



GENETIC ANALYSIS OF YIELD AND ITS COMPONENTS IN SOYBEAN [*Glycine max* (L.) Merrill]

A.T. ADSUL^{1*}, V.P. CHIMOTE², M.P. DESHMUKH³ and D.S. THAKARE¹

¹ Department of Genetics and Plant Breeding, Mahatma Phule Krishi Vidyapeeth (M.P.K.V.), Rahuri-413 722 India

² State Level Biotechnology Centre, M.P.K.V., Rahuri, Ahmednagar India

³ Agricultural Research Station, Kasbe Digraj, Sangli, India

*Corresponding author's email: amitadsul444@gmail.com

Co-authors' email addresses: vpchimote@gmail.com, drmpdeshmukh@gmail.com, dilipthakare55@gmail.com

SUMMARY

For improvement of yield, gene action studies are of immense use as they help in deciding suitable breeding strategy. For the present investigation four soybean genotypes were selected for effecting four crosses. Out of them two (DS-228 and MAUS-71) are well adopted, notified high yielding varieties, with low seed longevity and two genotypes (Birsa Soya-1 and Kalitur) with low yield but have high seed longevity. Additive gene action was found predominant in inheritance of yield and yield contributing characters viz., number of primary branches per plant, number of clusters per plant, number of pods per cluster, 100 seed weight and yield per plant. Both additive and non-additive gene effects were significantly involved in the expression of nine quantitative traits with duplicate epistasis. Duplicate epistasis was significantly importance in inheritance of most traits studies. Biparental mating design should be used to improve these characters

Key words: Additive, non-additive gene effects, biparental mating design, duplicate epistasis

Key findings: The gene action in four crosses was mostly additive and additive x additive contributed with greater magnitude towards yield and yield contributing characters. These characters can be improved by biparental mating design.

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INTRODUCTION

Soybean [*Glycine max* (L.) Merrill] is an important legume crop belongs to family Leguminosae, subfamily Papilionaceae, genus *Glycine*. It has been domesticated from *Glycine soja* Sieb & Zucc in northeast China where first written record dated back to 2328 B.C. (Hymowitz and Newell, 1980; Shimamoto, 2001; Smith and Huyser, 1987). It has been cultivated at broadly diverse geographical locations and under many different growing conditions, particularly in the America and Asia.

The importance of soybean in India has been recognized as indicated by the

increased area under soybean to the tune of 6.25 million hectares which comes to 12% of world's soybean area. However, the average productivity of soybean in India is 1392 kg/ha. As per survey conducted by SOPA, the estimated soybean production in India for 2014 was 10.44 million tons. The average productivity of soybean in USA and Brazil is 2620 kg/ha and 2290 kg/ha, respectively, (Anonymous, 1997). Thus there is a great potential for improving soybean productivity in India. In Maharashtra state the area under soybean cultivation during 2014 was 3.8 million hectares with the yield being 808 kg per hectare. This is mainly due to occurrence of low germination and uneven distribution of

monsoon rains besides lack high yielding varieties.

Soybean has become a miracle crop of the twentieth century and is often designated as a 'golden bean' (Sonawane, 2006). Soybean proteins have high nutritional quality and good functionality for foods. Soybean is also the lowest-cost producer of vegetable oil. Soybean seed contains approximately 37-41% protein, 18-21% oil, 30-40% carbohydrate, and 4-5% ash (Hulse, 1996). It's one of the world's leading sources of vegetable oil and plant protein, both of which are very well adapted to the nourishment of human beings. The increase in soybean production and uses as human food has been very rapid during the last few decades compared with that of many other major crops, and continuous growth is considered very important for stabilizing the world food supply. Its capacity for protein and oil production makes it a significant contributor to human nutrition, and its characteristic symbiosis with root bacteroids makes it a very important crop in research.

The information regarding gene action involving in control of inheritance for yield and yield contributing characters through generation mean analysis is immense use to plant breeder to decide suitable breeding strategy for improvement of quantitative characters. Seed yield is an important trait as it measures the economic productivity of the crop, but its inheritance is extremely complex. The classical breeding systems that make use of additive genetic variance will be effective breeding procedures for improving the seed yield. To exploit the existing genetic variability present in breeding material for seed yield as efficiently as possible the breeder would need the basic information regarding the inheritance of grain yield and its closely related components for devising an efficient selection programme (Bhor *et al.*, 2014). Keeping this in view, this study was undertaken to identify gene action for yield contributing traits in crosses between parents differing for seed longevity and yield.

