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GENE ACTION STUDY FOR YIELD AND YIELD CONTRIBUTING CHARACTERS IN GROUNDNUT, *ARACHIS HYPOGAEA* (L.)

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ABSTRACT

The study was carried out to investigate genetic nature and magnitude of gene effect for yield contributing character in groundnut by using six parameter model of generation mean analysis. Two crosses *viz.*, SBXI × Phuleunnati and SBXI × Girnar 4 were made involving two parents during *Kharif* 2021. Six generations (P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2) were obtained by mating two male parents with common female and further studied for nine quantitative characters. The significant analysis showed the presence of additive, dominant, and epistatic gene interactions. Hence F_1 , F_2 , BC_1 and BC_2 generations of each cross were evaluated along with their parents to assess the nature of gene action involved for various characters which in turn helps in formulating an effective and sound breeding programme in groundnut. Additive gene action along with additive × additive (i) followed by dominance (h) was found significant for the characters *viz.*, days to maturity, dry pod yield, shelling %, harvest index, sound mature kernel. For improvement of these characters, one should follow the simple selection in early segregating generations. For pod yield and its components, the dominant component (h) and dominance × dominance (l) gene interaction was found significant for most of the characters *viz.*, days to maturity, dry pod yield per plant, shelling %, harvest index, these characters can be improved by postponing selection in later generations.

Key words : Six parameter model, Generation mean analysis, Gene action, Groundnut.

Introduction

Groundnut, ‘the unpredictable legume’ is also known as earthnut, peanut, monkey nut and manilla nut. It is the 13th most important food crop and 4th most important oilseed crop of the world. Groundnut kernels have about 25% protein which is 1.3 times higher than meat, 2.5 times higher than eggs and 8 times higher than fruit. The oil content in kernels ranges from 40-50% and is extensively used for cooking (culinary oil) and for preparing vegetable oil (vanaspati). Its oil is also used for the preparation of soaps, cosmetics, cold cream and for various industrial uses. Its oil is now used in pharmaceutical as a substitute to oleic oil. Groundnut kernels are consumed directly as raw, roasted, boiled or fried. Groundnut haulms is a very good palatable (8-11%

protein) fodder for cattle, when fed in green state. The groundnut cake have immense value as feeding material for livestock and organic manure. It contains 8% N, 1.4% P_2O_5 and 1.2% K_2O .

Knowledge of gene action in plant breeding helps in selection of parents for use in the hybridization programmes, in choice of appropriate breeding procedure for the genetic improvement of various quantitative characters and also in estimation of some other genetic parameters. Gene action is measured in terms of components of genetic variance and is of three types, *viz.*, additive, dominance and epistatic gene action. Additive genetic variance is a pre-requisite for genetic gain under selection, because this is the only genetic variance which responds to selection. In addition to

additive variation, it has been suggested that non-additive variance (dominance and epistasis) may also be involved in the inheritance of many quantitative characters in groundnut. In spite of the limited scope of exploitation of non-allelic interactions in groundnut, the information on non-allelic interactions would be of value to groundnut breeders to formulate appropriate breeding procedures. The variation due to dominance effects and their interactions cannot be exploited effectively in crops like groundnut while the additive type of epistasis is potentially useful, as it can be fixed in homozygous cultivars. Hence insight into the nature of gene action involved in the expression of various characters is essential to a plant breeder for starting a judicious breeding programme.

Materials and Methods

Experiment location : The experiment was conducted in randomized block design with three replications during year 2021-2023 at Groundnut Farm, Post Graduate Institute, M.P.K.V., Rahuri, Maharashtra, India.



Fig. 1 : Experimental plot.

Experimental material : The material for this study comprised of two crosses *viz.*, SBXI \times Phuleunnati and SBXI \times Girnar 4. The parents were crossed to synthesize F_1 hybrids. The further advancement made to assess the nature of gene action by generation mean analysis. Generations *viz.*, P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 populations in each cross were developed to study the genetic interactions. The spacing adopted was 30 \times 10 cm and the recommended cultural practices were followed throughout the crop growing period.

