr graph for hydrocyanic acid content

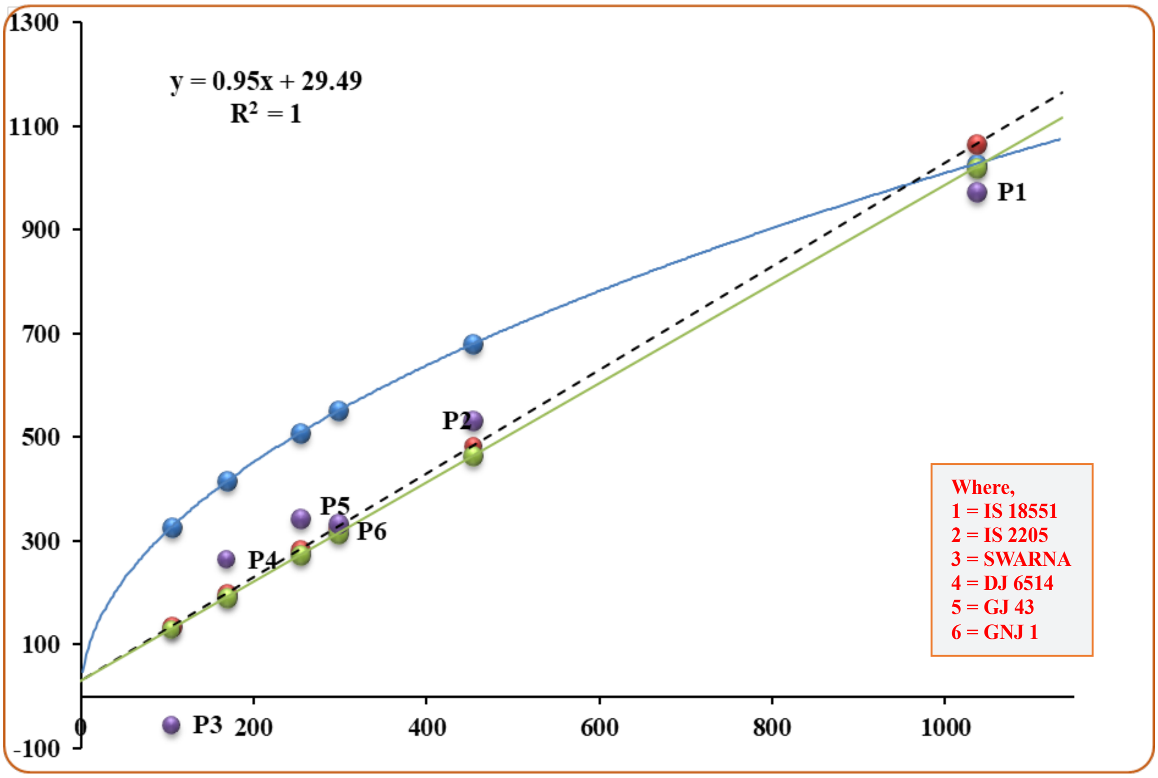

Fig. 9. Wr, Vr graph for grain yield per plant

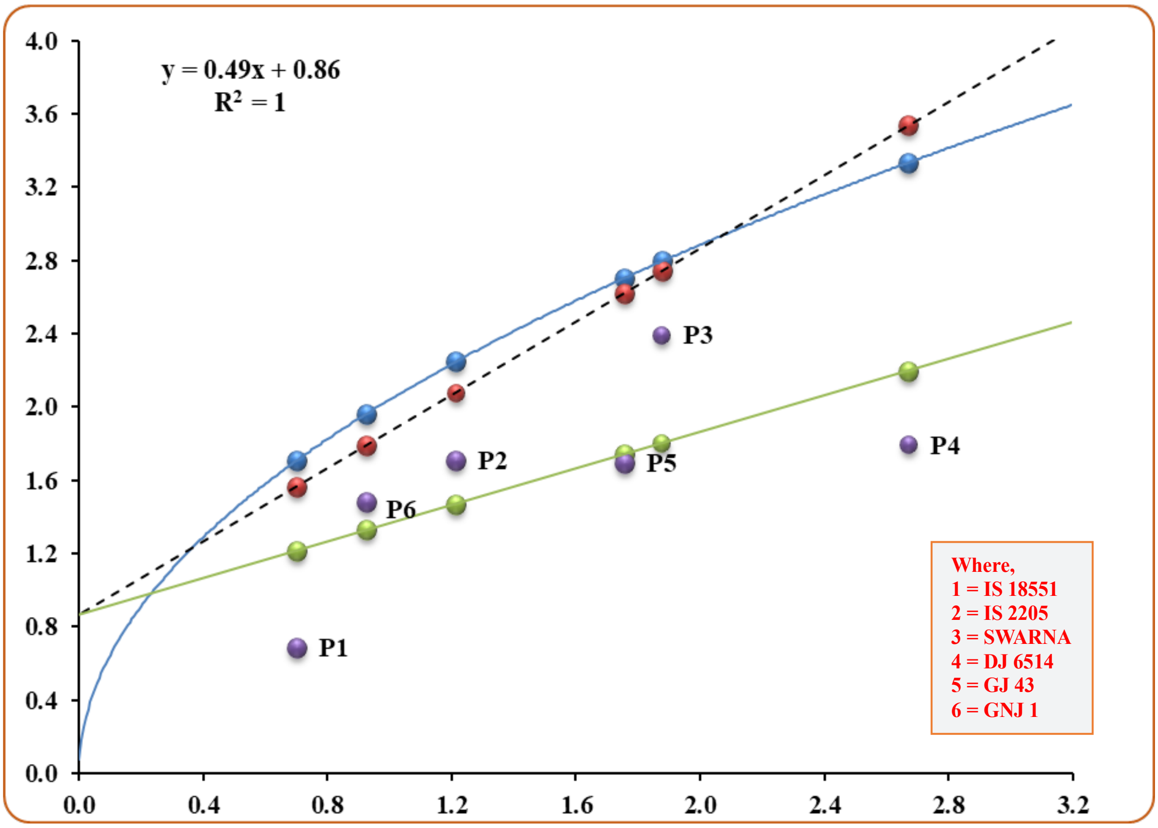