MATERIALS AND METHODS

This investigation was conducted at Post Graduate Institute Research Farm, Botany Farm, MPKV, Rahuri during the period from 2013-2014. Four crosses viz., DS-228 (Phule

Kalyani) x Kalitur, DS-228 (Phule Kalyani) × Birsa soya-1, MAUS-71 (Samrudhi) × Birsa soya-1 and MAUS-71 (Samrudhi) × Kalitur. Crosses were affected in *kharif* 2013 and early summer 2013 to produce the F₁ seeds. In early summer 2013 F₁s seeds sown and F₂s seeds were made. Backcrosses BC₁F₁s and BC₂F₁s of four crosses were also made in early summer 2013 within the stipulated period. The seeds of four genetically diverse genotypes were obtained from the Soybean Breeder, Agricultural Research Station, Kasbe Digraj, Dist. Sangli. On the basis of low and high seed longevity of soybean four soybean genotypes were selected for present investigation. Out of four genotypes two (DS-228 and MAUS-71) were well adopted, notified better yielding varieties, with low seed longevity and two genotypes (Birsa Soya-1 and Kalitur) with low yield but have high seed longevity.

The experiment was laid out in randomized complete block design (RCBD) with three replications in *kharif* 2014. The experimental material consisted of 24 treatments consisting of 6 parents, 4F₁s, 4F₂s, 4BC₁F₁s, 4BC₂F₁s, of four crosses [DS-228 (Phule Kalyani) × Kalitur, DS-228 (Phule Kalyani) × Birsa soya-1, MAUS-71 (Samrudhi) × Birsa soya-1 and MAUS-71 (Samrudhi) × Kalitur]. The parents, F₁s, F₂s, and back crosses were randomized separately in each of the three replications. Sowing was done in rows of 5m length and 45 cm apart accommodating 50 plants at 10 cm distance in a row. One row was assigned to P₁s, P₂s, F₁s, B₁s and B₂s and six rows to F₂s. This has permitted for raising of 50 plants in each of P₁s, P₂s, F₁s, BC₁F₁s and BC₂F₁s and 300 plants in each of the F₂s, in each of the three replications for each cross. Fertilizer dose of 50 kg N and 75 Kg P₂O₅/ha for irrigated situation was applied at the time of sowing. The experiment was sown on 5th of July 2014. All inter-culturing operations were carried out regularly as per need and stage of crop growth.

The observations were recorded on the nine quantitative characters on five random plants from parents and F₁s; 10 plants from backcrosses and 20 plants from F₂s generations of all the three crosses for each replication. Data were first tested for non-allelic interaction by Individual scaling test- A, B, C and D given by Mather (1949). Further analysis of data was performed according to the method of "Joint scaling test" given by

Cavalli (1952). For computation of gene effects for grain yield and its components with six basic generations, Hayman's (1958) six parameter models were used. Statistical analysis of data was done on a personal computer using software packages including MS EXCEL, SAS and INDOSTAT for different purposes.

RESULTS AND DISCUSSION

The results obtained in the present investigation for individual and joint scaling

test are presented in Table 1 and Table 2 respectively. All nine quantitative characters for four crosses contributed significantly in individual and joint scaling tests. These nine quantitative characters for all four crosses indicated presence of epistasis. The results of gene effects are presented in Table 3 and 6 and are discussed as below. Individual scaling test i.e. A, B, C and D of Mather (1949) and Joint scaling test of Cavalli, (1952) were used to detect presence of epistasis by using the data of various generations in all four crosses. The results of this study can help in devising proper breeding strategies as per trait desired.

Table 1. Estimation of individual scaling test for detecting non-allelic interactions for yield contributing traits in soybean.