Statistical analysis : Action of the genes controlling quantitative characters can be described by the use of gene models. Mean of five generations *viz.*, P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 were used to estimate genetic parameters following a perfect fit solution given by Cavalli (1952). The mid-parental effect (m) and the types of gene action *viz.*, additive (d), dominance (h), additive \times additive (i), additive \times dominance and dominance \times dominance (l) were determined using six parameter model of generation mean analysis. The adequacy of simple additive-dominance model was detected by employing

A, B, C and D scaling test suggested by Mather and Jinks (1971). The additive-dominance model was considered inadequate when any one of the four scaling test was significant or if chi square value for all traits was significant.

Results and Discussion

A good knowledge on the genetic systems controlling expression of the characters facilitates the choice of the most efficient breeding and selection procedure. The generation mean analysis with first degree statistics were adopted to detect nonallelic interaction component of the mean of the phenotypic distribution. Mean of six generations *viz.*, P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 of each cross are presented in Tables 1 and 2 and the results of scaling test and genetic parameters in each cross (Tables 3 and 4) are discussed character wise, hereunder. The mean performance for different characters varied over six generations for two crosses (Tables 1 and 2). The F_1 's means of all the two crosses founded as mid parental value over both the parent or exceeds over better parent, indicating their dominance (incomplete) genetic control in respective cross for different traits. The parents, SB-XI and Girnar 4 was earliest in day to 50 per cent flowering and days to maturity, parent Phule Unnati was better for yield contributing characters, whereas F_1 of cross-I (SB-XI \times Phule Unnati) recorded highest shelling per cent and harvest index. It was also observed that the F_1 of cross-II (SB-XI \times Girnar 4) was close to better parents for yield contributing characters. This implies that due consideration should be given to the per se performances of the generations along with the gene actions inferred therein, while selecting for improvement in the respective cross (s).

Scaling test : Scaling test was applied to detect the presence/ absence of epistasis. Estimates of scaling test revealed the presence of non-allelic interactions, indicating the inadequacy of additive-dominance model for all the characters in both the crosses.

Genetic parameters : Gene effects *viz.*, mid-parental effect (m), additive (d), dominance (h), additive \times additive (i), additive \times dominance and dominance \times dominance (l) were computed using a six parameter model of generation mean analysis since scaling tests were significant. The six generation of all two crosses were used to estimates the gene effects *viz.*, [m], [d], [h], [i], [j] and [l] in respect of traits associated with pod yield wherever, the scaling test and joint scaling test were highly significant indicating inadequacy of the simple additive-dominance model to explain the genetic control.

The estimates of m (mean), major genetic effects d

Table 1 : Mean performance and standard error of six generations for nine characters of groundnut for in the cross (I) SBXI × Phule Unnati.

Generations	Mean±SE	Days to flowering	Days to maturity	Number of branches/plant	Number of mature pods/plant	Dry pod yield (g/plant)	100 kernel weight (g/plant)	Shelling %	Harvest Index	SMK (%)
P ₁	Mean	44.00	116.13	5.93	16.66	10.70	29.55	63.96	43.95	90.33
	±SE	0.51	0.47	0.34	0.77	0.47	0.56	0.89	0.63	0.93
P ₂	Mean	50.13	122.40	9.93	23.33	23.38	39.67	68.29	58.96	94.60
	±SE	0.59	0.35	0.33	1.01	0.84	0.43	0.55	0.70	0.32
F ₁	Mean	46.93	115.60	6.26	20.26	19.08	38.04	69.75	59.08	92.20
	±SE	0.37	0.30	0.26	1.32	0.95	1.16	0.53	0.58	0.67
F ₂	Mean	46.23	124.95	7.41	21.95	18.98	37.93	67.92	55.02	90.98
	±SE	0.31	0.18	0.15	0.46	0.35	0.21	0.39	0.45	0.30
BC ₁	Mean	42.20	116.0	6.80	18.56	14.30	33.61	67.85	43.56	91.59
	±SE	0.24	0.24	0.19	0.84	0.23	0.23	0.40	0.29	0.29
BC ₂	Mean	49.33	123.00	8.76	26.21	20.23	39.11	67.85	58.36	92.80
	±SE	0.21	0.20	0.22	1.04	0.51	0.30	0.35	0.56	0.23

SMK- Sound mature kernel, SE- Standard error.

and h and non-allelic gene interactions [i, j and l] based on six parameter model (Hayman, 1958) for the traits associated with dry pod yield and its components in groundnut are presented in Table 4.

