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Research Article

Genetic study for yield and yield components in crosses between trypsin inhibitor free and expressing soybean [*Glycine max* (L.) Merrill.] genotypes

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Abstract
In the present investigation, gene action was investigated for six yield contributing traits in Soybean. Six crosses were made between three Kunitz trypsin inhibitor expressing and two Kunitz trypsin inhibitor-free soybean parents during summer 2017. Dominant gene action was found predominant in the inheritance of yield and yield contributing characters like yield per plant and 100 seed weight in cross P. Sangam × NRC 101 and P. Sangam × NRC 102. Both additive and dominance gene effects were significantly involved in the expression of yield per plant in crosses P. Kimya × NRC 101 and P. Kimya × NRC 102 with duplicate epitasis. Biparental mating design is suggested to improve these characters. Complementary epistasis was observed in cross P. Agrani × NRC 101 for days to 50% flowering, plant height and yield per plant and in cross P. Kimya × NRC 101 for plant height, 100 seed weight and pods per plant thereby suggesting that, the selection can be practiced in F_3 generation onwards for the improvement of these characters. Trypsin inhibitor-free genotype showed additive gene action.

Key words
Trypsin inhibitor-free, Soybean Gene action, Selection. Dominance, epistasis, Additive gene effects,

INTRODUCTION

Soybean [*Glycine max* (L.) Merrill.]. is considered as "golden bean" due to its dual qualities *viz*; high protein (40%) and oil (18 to 20%) content, and Oil comprising 85 % poly-unsaturated fatty acids (linoleic and linolenic acid) (Balsubramaniyan and Palaniappan 2003). The estimates of world soybean area, production and productivity for 2017-18 are 126.6 million ha, 346.31 million tons and 2.74 t/ha, against the 2016-17 figures of 121.10 million ha, 348.85 million tons and 2.88 t/ha (Anonymous, 2017a). The world largest soybean producers are USA (31.9 %), Brazil (31.8 %), Argentina (17.6 %) China (3.8 %) and India (3.6 %) (Anonymous, 2017b). In India, three states Madhya Pradesh (5.72 m ha), Maharashtra (3.94 m ha) and Rajasthan (0.94 m ha) together contribute for about 92% of area and production of soybean (Anonymous, 2017c).

The classical breeding systems assume that, making use of additive genetic variance will be effective breeding procedures for improving the seed yield. To exploit the existing genetic variability present in the breeding material for seed yield as efficiently as possible, the breeder needs the basic information regarding the inheritance of grain yield and its closely related component traits for devising an efficient selection program. For genetic improvements of the crop, the breeding method to be adopted depends mainly on the nature of gene action involved in governing the expression of quantitative traits. The presence or absence of epistasis can be detected by the analysis of generation means using the scaling test, which measures epistasis accurately, whether it is complimentary or duplicate at the digenic level.

MATERIAL AND METHODS

The present study was conducted at Post Graduate Institute Research Farm-Botany Section; M.P.K.V., Rahuri, during the period from 2016-17 to 2018- 2019. The parents *viz* P. Agrani, P. Sangam and P. Kimya (Trypsin inhibitor expressing) and NRC 101 and NRC 102 (trypsin inhibitor-free) were used for effecting six crosses obtained *viz*. P. Agrani × NRC 101 (Cross I), P. Agrani × NRC 102 (Cross II), P. Sangam × NRC 101 (Cross III), P. Sangam

× NRC 102 (Cross IV), P. Kimya × NRC 101 (Cross V) and P. Kimya × NRC 102 (Cross VI) during in Summer 2017 and *Kharif* 2017 to produce the F_1 Seeds. In early *Kharif* 2017, F_{1s} were sown and F_2 seeds were obtained which were sown in summer 2018 to get F_3 seeds. The experiment was laid out in Randomized Block Design (RBD) with three replications at PGI Research farm, M.P.K.V., Rahuri, during *Kharif* 2018. Sowing was done in rows of 1.5 m. and 30 cm apart at 10 cm distances in a row (medium soil). One row was assigned to P_1s, P_2s, F_1s, while two rows to each of the F_2 and F_3. This permitted for raising of 15 plants in each P_1, P_2, F_1, 30 plants in each of the F_2 and F_3, with three replications in each cross. The fertilizer dose of 50 kg N and 75 Kg P_2O_5/ha for was applied at the time of sowing. Regular operations like thinning, weeding, irrigation and plant protection were carried out regularly as per need and stage of crop growth. The observations were recorded on the quantitative characters on random 5 plants from Parents and F_1s; 20 plants from each F_2 and F_3 generations of all the six crosses for each replication. The C and D scaling test of Mather (1949) was carried out to have an idea regarding the presence or absence of non-allelic interactions. Further analysis of data was performed according to the method of the "joint scaling test" given by Cavalli (1952). Jinks and Jones (1958) three parameter model and Hayman's (1958) five parameter model were used. For the computation of gene effects for grain yield and yield attributing character with five generations.