Traits	Scaling tests	DS-228 x	DS-228 x	MAUS-71 x	MAUS-71 x
		Kalitur	Birsa soya-1	Birsa soya-1	Kalitur
Days to flowering	A	-1.210**	-1.515**	-3.650**	-2.403*
	B	0.221	-0.708	-2.224**	-0.189
	C	-1.544	1.625	-6.750**	0.345
	D	-0.278	1.924**	-0.438	1.469**
Days to maturity	A	7.481**	9.805**	3.691**	-1.917**
	B	1.029	-4.195**	-1.750	4.135**
	C	8.498**	-5.708**	-1.722	-1.896*
	D	-0.006	-5.659**	-1.831*	-2.057**
Plant height (cm)	A	-38.733**	-7.637**	9.400**	-25.000**
	B	14.133**	2.589	19.769**	19.867**
	C	-12.000*	-1.876	-12.460**	-30.956**
	D	6.300*	1.586	-20.815**	-12.911**
Number of primary branches/Plant	A	-1.791**	-1.670**	-2.214**	-1.149**
	B	-1.969**	0.347	-2.395**	-0.923*
	C	-0.610	-1.193	-4.272**	-2.863**
	D	1.575**	0.065	0.168	-0.395
Number of clusters/Plant	A	-10.777**	-9.073**	-7.981**	-8.293**
	B	-7.149**	-0.725	-6.241**	-5.968
	C	43.602**	-2.847	-24.192**	6.171
	D	30.764**	3.476	-4.985*	10.216*
Number of pods/Cluster	A	1.425**	-1.983**	-2.255**	1.369**
	B	0.265	-1.863**	-1.703**	-0.143
	C	1.269	-1.767**	-1.825**	1.257**
	D	-0.211	1.040**	1.066**	0.015
Number of pods/plant	A	-24.483**	20.772*	-13.127**	-9.301**
	B	-9.837**	23.161**	24.773**	-21.300**
	C	-6.898**	50.878**	-1.993	-5.985
	D	13.711**	3.473	-6.819	12.308**
100 seed weight (g)	A	2.039**	-2.414**	-1.189**	2.267**
	B	-1.649**	-2.374**	-1.381**	-0.877**
	C	3.354**	-5.033**	1.839**	-2.156**
	D	1.482**	-0.123	2.204**	-1.773**
Yield/plant (g)	A	22.795**	-7.699**	-10.519**	-7.950*
	B	11.893**	11.145**	-14.811**	-12.810**
	C	3.790	-6.382	-22.158**	-6.809
	D	-15.449**	-4.914*	1.586	6.976*

*, ** Significant at 5% and 1% level of significance, respectively.

Table 2. Estimation X2 for joint scaling test for yield contributing traits for four crosses in soybean.

Traits	DS-228 x Kalitur	DS-228 x Birsa soya-1	MAUS-71 x Birsa soya-1	MAUS-71 x Kalitur
Days to flowering	11.24*	18.35**	61.46**	25.83**
Days to maturity	82.47**	87.93**	27.24**	49.24**
Plant height (cm)	977.38**	37.27**	241.56**	62.37**
Number of primary branches/plant	38.52**	21.95**	37.68**	17.65**
Number of clusters/plant	521.29**	42.81**	34.89**	9.65*
Number of pods/cluster	17.89**	301.88**	180.29**	64.63**
Number of pods/plant	270.79**	19.65**	67.00**	168.50**
100 seed weight (g)	62.51**	50.73**	137.78**	336.56**
Yield/plant (g)	47.35**	30.43**	15.41**	23.98**

*,** Significant at 5% and 1% level of significance, respectively.

Table 3. Estimation of gene action for various characters in cross-I [DS-228 (Phule Kalyani) x Kalitur].

Traits	m	d	h	I	J	L	Types of Epistasis
Days to flowering	35.51** (0.20)	-1.03** (0.24)	0.89 (1.00)	0.55 (0.96)	-0.71* (0.28)	0.43 (1.39)	—
Days to maturity	103.59** (0.25)	4.01** (0.60)	-1.25 (1.61)	0.01 (1.58)	3.22** (0.63)	-8.52** (2.68)	—
Plant height (cm)	59.86** (1.47)	-53.56** (1.28)	1.26 (6.52)	-12.60 (6.43)	-26.43** (1.55)	37.20** (8.09)	—
Number of primary branches/plant	5.15** (0.15)	-0.41* (0.18)	-2.33** (0.77)	-3.15** (0.72)	0.08 (0.23)	6.91** (1.13)	Duplicate
Number of clusters/plant	47.02** (0.65)	-9.81** (0.48)	-60.75** (3.47)	-61.52** (2.79)	-1.81 (1.17)	79.45** (5.25)	Duplicate
Number of pods/ Cluster	3.01** (0.14)	1.13** (0.15)	-0.29 (0.67)	0.42 (0.65)	0.58** (0.19)	-2.11* (0.91)	—
Number of pods/ Plant	108.02** (0.49)	-14.70** (1.16)	-17.07** (3.10)	-27.42** (3.05)	-7.32** (1.20)	61.74** (5.17)	Duplicate
100 seed weight (g)	15.27** (0.10)	3.85** (0.19)	-2.20** (0.62)	-2.96** (0.55)	1.84** (0.31)	2.57* (1.03)	Duplicate
Yield/Plant (g)	37.20** (1.48)	13.53** (1.72)	27.89** (7.23)	30.89** (6.86)	5.45** (2.39)	-65.58** (10.17)	Duplicate

Table 4. Estimation of gene action for various characters in cross-II [DS-228 x Birsa soya-1].