The parameter [m] was significant in both two crosses (SBXI × Phule Unnati, SBXI × Girnar 4 for all the characters which were studied for dry pod yield and its components in Groundnut. The gene effect estimated by using perfect fit model in respect of traits associated with dry pod yield and its components have been presented in Table 4 and discussed traits wise below.

Days to 50% flowering : The estimates of genetics parameters in the cross SBXI × Phule Unnati, it was observed that additive 'd' (7.13) was positively significant. The magnitude of additive component is greater than dominance 'h'. The interaction components additive x dominance 'j' (4.06) and dominance × dominance 'l' (6.80) were estimated positively significant. Opposite sign observed for genetic component dominance 'h' and dominance × dominance 'l', with presence of duplicate epistasis.

In the cross SBXI × Girnar 4, estimates of genetics parameters, it was observed that additive 'd' (1.78) was positively significant. The magnitude of additive component is greater than dominance 'h'. The interaction component additive × additive 'i' (-3.63) was observed negatively significant, while additive x dominance 'l' (9.00) were estimated positively significant. The magnitude of additive (d) gene action for both the crosses was higher than dominance 'h' the in both the crosses. Opposite sign observed for genetic component dominance 'h' and dominance x dominance 'l', with presence of duplicate epistasis. The presence of additive, dominance and epistatic interactions for this trait were earlier reported by, Jaylakshmi *et al.* (2002), Suneetha *et al.* (2006), Boraih *et al.* (2015).

Days to maturity : The estimates of genetics parameters in the cross SBXI × Phule Unnati, it was observed that additive 'd' (-6.96) and dominance 'h' (-25.43) were negatively significant. The interaction components additive × additive 'i' (-21.76), additive x dominance 'j' (-3.83) and component dominance x dominance 'l' (-13.43) was found negatively significant. Opposite sign observed for genetic component dominance 'h' and dominance × dominance 'l', with presence of duplicate epistasis.

In the cross SBI-XI × Girnar 4, estimates of

Table 2 : Mean performance and standard error of six generations for nine characters of groundnut in the cross (II) SBXI × Girmar 4.

Cross No. II	Generations	Mean ± SE	Days to flowering	Days to maturity	Number of branches/plant	Number of mature pods/plants	Dry pod yield (g/plant)	100 kernel weight (g/plant)	Shelling %	Harvest Index	Sound Mature Kernel (%)
SBXI × Girmar 4	P ₁	Mean	39.46	115.93	6.73	16.93	11.97	31.79	62.70	46.03	88.73
		±SE	0.50	0.37	0.24	0.30	0.33	0.67	0.65	0.68	0.80
	P ₂	Mean	42.80	121.60	9.93	25.20	21.17	40.23	69.61	57.70	93.40
		±SE	0.66	0.39	0.30	0.82	0.71	0.60	0.37	0.67	0.55
	F ₁	Mean	43.06	119.13	8.06	17.06	17.49	36.24	66.28	55.48	90.26
		±SE	0.53	0.32	0.22	0.94	0.38	0.70	0.82	1.21	0.67
	F ₂	Mean	41.66	122.44	8.10	20.80	18.72	37.08	67.66	56.48	92.48
		±SE	0.19	0.16	0.11	0.39	0.36	0.29	0.27	0.27	0.28
	BC ₁	Mean	39.86	116.20	6.98	16.26	14.17	34.41	63.80	47.78	89.65
		±SE	0.23	0.20	0.18	0.29	0.34	0.41	0.32	0.36	0.50
	BC ₂	Mean	41.65	121.58	8.70	24.93	21.47	40.17	68.54	57.14	92.21
		±SE	0.24	0.17	0.19	0.41	0.55	0.21	0.33	0.29	0.34