RESULT AND DISCUSSION

The results obtained in the present investigation for, individual and joint scaling test are presented in **Table 1.** The test revealed significant gene interaction for 30 out of 36 cross traits combination except *viz.* days to maturity (Cross-P. Agrani × NRC 102 and P. Kimya × NRC 101); pods per plants (Cross-P. Sangam × NRC 101 and P. Sangam × NRC 102) and the seed yield per plant (Cross-P. Agrani × NRC 101 and Cross-P. Sangam × NRC 102), which indicated the only presence of simple additive and dominance model. The results of gene effects are presented in **table 2**.

Table 1. Estimates of individual and joint scaling test (. $\div^2$) for detecting non allelic interaction for yield and yield contributing characters in soybean.

Sr. No.	Characters	Cross name: Phule Agrani × NRC 101			Phule Agrani × NRC 102			Phule Sangam × NRC 101 C-			Phule Sangam × NRC 102			Phule Kimya × NRC 101			Phule Kimya × NRC 102						
		C-I			C-II			C-III			C-IV			C-V			C-VI						
		C	D	X^2	C	D	X^2	C	D	X^2	C	D	X^2	C	D	X^2	C	D	X^2	C	D	X^2
01	DF	23.00**	-1.70^{NS}	90.48**	-2.80^{NS}	0.50^{NS}	1.35^{ns}	2.33^{NS}	13.03**	838.96**	0.00^{NS}**	8.50**	54.99**	-1.93^{NS}	-2.73^{NS}	3.60^{ns}	7.06**	-6.63**	16.59**
02	DM	23.20**	-14.00**	39.17**	5.66^{ns}	-28.06**	212.43**	-23.46**	-21.46**	36.01**	-28.33**	16.20**	67.97**	-4.46^{ns}	-9.06*	13.32**	-0.66^{ns}	-13.93**	234.24**
03	PH (cm)	18.93**	1.70^{ns}	22.06**	-26.93**	38.90**	43.06**	-32.00**	-11.23**	165.89**	-24.66**	-2.00^{ns}	58.14**	7.66*	-34.63**	39.51**	-19.26**	-36.86**	869.31**
04	100 SWT (g)	-1.81^{ns}	6.13**	33.99**	-4.98**	5.22**	25.46**	-5.68**	-9.71**	237.94**	-3.17*	-12.10**	133.59*	-5.93**	-4.85**	65.80**	2.86*	4.82**	24.84**
05	PPP	-26.60**	-9.06**	489.06*	-13.20**	-12.20**	192.18**	8.00^{ns}	-7.03^{ns}	2.48^{ns}	10.67ns	-8.90 ns	1.49^{ns}	-36.46*	79.36**	18.72**	9.93**	2.33^{ns}	38.16**
06	SYP (g)	-3.66**	-3.22**	47.05**	4.00^{ns}	-2.55^{ns}	1.67^{ns}	-1.20^{ns}	-15.11**	67.26**	2.26^{ns}	-3.30^{ns}	1.87^{ns}	-1.19^{ns}	-9.39**	12.89**	2.43^{ns}	-10.002**	93.93**

*, ** Significant at P = 0.05 and 0.01 per cent levels, respectively.
C= Dominance D= Additive
DF = days to flowering
DM = days to maturity
100SW= 100 seed weight
PPP= pods per plant
SYP= seed yield per plant