Traits	m	d	h	I	J	L	Types of Epistasis
Days to flowering	37.06** (0.20)	-1.45** (0.27)	-3.56** (1.03)	-3.84** (1.00)	-0.40 (0.33)	6.07** (1.48)	Duplicate
Days to maturity	102.62** (0.22)	3.08** (0.75)	9.57** (1.86)	11.31** (1.75)	7.00** (0.83)	-16.92** (3.38)	Duplicate
Plant height (cm)	33.27** (0.25)	-6.24** (0.98)	-0.21 (2.35)	-3.17 (2.21)	-5.11** (1.14)	8.22 (4.35)	—
Number of primary branches/plant	4.95** (0.15)	-0.88** (0.20)	-0.63 (0.78)	-0.13 (0.73)	-1.00** (0.27)	1.45 (1.15)	—
Number of clusters/plant	34.00** (1.05)	-9.24** (0.80)	-5.63 (4.74)	-6.95 (4.53)	-4.17** (1.55)	16.74** (6.03)	—
Number of pods/cluster	3.69** (0.06)	0.02 (0.07)	-1.49** (0.30)	-2.08** (0.29)	-0.06 (0.10)	5.92** (0.42)	Duplicate
Number of pods/plant	141.42** (2.83)	-24.49** (5.05)	-34.32* (15.78)	-6.94 (15.17)	-1.19 (5.07)	-36.98 (24.72)	—
100 seed weight (g)	15.88** (0.14)	-0.67** (0.15)	-0.49 (0.71)	0.24 (0.64)	-0.02 (0.27)	4.45** (1.06)	—
Yield/Plant (g)	36.50** (1.05)	-10.64** (1.22)	5.24 (5.13)	9.82* (4.86)	-9.42** (1.77)	-13.27 (7.23)	—

*,** Significant at 5% & 1% level of significance, respectively. Figure in parentheses indicates standard error.

Table 5. Estimation of gene action for various characters in cross-III [MAUS-71 x Birsa soya-1]

Traits	m	d	h	I	J	l	Types of Epistasis
Days to flowering	35.06** (0.19)	-1.71** (0.29)	0.92 (1.05)	0.87 (0.99)	-0.71** (0.34)	4.99** (1.59)	–
Days to maturity	102.75** (0.21)	-1.31 (0.73)	0.62 (1.73)	3.66* (1.69)	2.72** (0.81)	-5.60 (3.15)	–
Plant height (cm)	29.55** (0.74)	-5.25** (0.74)	34.15** (3.61)	41.63** (3.32)	-5.18** (1.00)	-70.79** (5.07)	Duplicate
Number of primary branches/plant	5.08** (0.17)	0.53* (0.20)	0.12 (0.86)	-0.33 (0.79)	0.09 (0.27)	4.94** (1.25)	–
Number of clusters/plant	33.37** (0.99)	0.87 (0.96)	12.38** (4.57)	9.97* (4.41)	-0.87 (1.33)	4.25 (6.03)	–
Number of pods/Cluster	3.47** (0.14)	-0.27** (0.09)	-1.31* (0.60)	-2.13** (0.59)	-0.27* (0.12)	6.09** (0.71)	Duplicate
Number of pods/Plant	133.36** (3.53)	-28.15** (3.08)	16.59 (15.46)	13.63 (15.44)	-18.95** (3.13)	-25.28 (18.86)	–
100 seed weight (g)	17.38** (0.12)	-0.50** (0.15)	-3.73** (0.62)	-4.40** (0.59)	0.09 (0.21)	6.97** (0.89)	Duplicate
Yield/plant (g)	40.25** (1.42)	-4.30** (1.12)	-1.37 (6.84)	-3.17 (6.11)	2.14 (1.73)	28.50** (9.50)	–

Table 6. Estimation of gene action for various characters in cross-IV [MAUS-71 (Samrudhi) x Kalitpur]