Fig. 10. Wr, Vr graph for crude protein content

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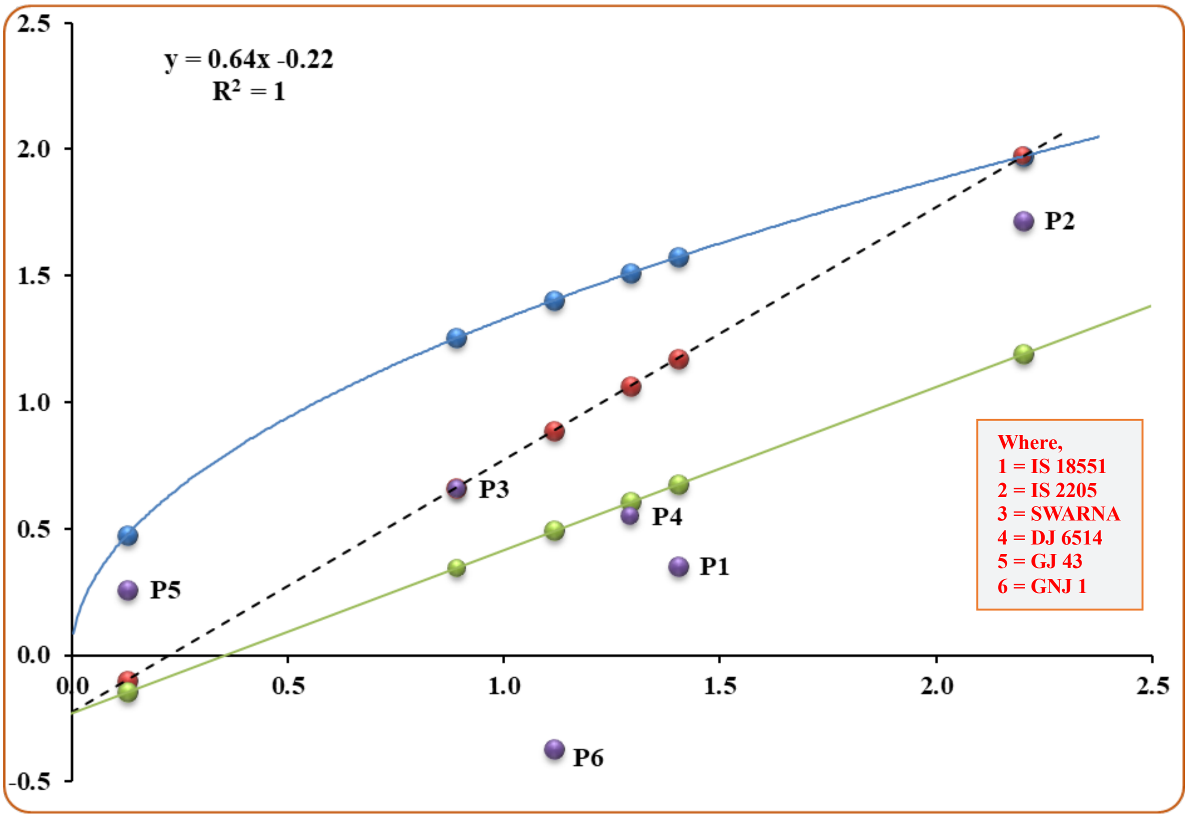