genetics parameters, it was observed that ‘d’ (-5.38) and ‘h’ (-13.83) were negatively significant. The interaction component ‘i’ (-14.20) and ‘j’ (-2.55) estimated negatively significant and ‘l’ (4.43) were observed positively significant component. Opposite sign observed for genetic component dominance ‘h’ and dominance × dominance ‘l’, with presence of duplicate epistasis. Role of additive and non-additive gene action for 100-kernel weight were earlier reported by Basu *et al.* (1988) in soybean crop while in groundnut by Gaurav *et al.* (2010), Pavithradevi (2013), Prabhu and Shinde (2016).

Number of branches per plant : In cross SBXI × Phule Unnati the estimates of genetic parameters only additive effect ‘d’ (-1.96) were significant. The interaction components ‘i’, ‘j’ and ‘l’ component were found non-significant and similar sign observed for genetic component dominance ‘h’ and dominance × dominance ‘l’, with presence of complimentary epistasis. The presence of complimentary epistasis was matched with the finding given by Mohan Vishnuvardhan (2011).

The estimates of genetics parameters in cross SBXI × Girmar-4, it was observed that, additive ‘d’ (-1.71) component were negatively significant. The interaction component ‘i’, ‘j’ and ‘l’ components were non-significant, respectively. Opposite sign observed for genetic component dominance ‘h’ and dominance × dominance ‘l’, indicate presence of duplicate epistasis. The duplicate type of epistasis was earlier noticed by Rahangdale and Raut (2002) and Nagarajan *et al.* (2022). The magnitude of additive component in both the crosses was higher and this finding are close agreement with the Shinde *et al.* (2016).

Number of mature pods per plant : From the estimates of genetic parameters, it was observed that additive gene effect [d] (-7.65) were negatively significant in cross SBXI × Phule Unnati. The interaction components [j] additive × dominance (-4.31) was estimated negatively significant. Dominance × dominance [l] was estimated non-significant. Opposite sign observed for genetic component dominance [h] and dominance × dominance [l], indicate presence of duplicate epistasis for number of mature pods per plant. The previous findings revealed the importance of additive type of effects for the trait by Shobha *et al.* (2010), Mohan Vishnuvardhan (2011). Duplicate type of epistasis was observed by the Kaw and Menon (1983) in groundnut, while similar results were reported by Nagarajan *et al.* (2022).

The estimates of genetic parameters in the cross

Table 3 : Estimates of individual and joint scaling tests for different traits for pod yield in two crosses of groundnut [SBXI × Phule Unnati, SBXI × Girnar 4].

S. no.	Characters	Crosses	Scaling tests				χ^2
			A	B	C	D	
1.	Days to 50% flowering	C-I	1.60*	-6.53**	-3.06	0.93	77.61**
		C-II	-2.56**	2.80**	-1.73	1.81**	18.96**
2.	Days to maturity	C-I	0.33	8.00**	30.10**	10.88**	859.65**
		C-II	-2.66**	2.43**	13.96**	7.10**	345.11**
3.	Number of branches / plant	C-I	1.40**	1.33**	1.26	-0.73	8.89**
		C-II	0.83	-0.60	-0.36	0.53	5.07**
4.	Number of mature pods / plant	C-I	0.20	8.83**	7.26*	-0.88	15.00**
		C-II	-1.46	7.60**	6.93**	0.40	47.83**
5.	Dry pods yield (g/plant)	C-I	-1.17	-1.98	3.68	3.42**	15.05**
		C-II	-1.12	4.28**	6.74**	1.79	24.57**
6.	100 kernel weight (g/plant)	C-I	-0.38	0.50	6.40*	3.14**	33.41**
		C-II	0.80	3.87**	3.83	-0.42	17.84**
7.	Shelling %	C-I	1.98	-2.33*	-0.08	0.13	8.99**
		C-II	-1.37	1.19	5.78**	2.97**	26.93**
8.	Harvest index	C-I	-15.91**	-1.32	-0.98	8.12**	282.39**
		C-II	-5.95**	1.09	11.22**	8.04**	143.28**
9.	Sound mature kernel	C-I	0.66	-1.20	-5.40**	-2.43**	19.36**
		C-II	0.30	0.76	7.26**	3.10**	19.57**

* Significant at 5% level, ** Significant at 1% level.