Traits	m	d	h	I	J	L	Types of Epistasis
Days to flowering	36.51** (0.20)	-0.62* (0.25)	-1.85 (1.05)	-2.93** (0.97)	-1.10** (0.31)	5.53** (1.52)	–
Days to maturity	100.77** (0.19)	-3.08** (0.42)	5.26** (1.18)	4.11** (1.15)	-3.02** (0.45)	-6.33** (1.95)	Duplicate
Plant height (cm)	57.44** (2.34)	-46.40** (2.72)	30.52** (11.40)	25.82* (10.86)	-22.43** (3.45)	-20.68 (15.98)	–
Number of primary branches/plant	5.04** (0.13)	-0.34 (0.23)	0.33 (0.73)	0.79 (0.69)	-0.11 (0.27)	1.28 (1.16)	–
Number of clusters/plant	44.66** (2.29)	-4.43* (1.84)	-9.52 (10.19)	-20.43* (9.89)	-1.16 (2.28)	34.69** (12.75)	–
Number of pods/Cluster	3.14** (0.13)	1.19** (0.10)	-0.03 (0.51)	-0.03 (0.49)	0.75** (0.12)	-1.19 (0.65)	–
Number of pods/Plant	136.40** (0.28)	8.45** (0.81)	-15.52** (2.64)	-24.61** (1.98)	5.99** (1.55)	55.21** (4.90)	Duplicate
100 seed weight (g)	14.63** (0.18)	4.26** (0.10)	4.14** (0.77)	3.54** (0.76)	1.57** (0.11)	-4.93** (0.89)	Duplicate
Yield/plant (g)	37.77** (1.64)	8.15** (1.25)	-5.39 (7.44)	-13.95* (7.02)	2.43 (1.71)	34.71** (9.63)	–

*,** Significant at 5% & 1% level of significance, respectively. Figure in parentheses indicates standard error.

The different types of gene effects estimated provide a test for gene action and are useful for analyzing the genetic architecture of a crop so as to achieve future improvement in desirable traits. The presence or absence of epistasis detected by the analysis of generation means using the scaling test, measures epistasis accurately, whether it is complimentary or duplicate. Significant results regarding nature of gene action and gene effects involved in the inheritance of yield and its components obtained in this study are

discussed below in relation to relevant literature cited earlier. The character days to flowering were the one most affected by the environment and therefore the selection of genotypes for this trait is not reliable. The character days to flowering also showed significant genotypic and phenotypic correlation with days to maturity meaning that the selection of plants which delay for reaching the reproductive stage yield late-maturing plants. A similar result was observed by (Romanato, 2013) who evaluates the

phenotypic and genotypic correlations between nine agronomic traits in 27 soybean genotypes.

Flowering time

In DS-228 (Phule Kalyani) × Kalitur, cross combination the predominance of additive gene effect (negative significant and desirable direction) with complementary epistasis was observed for the trait days to flowering and hence it can be exploited effectively by selection for the improvement of the character. These findings are in agreement with earlier reports of (Agrawal *et al.*, 1999), Rahangdale and Raut (2002), (Sayad *et al.*, 2005) and (Datt *et al.*, 2011). In another cross DS-228 (Phule Kalyani) × Birsa Soya-1 the dominance gene effect (h) was significant and greater in magnitude than the additive gene effect (d) with duplicate epistasis, therefore, indicating a predominant role of dominance gene action in controlling these traits in soybean. These findings are in agreement with earlier reports of (Sharma *et al.*, 1993), Halvankar and Patil (1993), (Khattab, 1998), (Sayad *et al.*, 2005) and (Bhor *et al.*, 2014). Additive gene effect (d) with additive × dominance (j) and additive gene effect (d) with additive × additive (i) epistasis was negative significant in crosses MAUS-71 (Samrudhi) × Birsa Soya-1 and MAUS-71 (Samrudhi) × Kalitur respectively indicating that expression of this trait was under the influence of additive gene action but for lateness. The additive effects could facilitate fixation of the combination of genes and therefore, selection for days to flowering in these crosses would give better response. These results were confirms the earlier reports of (Ma *et al.*, 1987), (Mehetre *et al.*, 1998), (Agrawal *et al.*, 1999); Rahangdale and Raut (2002) and (Sayad *et al.*, 2005). The significant additive x additive non-allelic interaction with duplicate epistasis was observed in crosses DS-228 (Phule Kalyani) × Kalitur and MAUS-71 (Samrudhi) × Kalitur for days to flowering suggesting the possibilities of obtaining transgressive segregants in later generations. The results are agreement with earlier reports of (Talwar *et al.*, 1986 a), Ghassemi and Yazdi-Samadi (1987) and Sharma and Phul (1994).