Additive gene effect and additive × additive (i) epistasis were positively significant for days to fifty percent flowering in all the crosses (except cross-II and Cross-V) indicating that the expression of this character was under the influence of an additive gene action but for lateness. The additive effects could facilitate fixation of the combination of genes and therefore, selection for days to 50 % flowering in these crosses would give a better response. The result isconfirmed with earlier reports of Thakare *et al.,* (2017); Rahangdale and Raut, (2002); Syad *et al.*, (2005) and Bhor *et al.,* (2014). In Cross P. Kimya × NRC 102, an additive gene effect (d) was equally important as non-additive (h) with duplicate epistasis; therefore, for the efficient utilization of fixable and nonfixable components of genetic variation, reciprocal recurrent selection or biparental mating was suggested for this cross. A similar finding was also reported by Halvankar and Patil (1993) Bhor *et al.* (2014) and Thakare *et al.* (2017).The positively significant additive × additive non-allelic interaction with duplicate epistasis for days to 50 % flowering was observed in three crosses *i.e* P. Sangam × NRC 101, P. Sangam × NRC 102 and P. Kimya × NRC 102 which suggested the possibilities of obtaining transgressive segregants in later generations. Similar results also reported by Bhor *et al.,* (2014) and Thakare *et al.*, (2017).

Table 2. Estimation of gene effect in six crosses for the quantitative traits in soybean.

Sr. No.	Crosses	Genetic parameters					Type of gene action
		m	d	h	i	l	
				Days to 50% flowering			
C-I	PHULE AGRANI × NRC 101	34.51**	5.60**	-2.30^{ns}	16.16*	-32.93**	Complementary
C-II	PHULE AGRANI × NRC 102	32.91**	5.56**	1.83^{ns}	-	-	Absence of inter allelic interaction
C-III	PHULE SANGAM × NRC 101	36.15**	9.66**	-9.43**	11.03**	14.26*	Duplicate
C-IV	PHULE SANGAM × NRC 102	38.15**	8.50**	-3.96*	11.33**	11.33*	Duplicate
C-V	PHULE KIMYA × NRC 101	35.16**	7.50**	5.00*	-	-	Absence of inter allelic interaction
C-VI	PHULE KIMYA x NRC 102	35.48**	7.96**	6.03**	21.53**	-18.26**	Duplicate
				Days to Maturity			
C-I	PHULE AGRANI × NRC 101	93.70**	10.40**	6.20**	34.00**	-49.60**	Duplicate
C-II	PHULE AGRANI × NRC 102	91.23**	8.83**	12.02**	37.32**	-44.97 **	Duplicate
C-III	PHULE SANGAM ×NRC 101	94.83**	15.40**	-15.62**	12.57**	59.91**	Duplicate
C-IV	PHULE SANGAM × NRC 102	93.36**	14.10**	-12.42**	12.67**	59.67**	Duplicate
C-V	PHULE KIMYA × NRC 101	92.90**	12.63**	1.00ns	30.56**	-6.13ns	Duplicate
C-VI	PHULE KIMYA × NRC 102	93.96**	12.00**	2.91*	33.17**	-17.68**	Duplicate
				Plant height			
C-I	PHULE AGRANI × NRC 101	53.51**	10.10**	-4.21^{ns}	22.22^{ns}	-22.97*	Complementary
C-II	PHULE AGRANI × NRC 102	49.61**	9.90**	-21.12**	-10.62*	87.77**	Duplicate
C-III	PHULE SANGAM × NRC 101	51.45**	14.90**	7.25**	31.95**	27.68**	Complementary
C-IV	PHULE SANGAM × NRC 102	52.73**	12.93**	3.15 ^{ns}	23.08**	30.22**	Complementary
C-V	PHULE KIMYA × NRC 101	52.98**	11.33**	19.83**	-47.03**	56.40**	Complementary
C-VI	PHULE KIMYA ×NRC 102	51.90	11.50**	28.86**	44.36**	-23.46**	Duplicate
				100 seed weight			
C-I	PHULE AGRANI × NRC 101	13.64**	-0.79**	-1.52ns	-5.99**	10.60**	Duplicate
C-II	PHULE AGRANI × NRC 102	12.26**	-1.56**	-3.34**	-7.44**	13.61**	Duplicate
C-III	PHULE SANGAM × NRC 101	13.66**	-0.03^{ns}	6.67**	5.47**	-5.48 ^{ns}	Duplicate
C-IV	PHULE SANGAM × NRC 102	15.36**	1.55**	8.09**	10.65**	-11.90^{ns}	Duplicate
C-V	PHULE KIMYA × NRC 101	13.26**	0.46**	1.74ns	3.17**	1.44^{ns}	Complementry
C-VI	PHULE KIMYA × NRC 102	13.46**	1.50**	-3.17**	0.26^{ns}	2.60^{ns}	Duplicate
				Pods per plant			
C-I	PHULE AGRANI × NRC 101	112.10**	4.96**	6.55ns	7.32^{ns}	-77.51^{ns}	Duplicate
C-II	PHULE AGRANI × NRC 102	84.06**	5.13**	6.84**	16.64**	0.44ns	Complementary
C-III	PHULE SANGAM × NRC 101	103.88**	9.70**	26.65**	-	-	Absence of inter allelic interaction
C-IV	PHULE SANGAM × NRC 102	102.38**	12.46**	6.41^{ns}	-	-	Absence of inter allelic interaction
C-V	PHULE KIMYA × NRC 101	82.71**	5.00**	-49.32**	-48.98**	-154.44**	Complementary
C-VI	PHULE KIMYA × NRC 102	108.16**	3.70**	-52.82**	-53.12**	56.97**	Duplicate
				Seed yield per plant (g)			
C-I	PHULE AGRANI × NRC 101	84.76**	4.96**	10.77**	11.54**	23.37**	Complementry
C-II	PHULE AGRANI × NRC 102	16.58**	-1.16**	-11.28**	-	-	Absence of inter allelic interaction
C-III	PHULE SANGAM × NRC 101	19.20**	-0.05ns	13.85**	9.77**	-18.54**	Duplicate
C-IV	PHULE SANGAM × NRC 102	20.05**	0.08ns	6.61**	-	-	Absence of inter allelic interaction
C-V	PHULE KIMYA × NRC 101	94.63**	3.70**	7.80**	7.50**	-10.13ns	Duplicate
C-VI	PHULE KIMYA × NRC 102	16.53**	0.55**	9.02**	8.17**	-16.57**	Duplicate

