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INHERITANCE STUDIES THROUGH GENERATION MEAN ANALYSIS FOR YIELD AND YIELD COMPONENTS IN SOYBEAN [*GLYCINE MAX* (L.) MERRILL]

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ABSTRACT

The present investigation was undertaken to study the genetics of yield and yield components in soybean through generation mean analysis. Four crosses *viz.*, DS-228 × Type-49(C-I), DS-228 × MACS-450 (C-II), JS-9305 × Type-49 (C-III) and JS-9305 × MACS-450 (C-IV) were made involving four parents during *kharif* 2021 to study the gene action for nine characters in soybean. Five generations (P_1, P_2, F_1, F_2 and F_3) were obtained by intermating diverse parents. Dominant gene action was observed in the inheritance of yield and yield contributing traits *viz.*, number of pods per plant, 100 seed weight (g) and yield per plant (g). Duplicate epistasis was observed for days to flower initiation in cross-I and cross-III, for days to maturity in all crosses except cross-I, for plant height (cm) in cross-IV, for number of clusters per plant in cross-I and cross-II and for number of pods per plant and 100 seed weight (g) in cross-I, cross-III and cross-IV therefore Bi-parental mating design may be used to improve these characters. Complementary epistasis was observed for the cross-II for days to flower initiation and number of primary branches per plant, in cross-III for number of pods per cluster and incross-IV for number of primary branches per plant and number of pods per cluster, which suggested that the selection will be practiced in F_3 generation onwards for improvement of these characters.

Key words : Soybean, Gene action, Inheritance, Epistasis, Generation mean analysis.

Introduction

The soybean is leguminous seed crop and economically the most important bean in the world. India ranks fourth globally in terms of soybean production. However, under 5% of the world's soybeans are produced in India. Soybean production is currently at 1.21 t/ ha, or around half of the global average productivity. Due in part to the excellent nutritional value of soybeans as a food source for humans and cattle as well as their importance as an industrial commodity, soybean production is increasing substantially. With the introduction and inception of commercial cultivation in India in late 60's, the crop is being cultivated in around 12.27 million

hectares with production of 12.99 million ton (2021-22). In a very short period of time, the crop was adopted by farmers as major *kharif* crop in Madhya Pradesh and afterwards the acreage increased in Maharashtra, Rajasthan, Chhattisgarh, Northern Karnataka, Gujarat and Northern Telangana. On an average Madhya Pradesh and Maharashtra produce 51 and 33 per cent of total production of soybean, respectively.

Breeders of soybeans need a foundational understanding of the nature of gene action involved in expressing many yield and yield components in order to optimize soybean production through genetic improvement of the crop. The nature of gene action involved in the

inheritance of yield and yield components was simultaneously determined using two genetic models, namely Cavalli (1952) and Hayman (1958). The breeding method to be used for crop genetic improvement mostly depends on the type of gene action controlling the expression of quantitative traits. The dominant variation and their interactions could not be exploited effectively in soybean, while the additive type of epistasis is potentially exploited, as it can be fixable. The scaling test, which assesses epistasis precisely whether it is complimentary or duplicate at the digenic level, can be used to analyses generation means in order to determine the presence or absence of epistasis. Considering the present study, the four crosses differing in seed longevity was undertaken to study the information on gene action involved in the control of yield and yield components through five parameter model of generation mean analysis.

Materials and Methods

The present investigation was conducted at Post Graduate Research Farm of Department of Agricultural Botany, Post Graduate Institute, Mahatma Phule Krishi Vidyapeeth Rahuri, Ahmednagar (M.S.) during the period from 2019-2020 and 2020-2021. Four crosses *viz*; DS-228 × Type-49(C-I), DS-228 × MACS-450 (C-II), JS-9305 × Type-49 (C-III) and JS-9305 × MACS-450 (C-IV) were effected in early Summer 2020, *Kharif* 2020 and Summer 2021 to produce the F_1 seeds. F_2 and F_3 advancement were attempted in *Kharif* 2020 and Summer 2021.