Maturity

In cross combination of DS-228 (Phule Kalyani) × Kalitur the predominance additive gene effect (negative significant and desirable direction) with complementary epistasis was observed for days to maturity and hence it can be exploited effectively by selection for the improvement of this trait. These findings were agreement with earlier reports of (Zhang *et al.*, 1987), (Mehetre *et al.*, 1998), (Agrawal *et al.*, 1999), Rahangdale and Raut (2002), (Sayad *et al.*, 2005) and (Datt *et al.*, 2011). In DS-228 (Phule Kalyani) × Birsa Soya-1 cross, the additive genetic effect (d) was equally important as non-additive (h) with duplicate epistasis, therefore, for efficient utilization of fixable and non-fixable components of genetic variation, reciprocal recurrent selection or biparental mating can be used in this cross. These findings were agreement with earlier reports of Halvankar and Patil (1993), (Khattab, 1998), (Sayad *et al.*, 2005) and (Shinde, 2010) and (Bhor *et al.*, 2014). Additive genetic effect (d) with additive × additive (i) and Additive genetic effect (d) with additive × dominance epistasis was negative and significant in crosses MAUS-71 (Samrudhi) × Kalitur and MAUS-71 (Samrudhi) × Birsa Soya-1 indicating the expression of this 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, selection for days to maturity in these crosses would give better response. The results confirms the earlier reports of (Ma *et al.*, 1987), (Mehetre *et al.*, 1998), (Agrawal *et al.*, 1999); Rahangdale and Raut (2002) and (Sayad *et al.*, 2005). The significant additive x additive non-allelic interaction with duplicate epistasis was observed in crosses DS-228 (Phule Kalyani) × Birsa Soya-1 and MAUS-71 (Samrudhi) × Kalitur for physiological maturity suggesting the possibilities of obtaining transgressive segregants in later generations. These results are in agreement with earlier reports of (Talwar *et al.*, 1986 b), Ghassemi and Yazdi-Samadi (1987) and Sharma and Phul (1994).

Plant height

Both additive (d) and dominance (h) gene effects were significant in the crosses MAUS-

71 (Samrudhi) × Birsa Soya-1 and MAUS-71 (Samrudhi) × Kalitur. The results are agreement with earlier reports of Harer and Deshmukh (1991), Halvankar and Patil (1993) and (Khattab, 1998), (Shinde, 2010) and (Bhoret *et al.*, 2014). Additive gene effect was significant in negative direction for in the cross DS-228 (Phule Kalyani) × Kalitur and DS-228 (Phule Kalyani) × Birsa Soya-1 for plant height of revealed that selection for this trait would be useful to start from the early segregating generation. The above findings confirms earlier finding of (Jackovic *et al.*, 1988), (Kang, 1990), Triller and Toledo (1996), (Mehetre *et al.*, 1998), (Agrawal *et al.*, 1999), Rahangdale and Raut (2002) and (Shinde, 2010). Among interaction components, estimates of additive × additive (i) component were positively significant in crosses MAUS-71 (Samrudhi) × Birsa Soya-1 and MAUS-71 (Samrudhi) × Kalitur. The cross MAUS-71 (Samrudhi) × Birsa Soya-1 recorded significant duplicate epistasis. Similar results were earlier reported by (Hanson *et al.*, 1967), (Ma *et al.*, 1987), and Maloo and Nair (2005), whereas an additive and additive × additive gene effect for this character was reported by (Datt *et al.*, 2011). Non additive gene action was predominant for cross II which was also reported by Croissant and Torrie (1971), (Alam *et al.*, 1984), (Talwar *et al.*, 1986 a), Ghassemi and Yazdi-Samadi (1987), Sharma and Phul (1994), (Khattab, 1998) and (Bhoret *et al.*, 2015). Significant dominant and dominant × dominant gene interaction was reported for crosses DS-228 (Phule Kalyani) × Birsa Soya-1 and MAUS-71 (Samrudhi) × Birsa Soya-1 for plant height. Rahangdale and Raut (2002) reported similar results for this character. The dominance (h) and dominance × dominance (l) effects are in the opposite direction, suggesting that duplicate type epistasis and indicating predominantly dispersed alleles at the interacting loci.

Number of primary branches per plant

Additive and dominance gene actions were found to be predominant in controlling the inheritance of number of primary branches per plant in the cross of DS-228 (Phule Kalyani) × Kalitur. These findings are in agreement with Ghassemi and Yazdi-Samadi (1987), (Kang, 1990), Halvankar and Patil (1993), Sharma

and Phul (1994) and (Khattab, 1998). The effect of dominant gene action for the trait should be eliminated through bulk selection method through which homozygosity could be achieved prior to the initiation of selection for the character. The opposite sign of (h) and (l) indicated duplicate epistasis for cross DS-228 (Phule Kalyani) × Kalitur and absence of non-allelic interactions for cross MAUS-71 (Samrudhi) × Kalitur was observed. Duplicate type of epistasis, which would limit the range of variability and thus slow down the pace of progress through selection, therefore, heterosis breeding would be advantageous. The importance of dominant gene action with duplicate epistasis for this trait confirms the earlier findings of (Li-Zeng Lu *et al.*, 1995), Rahangdale and Raut (2002), (Shinde, 2010), (Datt *et al.*, 2011) and (Bhor *et al.*, 2014) for this trait. Talwar and Singh (1983), Harer and Deshmukh (1991) and (Khattab, 1998) observed both additive and non-additive gene effects for this trait.