SBXI × Girnar-4, additive gene effect [d] (-8.66) and dominance gene effect [h] (-4.80) were recorded negatively significant. The interaction component additive × dominance [j] (-4.53) were negatively significant. Complimentary gene interaction based on the similar signs of [h] and [l] components was noticed in this cross combination, which is supported by Shobha *et al.* (2010), Prabhu *et al.* (2016) and Shrivalli *et al.* (2016) noticed the role of additive gene action for this trait.

Dry pods yield per plant (g) : In cross SBXI × Phule Unnati, additive [d] (-5.93) and dominance [h] (-4.80) component was observed negatively significant. The interaction component additive × additive [i] (-6.84) and dominance × dominance [l] (10.01) was negatively and positively significant, respectively, while additive × dominance [j] (0.40) was positively non-significant. Opposite sign observed for genetic component dominance [h] and dominance × dominance [l], with presence of duplicate epistasis. The magnitude of additive gene effect was higher, which indicate the predominance of additive gene action for the pod yield per plant trait.

The estimates of genetic parameters in cross SBXI × Girnar-4, it was observed that, additive [d] (-7.30) component was negatively significant. The interaction component additive × dominance [j] (-2.70) component was negatively significant. Opposite sign observed for genetic component dominance [h] and dominance × dominance [l], with presence of duplicate epistasis for earhead length. Gaurav *et al.* (2010), Shoba *et al.* (2010) and Nagrajan *et al.* (2022) reported additive gene action to be involved in the inheritance of this trait. However, non-additive gene action holds good for this trait were reported by Savithamma *et al.* (2010) and Pavithradevi (2013).

100 Kernel weight (g) : The estimates of genetic parameters in cross SBXI × Phule Unnati, additive [d] (-5.50) positively significant. The interaction components additive × additive [i] (-6.28) and dominance × dominance [l] (6.15) component was negatively and positively significant, respectively, Whereas, additive × dominance [j] (-0.73) was negatively non-significant. Opposite sign observed for genetic component dominance [h] and dominance × dominance [l], with presence of duplicate

Table 4 : Estimates of genetic effects for different traits for pod yield in two crosses of groundnut [SBXI × Phule Unnati, SBXI × Girmar 4].