The experiment was laid out in randomized block design (RBD) with three replications in *Kharif* 2021 for studying yield and yield components. The experimental material consisted of 20 treatments consisting of 5 parents, $4F_1$'s, $4F_2$'s and $4F_3$'s, of four crosses (DS-228 × Type-49(C-I), DS-228 × MACS-450 (C-II), JS-9305 × Type-49 (C-III) and JS-9305 × MACS-450 (C-IV)). The parents and F_1's, of each cross were randomized separately in each of the three replications. The segregating generation F_2's and F_3's of four crosses were non-replicated sown in single block. Sowing was done in rows of 5m length and 45 cm apart accommodating 30 plants at 15 cm distance in a row. One row was assigned to P_1's, P_2's and F_1's, this has permitted for raising of 30 plants in each of P_1's, P_2's and F_1's, in each of the three replications for each cross. The segregating generations F_2's and F_3's of each cross was assigned 30 and 6 rows permitted for raising of 300 plants in each of the F_2's and 60 plants in F_3's was grown in single block without replication. The observations were recorded on nine quantitative characters on random 10 plants from parents

and F_1 in each replication; 120 plants from F_2 and 60 plants from F_3 generations of all the four crosses. Data were tested for non-allelic interaction by Individual scaling test- 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). To compute gene affects for grain yield and its components with five basic generations, Mather's (1949) three parameter model and Hayman's (1958) five parameter models were used.

Results and Discussion

The results obtained in the present investigation; the analysis of variance was presented in Table 1. Mean sum of squares were significant either 5% or 1% level. This indicated for presence of significant variability in the parental material used and their segregating generations. The significant individual and joint scaling tests were observed for maximum characters in all crosses indicated presence of epistasis are presented in Table 2. The results of gene effects are presented in Table 3 are discussed below.

Days to flower initiation

In DS-228 × Type-49 cross combination the additive gene effect (h) was significant and greater in magnitude than the dominance gene effect (d) with duplicate epistasis, therefore, indicating a predominant role of additive gene action in controlling these traits in soybean. Additive genetic effect (d) in cross DS-228 × MACS-450 was negative and significant indicating the expression of this trait was under the influence of additivegene action but for lateness. InJS-9305 × Type-49 cross, duplicate epistasis was reported and significant negative additive gene effect observed, suggesting that early segregating generation should be the target of selection for this trait. These findings are in agreement with earlier reports of Mehetre *et al*. (1998), Agrawal *et al*. (1999), Rahangdale and Raut *et al*. (2002), Sayad *et al*. (2005), Adsul *et al*. (2016), Thakare *et al*. (2017) and Adetiloye *et al*. (2023). In JS-9305 × MACS-450 cross combination, there was absence of inter-allelic gene action nor non-allelic gene interaction as a result of internal gene effect cancellation or desperation in gene interaction.

Days to maturity

The expression of this trait in cross DS-228 × Type-49 was influenced by additive gene action, but for lateness, as indicated by the negative and considerable additive genetic effect (d) and non-allelic gene interaction was absent in this crossit indicates internal cancelation of gene effect because of balanced action of different loci having positive and negative increment and ultimately

Table 1 : Analysis of variance (M.S.S.) for yield and yield components in soybean.

Characters	Cross - I		Cross - II		Cross - III		Cross - IV	
	Treatment	Error	Treatment	Error	Treatment	Error	Treatment	Error
	(4)	(8)	(4)	(8)	(4)	(8)	(4)	(8)
Days to flower initiation	11.603**	0.090	38.676**	0.097	8.431**	1.104	15.402**	0.241
Days to maturity	57.043**	0.103	29.514**	1.270	91.644**	0.093	47.352**	0.100
Plant height (cm)	106.643**	11.254	40.197**	3.317	76.445**	1.445	118.257**	4.509
Number of primary branches/plants	2.985**	0.288	0.605*	0.151	0.621*	0.158	0.659**	0.058
Number of clusters/plants	107.060**	5.057	32.356*	5.363	227.067**	5.469	89.299*	12.780
Number of pods / clusters	1.156**	0.055	0.305*	0.078	0.773**	0.037	0.782**	0.079
Number of pods / plants	715.827**	6.735	383.942**	15.633	3752.508**	38.283	2631.519**	31.754
100 seed weight (g)	6.795**	0.320	2.140*	0.410	6.873**	0.171	2.579*	0.414
Yield / plant (g)	38.835**	3.414	145.596**	13.011	34.532**	4.925	238.263**	13.898

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

    Cross-I : DS-228 (Phule Kalyani) x Type-49

    Cross-II: DS-228 (Phule Kalyani) x MACS-450

    Cross-III: JS-9305 x Type-49

    Cross-IV: JS-9305 x MACS-450

contributes to generation mean effect. In all crosses, duplicate epistasis was observed except cross-I. Biparental mating can therefore be employed to utilize both fixable and non-fixable components of genetic variation for this trait. These results confirm the earlier reports of Zhang *et al*. (1987), Agrawal *et al*. (1999), Rahangdale and Raut *et al*. (2002), Shinde *et al*. (2010), Datt *et al*. (2011), Adsul *et al*. (2016), Thakare *et al*. (2017) and Adetiloye *et al*. (2023).