Number of clusters per plant

An additive and dominance gene action with duplicate epistasis was in the inheritance of number of clusters per plant per plant in the cross of DS-228 (Phule Kalyani) × Kalitur. These findings are in agreement with Ghassemi and Yazdi-Samadi (1987), (Kang, 1990), Halvankar and Patil (1993), Sharma and Phul (1994) and (Khattab, 1998). The perusal of data indicated significant non additive (dominance and epistasis) gene actions in the inheritance of this trait in the cross MAUS-71 (Samrudhi) × Birsa Soya-1, which revealed that number of clusters per plant was predominantly under non-additive genetic control. The high magnitude of dominance effect suggested that selection of high yielding genotypes would be postponed till later generation when the dominant effect could be diminished. Similar results were reported by Rahangdale and Raut (2002), (Shinde, 2010) and (Datt *et al.*, 2011). In cross MAUS-71 (Samrudhi) × Birsa Soya-1 complementary epistasis observed which can help in selection in F₃ onwards for improvement of this trait. (Bhatade *et al.*, 1977), and Rahangdale and Raut (2002) reported additive gene action in inheritance of this trait. Both additive and dominance gene effects were significant in all crosses. (Singh *et al.*, 1974) observed both

additive and dominant gene action for this trait.

Number of pods per cluster

Significant additive and non-additive (dominance and epistasis) gene actions with complementary epistasis was observed for the inheritance of this trait in the cross MAUS-71 (Samrudhi) × Birsa Soya-1 which revealed that trait number of pods per clusters can be improved by selections in F₃ generations onwards. Similar results were reported by Lal and Fazlul Haque (1972). (Agrawal, 1999) and Rahangdale and Raut (2002) reported that additive gene action plays an important role in inheritance of this trait. Importance of duplicate epistasis in control of this character was reported by Rahangdale and Raut (2002). (Singh *et al.*, 1974) observed both additive and dominant gene action for this trait.

Number of pods per plant

Predominance of additive gene effect was found for the cross MAUS-71 (Samrudhi) × Birsa Soya-1. These results are in agreement with reports of Diaz and Velazquez (1985), Ghassemi and Yazdi-Samadi (1987), Halvankar (1988), Harer and Deshmukh (1991), Halvankar and Patil (1993), Sharma and Phul (1994), Khattab (1998), Sayad *et al.* (2005) and Maloo and Nair (2005). The additive and dominance gene effects were significant for crosses DS-228 (Phule Kalyani) × Kalitur, DS-228 (Phule Kalyani) × Birsa Soya-1 and MAUS-71 (Samrudhi) × Kalitur. Among inter-allelic interactions, negatively significant additive x additive component was observed for the crosses DS-228 (Phule Kalyani) × Kalitur and MAUS-71 (Samrudhi) × Kalitur. Duplicate epistasis was significant for crosses DS-228 (Phule Kalyani) × Kalitur and MAUS-71 (Samrudhi) × Kalitur. The predominance of additive gene action for this character was earlier reported by (Budak, 1986), (Ecochard, 1986), Malik and Singh (1987), (Rajput *et al.*, 1987), (Mehetre *et al.*, 1998) and (Agrawal *et al.*, 1999). Duplicate epistasis controlling this character was reported by (Li-Zeng Lu *et al.*, 1995), Rahangdale and Raut (2002) and (Datt *et al.*, 2011). Significant dominant x dominant interaction was reported by Maloo and Nair (2005) for this character. Both additive and

non-additive gene effects were reported to be equally important for this trait in the studies of (Kunta *et al.*, 1985), Harer and Deshmukh (1991), (Khattab, 1998), Ganesamurthy and Seshadri (2002), (Sayad *et al.*, 2005) and (Shinde, 2010). The significant values of additive and the non-allelic gene interactions i.e. additive × additive (i), additive × dominance (j) and dominance × dominance (l) for number of pods per plant in crosses DS-228 (Phule Kalyani) × Kalitur and MAUS-71 (Samrudhi) × Kalitur showed less complexity in the inheritance of the trait. These results are in agreement with earlier reports of (Mehetre *et al.*, 1998) and (Agrawal *et al.*, 1999).