Character	Cross	Genetic Components							Type of epistasis
		m	d	h	I	j	i		
Days to 50% flowering	C-I	46.23** (0.31)	7.13** (0.32)	-2.00 (1.51)	-1.86 (1.99)	4.06** (0.26)	6.80** (4.44)	Duplicate	
	C-II	41.66** (0.19)	1.78** (0.34)	-1.70 (1.24)	-3.63** (1.03)	0.11 (0.54)	9.00** (2.08)	Duplicate	
Days to maturity	C-I	124.95** (0.18)	-6.96** (0.31)	-25.43** (1.07)	-21.76** (0.98)	-3.85** (0.43)	13.43** (1.73)	Duplicate	
	C-II	122.4** (0.16)	-5.38** (0.27)	-13.83** (0.95)	-14.20** (0.86)	-2.55** (0.38)	14.43** (1.52)	Duplicate	
Number of branches / plant	C-I	7.41** (0.15)	-1.96** (0.29)	-0.20 (0.92)	1.46 (0.72)	0.03 (0.38)	-4.20 (1.51)	Complementary	
	C-II	8.10** (0.11)	-1.71** (0.27)	-1.33 (0.76)	-1.06 (0.70)	-0.11 (0.33)	2.50 (1.32)	Duplicate	
Number of mature pods/plant	C-I	21.95** (0.46)	-7.65** (1.34)	2.03 (3.58)	1.76 (3.27)	-4.31** (1.48)	-10.80 (6.40)	Duplicate	
	C-II	20.80** (0.39)	-8.66** (0.51)	-4.80* (2.15)	-0.80 (1.88)	-4.53** (0.67)	-5.33 (3.32)	Complementary	
Dry pods yield (g/plant)	C-I	18.98** (0.35)	-5.93** (0.56)	-4.80* (2.09)	-6.84** (1.80)	0.40 (0.74)	10.01** (1.80)	Complementary	
	C-II	18.72** (0.36)	-7.30** (0.64)	-2.67 (2.02)	-3.58 (1.95)	-2.70** (0.75)	0.43 (3.17)	Duplicate	
100 kernel weight (g/plant)	C-I	37.93** (0.21)	-5.50** (0.38)	-2.85 (1.67)	-6.28** (1.15)	-0.44 (0.52)	6.15* (3.00)	Duplicate	
	C-II	37.08** (0.29)	-5.75** (0.46)	-1.07 (1.73)	0.84 (1.51)	-1.53** (0.65)	-5.52* (2.78)	Complementary	
Shelling %	C-I	67.92** (0.39)	-0.005 (0.54)	3.35 (2.05)	-0.26 (1.91)	2.16** (0.75)	0.61 (3.06)	Complementary	
	C-II	67.66** (0.27)	-4.73** (0.46)	-5.82** (1.71)	-5.95** (1.45)	-1.28** (0.59)	6.13* (2.83)	Duplicate	
Harvest index	C-I	55.02** (0.45)	-14.80** (0.63)	-8.62** (2.34)	-16.25** (2.21)	-7.29** (0.79)	33.49** (3.48)	Duplicate	
	C-II	56.48** (0.27)	-9.36** (0.46)	-12.46** (1.94)	-16.08** (1.43)	-3.52** (0.67)	20.93** (3.38)	Duplicate	
Sound mature kernel	C-I	90.98** (0.30)	-1.20** (0.38)	4.59** (1.67)	4.86** (1.44)	0.93 (0.62)	-4.31 (2.58)	Duplicate	
	C-II	92.48** (0.28)	-2.56** (0.61)	-7.00** (1.86)	-6.20** (1.66)	-0.23 (0.78)	5.13 (3.16)	Duplicate	

epistasis.

In cross SBXI × Girmar-4, additive component [d] (-5.75) was negatively significant. The interaction components additive × dominance [j] (-1.53) and dominance × dominance [I] (-5.52) component was found negatively significant, respectively. Similar sign observed for genetic component dominance [h] and dominance × dominance [I], with presence of complementary epistasis for 100 kernel weight. Role of additive and non-additive gene action for 100-kernel weight were earlier reported by Gaurav *et al.* (2010), Pavithradevi (2013) and Prabhu *et al.* (2016), respectively.

Shelling (%) : From the estimates of genetic parameters in cross SBXI × Phule Unnati, it was observed that additive gene effect [d] (-0.54) and dominance gene effect 'h' (3.28) were negatively and positively non-significant, respectively. The interaction components component [j] additive × dominance (2.16) was estimated positively significant. Similar sign observed for genetic component dominance [h] and dominance × dominance [I], with presence of complimentary epistasis for shelling %.

The estimates of genetic parameters in the cross SBXI × Girmar-4, additive gene effect [d] (-4.73) and dominance gene effect [h] (-5.82) were recorded negatively significant. The interaction components additive × additive [i] (-8.18), additive × dominance [j] were negatively significant and dominance × dominance [I] (6.13) was positively significant. Duplicate gene interaction based on the

opposite signs of [h] and [l] components was noticed in this cross combination. Both the crosses involve additive and non-additive type of gene action significant for the shelling % supported by Jayalkshmi *et al.* (2002) and Suneetha *et al.* (2006).