*, ** Significant at P = 0.05 and 0.01 per cent levels, respectively.
m= mean effect
d= additive effect
h= dominance effect
i= additive × additive effect
l= dominance × dominance effect

Additive gene effect and additive × additive epistasis was (i) positively significant in all the crosses for days to maturity indicating that, the expression of character was under the influence of additive gene action but for lateness. The additive effects could facilitate fixation of the combination of genes and therefore, the selection for days to maturity in this crosses would give a better response. Similar finding was also reported by Bhor *et al.,* (2014); Thakare *et al*., (2017); Syad *et al*., (2005). The significant additive × additive (i) non-allelic interaction with duplicate epistasis was observed in all the crosses for days to maturity which suggests the possibilities of obtaining transgressive segregants in later generations which was also reported by Bhor *et al,.* (2014); Thakare *et al.,* (2017); Sharma and Phul, (1994).For plant height, bBoth additive (d) and non-

additive (h) gene effects were positively significant in the crosses *i.e* P. Sangam × NRC 101, P. Kimya × NRC 101 and P. Kimya × NRC 102. The similar result were also reported by Bhor *et al*., (2014); Thakre *et al*., (2017); Shinde (2010). Among the interaction components, estimates of additive × additive (i) components was positively significant in two crosses i.e. P. Sangam × NRC 101, P. Sangam × NRC 102 with complementary epistasis. In the cross, P. Kimya × NRC 102 positively significant duplicate epistasis was observed. These results are in agreement with earlier reports of Bhor *et al*., (2014); Thakare *et al.,* (2017) and Maloo and Nair, (2005). Additive gene effect was observed for the trait 100 seed weight in crosses P. Sangam × NRC 102 and P. Kimya × NRC 101 and P. Kimya × NRC 102. Similar results were also reported by Bhor *et al*. (2014) ; Thakare *et al.,* (2017); Agrawal *et al*., (1999)

Additive × additive (i) interaction was positively significant in the crosses P. Sangam × NRC 101, P. Sangam × NRC 102 and P. Kimya × NRC 101. The result are in conformity with earlier reports of Thakare *et al.,* 2017; (1988); Sharma and Phul, (1994) and Bhor *et al.,* (2014).