Seed weight

Additive and dominance gene actions with duplicate epistasis in the inheritance of 100 seed weight in the crosses of DS-228 (Phule Kalyani) × Kalitur, MAUS-71 (Samrudhi) × Kalitur and MAUS-71 (Samrudhi) × Birsa Soya-1. These findings are in agreement with Ghassemi and Yazdi-Samadi (1987), (Kang, 1990), Halvankar and Patil (1993), Sharma and Phul (1994) and (Khattab, 1998). Predominance of additive gene effect was observed for the trait in cross DS-228 (Phule Kalyani) × Birsa Soya-1. These results are in agreement with the earlier reports of Srinivas and Sutakom (1986), (Zhang *et al.*, 1987), Malik and Singh (1987), (Pushpendra Ram, 1987), (Surlan-Momirovic, 1987), (Kang, 1990), Harer and Deshmukh (1991), Halvankar and Patil (1993), (Mehetre *et al.*, 1998) and (Agrawal *et al.*, 1999). Among non-allelic interaction all three additive × additive (i), additive × dominance (j) and dominance × dominance (l) effects were significant for the cross DS-228 (Phule Kalyani) × Kalitur and MAUS-71 (Samrudhi) × Kalitur. Additive × dominance (j) component was significant for all three crosses. Additive x additive non-allelic gene interaction for inheritance of this character was reported by (Ma *et al.*, 1987). Similar results were also reported by Ghassemi and Yazdi-Samadi (1987), (Jackovic *et al.*, 1988), Sharma and Phul (1994) and Maloo and Nair (2005). Duplicate epistasis was observed for crosses DS-228 (Phule Kalyani) × Kalitur, MAUS-71 (Samrudhi) × Birsa Soya-1 and MAUS-71 (Samrudhi) × Kalitur. Duplicate epistasis was also reported by (Li-Zeng Lu, 1995), Rahangdale and Raut (2002) and (Datt

et al., 2011). Biparental mating was suggested for duplicate epistasis. Complimentary epistasis was observed for cross DS-228 (Phule Kalyani) × Birsa Soya-1 which suggests that improvement in the character can be possible by selection in F₃ generation onwards such that the desired recombinants become available in the population. The result supports the findings of (Singh *et al.*, 1974), Sharma and Phul (1994) and Maloo and Nair (2005).

Yield per plant

Significant additive and non-additive (dominance and epistasis) gene actions with duplicate epistasis was observed for the inheritance of yield trait in the cross DS-228 (Phule Kalyani) × Kalitur. Similar results were reported by Lal and Fazlul Haque (1972). (Agrawal, 1999) and Rahangdale and Raut (2002) reported that additive gene action plays an important role in inheritance of this trait. Importance of duplicate epistasis in control of this character was also reported by Rahangdale and Raut (2002). (Singh *et al.*, 1974) observed both additive and dominant gene action for this trait. The selection 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. Duplicate epistasis involving in the inheritance of this trait was reported by Rahangdale and Raut (2002) and (Datt *et al.*, 2011). The involvement of non-additive gene action in control of this trait was reported by Ghassemi and Yazdi-Samadi (1987), (Jackovic *et al.*, 1988), (Halvankar, 1988), Halvankar and Patil (1993), Sharma and Phul *et al.* (1994), Triller and Toledo (1996), (Khattab, 1998), (Sayad *et al.*, 2005) and (Shinde, 2010). Significant additive × additive gene effects for controlling this trait were observed for crosses DS-228 (Phule Kalyani) × Kalitur, DS-228 (Phule Kalyani) × Birsa Soya-1 and MAUS-71 (Samrudhi) × Kalitur. Similar results were reported by (Hanson *et al.*, 1967) and (Ma *et al.*, 1987). The importance of both additive and non-additive gene effects are equally important as reported by (Singh *et al.*, 1974), Talwar and Singh (1983), (Alam *et al.*, 1984), Harer and Deshmukh (1991) and (Sayad *et al.*, 2005).

CONCLUSION

Mean values of F₁ from all crosses exceeded than of better parent for most of the yield contributing characters *viz.*, plant height, primary branches per plant, clusters per plant, pods per clusters, pods per plant, 100 seed weight and seed yield per plant. The gene action in four crosses was mostly additive and additive × additive contributed with greater magnitude towards yield and yield contributing characters *viz.*, number of primary branches per plant, number of clusters per plant, number of pods per cluster, 100 seed weight and yield per plant. These characters can be improved by progeny row selection from respective crosses. The high magnitude of dominance effect suggested that selection of high yielding genotypes could be postponed till later generation when the dominant effect would be diminished. Significant additive and non-additive (dominance and epistasis) gene actions with complementary epistasis was observed for the inheritance of number of pods per clusters in the cross of MAUS-71 (Samrudhi) × Birsa Soya-1, revealed that the trait can be improved by selections in F₃ generations onwards. Significant additive and non-additive gene actions with duplicate epistasis were observed for the inheritance of seed yield per plant in the cross of DS-228 of (Phule Kalyani) × Kalitur. The selection 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.

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