Plant height

The additive gene effect was shown to be significantly inverse in DS-228 × Type-49 cross for this trait, suggesting that early segregating generation selection for this trait would be desirable. In DS-228 × MACS-450 cross, duplicate epistasis was reported. Consequently, bi-parental mating can be used to utilize both fixable and non-fixable components of genetic diversity. Inter-allelic gene action was absent in JS-9305 × Type-49 cross *i.e.* absence of gene action and non-allelic gene interaction due to desperation of interaction of gene or internal cancelation of gene effects. The plant height of JS-9305 × MACS-450 cross showed a significant additive gene effect with negative direction, suggesting that early segregating generation selection for this trait would be desirable. These results confirm the earlier reports of Zhang *et al*. (1987), Agrawal *et al*. (1999), Rahangdale and Raut (2002), Shinde *et al*. (2010), Datt *et al*. (2011), Adsul *et al*. (2016), Thakare *et al*. (2017) and Adetiloye

et al. (2023).

Number of primary branches per plant

Additive gene effect was significant in negative direction in cross-I and cross-III for number of primary branches per plant revealed that selection for this trait would be useful to start from the early segregating generation. Non-allelic gene interaction was absent in DS-228 × MACS-450 cross. It indicates internal cancelation of gene effect because of balanced action of different loci having positive and negative increment and ultimately contributes to generation mean effect. The dominance gene effect (h) was significant and greater in magnitude than the additive gene effect (d), therefore, indicating a predominant role of dominance gene action in controlling this trait in JS-9305 × MACS-450. These results confirm the earlierreports of Nagarajan *et al*. (2022).

Number of clusters per plant

The number of primary branches per plant showed a significant negative additive gene effect in cross DS-228 × Type-49, suggesting that early segregating generation selection for this trait would be desirable. In cross DS-228 × MACS-450, duplicate epistasis was detected. Biparental mating can therefore be employed to utilize both fixable andnon-fixable components of genetic diversity for this trait. The dominance gene effect (h) was significant and greater in magnitude than the additive

Table 2 : Estimates of individual and joint scaling test (χ^2) for detecting non allelic interaction for yield and yield components in soybean.

Traits	Scaling tests	DS-228 x Type-49	DS-228 x MACS-450	JS-9305 x Type-49	JS-9305 x MACS-450
Days to flower initiation	C	-2.633*	4.300**	-5.800**	-2.500
	D	-6.200**	5.000**	1.067	-3.167
	χ^2	53.206**	26.300**	25.311**	7.855*
Days to maturity	C	-3.467	-7.767**	-6.700**	-3.533**
	D	-2.533	-12.133**	-8.100**	-7.033**
	χ^2	5.343	129.008**	71.428**	33.645**
Plant height (cm)	C	0.500	5.500	7.300	16.933**
	D	5.633	1.033	-0.100	11.367*
	χ^2	1.106	2.144	4.121	38.859**
Number of primary branches/plants	C	-4.567**	0.267	-0.133	-2.000**
	D	-3.333**	-1.533	-1.000	2.000*
	χ^2	70.613**	3.961	3.766	22.511**
Number of clusters/plants	C	19.900**	12.233**	5.400	4.195
	D	11.533**	2.067	-1.200	2.702
	χ^2	63.190**	16.505**	2.257	2.569
Number of pods/clusters	C	-0.533	1.467**	-1.067**	-0.867*
	D	-3.900**	-1.167*	0.067	0.400
	χ^2	88.776**	14.035**	12.114**	7.894*
Number of pods/plants	C	35.967**	-2.900	66.933**	44.400**
	D	27.933**	-4.167	59.467**	38.567**
	χ^2	80.145**	2.837	391.177**	128.921**
100 seed weight (g)	C	-5.745	-0.096	-1.114	-3.282**
	D	-5.987	-0.971	-4.014**	-5.471**
	χ^2	55.513**	0.576	39.420**	46.770**
Yield /plant (g)	C	3.433	6.867	1.800	10.800*
	D	0.867	3.467	8.133	8.533
	χ^2	1.558	5.825	3.255	9.423*

gene effect (d), therefore, indicating a predominant role of dominance gene action in controlling this trait in cross-III and cross-IV. Non-allelic gene interaction was absent in these cross indicates internal cancelation of gene effect. These findings are in agreement with earlier reports of Adsul *et al.* (2016), Thakre *et al.* (2017) and Adetiloye *et al.* (2023).