Fig. 11. Wr, Vr graph for total phenol content

Table 6. Estimates of genetic parameters by Griffing's method *vs* and Hayman's method for 12 traits in sorghum

Name of character	Parameters		Status of Hayman's analysis
	δ²GCA / δ²SCA	$\sqrt{H_1/D}$	
Seedling vigour	Over dominance (0.02)	Partial dominance (0.31)	Valid
Seedling glossiness	Over dominance (0.83)	Partial dominance (0.76)	Valid
Days to flowering	Over dominance (0.81)	Partial dominance (0.63)	Valid
Total plant height	Over dominance (0.76)	Partial dominance (0.88)	Valid
Shoot fly dead heart at 14 DAE	Over dominance (0.63)	Over dominance (1.01)	Valid
Shoot fly dead heart at 21 DAE	Over dominance (0.83)	Partial dominance (0.86)	Valid
Shoot fly dead heart at 28 DAE	Over dominance (0.75)	Partial dominance (0.88)	Valid
Hydrocyanic acid content	Over dominance (0.16)	Over dominance (1.79)	Valid
1000-grain weight	Over dominance (0.55)	Over dominance (1.16)	Partially valid
Grain yield per plant	Over dominance (0.67)	Dominance (0.97)	Valid
Crude protein content	Over dominance (0.82)	Partial dominance (0.94)	Valid
Total phenol content	Over dominance (0.24)	Over dominance (1.57)	Valid

regression line in the Wr-Vr graph for hydrocyanic acid content, crude protein content and total phenol content showing considerable genetic diversity among the parents for these traits. The parental line IS 18551 had maximum recessive genes for days to flowering and shoot fly dead heart at 28 DAE. IS 2205 had maximum recessive genes for seedling vigour, shoot fly dead heart at 14 DAE, shoot fly dead heart at 21 DAE and total phenol content, while SWARNA had maximum recessive genes for total plant height. Similarly, the parent SWARNA had maximum dominant genes for increasing grain yield per plant. The parent GJ 43 had high frequency of dominant genes for total phenol content, while IS 18551 possessed maximum dominant genes for reducinghydrocyanic acid content.

The evidence obtained from Griffing and Hayman diallel analyses relating to the nature of gene action controlling different traits are summarized in **Table 6** for comparable evaluation. Perusal of the table lead to draw the conclusion that both the analyses gave more or less the same picture with regard to the magnitude of additive and non-additive genetic effects for respective traits.

The *gca* effects of parents explicated that the parent IS 18551 was found good general combiner for seedling vigour, seedling glossiness, total plant height, shoot fly dead heart at 14, 21 and 28 DAE, hydrocyanic acid content and total phenol content. The parent IS 2205 was good general combiner for seedling glossiness, total plant height, shoot fly dead heart at 14, 21 and 28 DAE and hydrocyanic acid content. The parent SWARNA was good general combiner for days to flowering, 1000-grain weight and grain yield per plant. Shoot fly resistance can be evaluated from a series of associated characters. These characters include seedling glossiness, seedling vigour; shoot fly dead heart at 14, 21 and 28 DAE. The cross IS 18551 × IS 2205 exhibited significant desirable *sca* effects for the character associated with shoot fly resistance. On the basis of all the genetic parameters, the crosses IS 18551 × IS 2205, IS 18551 × SWARNA and GJ 43 × GNJ 1 were found promising as they expressed high *sca* effects. These three crosses having potential to generate desirable segregants for selection of superior plants for grain yield and shoot fly resistance attributes. The Griffing and Hayman analyses gave more or less the same picture with regard to the magnitude of additive and non-additive genetic effects for shoot fly resistance and grain yield attributes.

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