Duplicate epistasis was observed in crosses P. Agrani × NRC 101, P. Agrani × NRC 102, P. Sangam × NRC 101, P. Sangam × NRC 102 and P. Kimya × NRC 102. Similar findings were also reported by Bhor *et al.,* (2014); Thakare *et al.,* (2017); Datt *et al*., (2011). Biparental mating is suggested for duplicate epistasis to improve the traits. Complimentary epistasis was observed for crosses P. Kimya × NRC 101 which suggests that improvement in the character of seed weight is possible by selection in F_3 generation onwards such that the desired recombinants become available in the populations as reported by Sharma and Phul, (1994).

The additive gene effect was positively significant observed for the pods per plant in all the crosses. Similar results were also reported by Bhor *et al*., (2014); Harer and Deshmukh, (1991); Halvankar and Patil (1993) ; Mehetre, *et al.,* (1998); Agrawal *et al*., (1999)Dominance (h) gene effect was positively significant in two crosses P. Agrani × NRC 102 and P. Sangam × NRC 101. These results are in agreement with earlier reports of Sayad *et al*., (2005); Mallo and Nair, (2005) Bhor *et al.,* (2014) ; Thakre *et al.,* (2017).

The additive and dominance gene effects were positively significant in crosses, P. Sangam × NRC 101 and P. Agarani × NRC 102. Among inter-allelic interactions, positively significant additive × additive component was observed in the cross P. Agrani × NRC 102 and dominance × dominance in cross P. Kimya × NRC 102. A similar result was also reported by Datt *et al*., (2011) Bhor *et al* .,(2014); Thakre *et al.,* (2017). The positively significant values of additive gene effect (d) were higher as compared to non-additive and this helps for the selection of the traits. For seed yield per plant the presence of significant dominance component (h) with the absence of non–allelic interactions in cross P. Sangam × NRC 102 revealed that yield of soybean was predominantly under non-additive genetic control as reported by Bhor *et al*.,(2014). The presence of duplicate epistasis in cross P. Sangam × NRC 101, cross-P. Kimya × NRC 101 and cross P. Kimya × NRC 102 for the yield trait can hinder progress and make it difficult to fix genotypes at a high level of manifestation. Duplicate epistasis may restrict the expression of a yield trait in early generations would not be effective for want of fixable components of variation. Such gene effects can however, be exploited by intermating the selected segregants and delaying the selections to the advanced generations. The results are confirmed with earlier reports of Rahangdale and Raout (2002); Datt *et al.,* (2011) Bhor *et al*., (2014).

Significant additive × additive gene effects for controlling this trait was observed in cross-P. Agrani × NRC 101, Cross-P. Sangam × NRC 101 Cross-P. Kimya × NRC 101 and Cross-P. Kimya × NRC 102. Bhor *et al.,* (2014) are also reported similar gene effects for yield traits. Duplicate epistasis was observed in Cross-P. Sangam × NRC 101 Cross-P. Kimya × NRC 101, and Cross-P. Kimya × NRC 102; hence, the simple selection procedure in the early segregating generations may not contribute significantly for the improvement of the traits governed by duplicate epistasis and dominance components could be successfully exploited in the later generations. It is, therefore, suggested that the selections for the improvement of all these traits, particularly seed yield should be delayed to the later generations of segregating populations in soybean.

It can be concluded that predominant additive gene effects in desirable direction were observed Cross P. Sangam × NRC 102 , Cross P. Kimya × NRC 101 and P. Kimya × NRC 102 for traits pods per plant. In cross P. Kimya × NRC 102 predominance of additive gene effects was observed for the trait 100 seed weight. In crosses P. Sangam × NRC 101, P. Kimya × NRC 101 and P. Kimya × NRC 102 predominance of additive × additive effect was higher as compared to dominance × dominance gene interaction for seed yield traits suggesting that the selections can be effectively applied for improvement of these traits.

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