Harvest index (g) : The estimates of genetic parameters in cross SBXI × Phule Unnati, it was observed that additive gene effect [d] (-14.80) and dominance gene effect 'h' (-8.62) were negatively significant. The interaction components additive × additive [i] (-16.25) and additive × dominance [j] (-7.29) were estimated negatively significant. The interaction component dominance × dominance [l] (33.49) component was estimated positively significant. Opposite sign observed for genetic component dominance [h] and dominance × dominance [l], with presence of duplicate epistasis for pod yield per plant.

In cross SBXI × Girnar 4, additive component [d] (-9.36) and dominance component [h] (-12.46) component observed negatively significant. The interaction component additive × additive [i] (-16.08) and additive × dominance [j] (-3.52) was negatively significant. The components dominance × dominance [l] (20.93) were positively significant. Opposite sign observed for genetic component dominance [h] and dominance × dominance [l], with presence of duplicate epistasis for harvest index. The additive gene effect for harvest index trait is supported by Chavadhari *et al.* (2017). Both crosses show that the additive and non-additive genetic components were equally important this finding matched with the previous finding given by Upadhyaya and Nigam (1999) and Jayalakshmi (2002), Mohan Vishnuvardhan (2011).

Sound mature kernel (%) : In cross SBXI × Phule Unnati, additive [d] (-1.20) was negatively significant while [h] (4.59) component was observed positively significant. The interaction components additive × additive [i] (4.86) were positively significant and the component additive × dominance [j] (0.93), dominance × dominance [l] (-4.31) was non-significant. Opposite sign observed for genetic component dominance [h] and dominance × dominance [l], with presence of duplicate epistasis. The magnitude of dominance gene effect is higher than additive component.

In cross SBXI × Girnar-4, additive [d] (-2.56) and dominance [h] (-7.00) genetic effect were observed negatively significant. The interaction components additive × additive [i] (-6.20) were estimate positively significant while additive × dominance [j] and dominance × dominance [l] (7.94) component was non-significant.

Opposite sign observed for genetic component dominance [h] and dominance × dominance [l], with presence of duplicate epistasis. Both additive and non-additive gene action reported for the sound mature kernel trait by Savitharma (2010).

Inferences based on the magnitudes of additive effects are not advisable, because the distribution of positive and negative gene effects in the parents may result in different degrees of cancellation of effects in the expression and thereby do not necessarily reflect in the magnitude of additive variance. However, dominance (h) and dominance × dominance (l) are independent of the degree of gene distribution due to which their combined estimates could be considered to be the best representative. So, practically these are the only components, which can safely be used to determine the type of epistasis, which may have influence on the observed performance of generations. For the same reason, emphasis has been given to the characters, which are governed by such gene effects for suggesting appropriate breeding method that should be followed to achieve higher expression of such characters.

The presence of duplicate epistasis would be detrimental for rapid progress, making it difficult to fix genotypes with increased level of character manifestation because the positive effects of one parameter would be cancelled out by the negative effects of another. Hence, early generation inter mating besides accumulating the favorable genes and maintaining heterozygosity in the population is likely to throw useful recombinants (Shoba *et al.*, 2010). Complementary epistasis helps in effective execution of pedigree breeding. Based on the criteria mentioned above, the possible exploitation of desirable crosses through pedigree breeding is presented in Table 3.

Conclusion

The characters governed by additive (d) gene effects and additive × additive (i) gene interaction effects are fixable. Also, the crosses which are governed by complementary epistasis where signs of dominance (h) gene effects and dominance × dominance (l) gene interaction effects are similar are also worth exploitation. Such crosses have the potentiality to produce transgressive segregants on the positive side. Pedigree method of breeding followed by simple selection in later segregating generations will be a meaningful breeding strategy to be followed in such crosses for the improvement of the characters under consideration. The generation means analysis of this study brought out the genetics of yield and its components in each of the four

cross combinations studied in detail. From the foregoing discussion, it may be concluded that in all the vegetative and reproductive characters, additively, dominance and one or more of the epistatic effects determined the expression. Considering the pod yield per plant, the cross SBXI × Phule unnati was judged as the best cross for further selection programme.

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