Number of pods per cluster

The dominance gene effect (h) was significant and greater in magnitude than the additive gene effect (d) in all crosses. Therefore, it indicates a predominant role of

dominance gene action in controlling this trait in soybean. Duplicate type of epistasis observed in cross- I and cross-II. Complementary type of epistasis observed in cross-III and cross-IV These results confirm the earlier reports of Ghassemi and Yazdi- Samadi (1987), Kang *et al.* (1990), Halvankar and Patil (1993), Sharma and Phul (1994), Khattab *et al.* (1998) and Thakare *et al.* (2017).

Number of pods per plant

As regards gene effects, the dominance gene effect (h) was significant and greater in magnitude than the additive gene effect (d) indicating a predominant role of

Table 3 : Estimation of gene action for yield and yield components.

Traits	Genetic parameters					Types of Epistasis
	m	**d**	**h**	**i**	**l**	
Days to flower initiation						
C- I: DS-228 × Type-49	37.45**±0.24	-2.51**±0.13	4.01**±0.81	-1.33±0.79	-4.75**±2.41	Duplicate
C-II:DS-228 × MACS-450	43.18**±0.29	-4.21**±0.12	1.76±1.26	-11.05**±1.09	0.93±3.29	Complementary
C-III:JS-9305 × Type-49	36.46**±0.22	-2.10**±0.21	-0.31±0.82	-5.87**±0.82	9.15**±2.36	Duplicate
C-IV:JS-9305 × MACS-450	40.80**±0.33	-3.11**±0.21	2.04±1.43	-	-	-
Days to maturity						
C- I: DS-228 × Type-49	102.30**±0.50	-6.10**±0.24	1.97±1.82	-	-	-
C-II:DS-228 × MACS-450	99.85**±0.30	-3.55**±0.18	8.07**±1.09	-0.30±1.04	-5.82±3.13	Duplicate
C-III:JS-9305 × Type-49	100.50**±0.27	-7.55**±0.20	5.60±1.07	-10.81**±0.99	-1.86**±2.91	Duplicate
C-IV:JS-9305 × MACS-450	99.21**±0.26	-5.40**±0.20	5.23**±1.11	6.70**±1.02	-4.66**±2.93	Duplicate
Plant height (cm)						
C- I: DS-228 × Type-49	54.06**±1.17	-7.68**±0.31	2.17±4.36	-	-	-
C-II:DS-228 × MACS-450	54.63**±1.00	-3.55**±0.29	6.24±4.19	-	-	-
C-III:JS-9305 × Type-49	51.46**±0.89	-6.81**±0.37	3.86±3.59	-	-	-
C-IV:JS-9305 × MACS-450	52.58**±0.77	-10.03**±0.48	8.14*±3.24	-24.82**±3.03	-7.42±9.08	Duplicate
Number of primary branches /plant						
C- I: DS-228 × Type-49	3.91**±0.12	-0.45**±0.15	1.14±0.47	0.56±0.51	1.64**±1.35	Complementary
C-II:DS-228 × MACS-450	4.40**±0.12	0.03±0.15	0.80±0.59	-	-	-
C-III:JS-9305 × Type-49	4.46**±0.12	-0.33*±0.13	0.48±0.52	-	-	-
C-IV:JS-9305 × MACS-450	4.00**±0.13	-0.43±0.10	1.06*±0.49	0.13±0.48	0.98*±1.41	Complementary
Number of clusters/plants						
C- I: DS-228 × Type-49	43.75**±0.73	-4.61**±0.36	5.14± 2.87)	-13.60**±2.59	-11.15±7.75	Duplicate
C-II:DS-228 × MACS-450	31.98**±0.74	-1.51**±0.34	6.87*±2.85	-2.37±2.61	-13.55±7.85	Duplicate
C-III:JS-9305 × Type-49	42.13**±0. 85	-8.80**±0.34	15.93**±3.75	-	-	-
C-IV:JS-9305 × MACS-450	37.34**±0.73	5.83**±0.43	7.36*±3.00	-	-	-
Number of pods/cluster						
C- I: DS-228 × Type-49	3.85**±0.58	-0.20**±0.05	3.87**±0.35	2.11**±0.26	-4.48**±0.75	Duplicate
C-II:DS-228 × MACS-450	3.95**±0.09	-0.36**±0.06	1.05**±0.37	0.28±0.35	-3.51**±1.04	Duplicate
C-III:JS-9305 × Type-49	3.70**±0.06	-0.13±0.07	0.97**±0.26	-0.48*±0.27	1.51*±0.74	complementary
C-IV:JS-9305 × MACS-450	3.50**±0.06	-0.33**±0.07	0.68**±0.21	-0.78**±0.24	1.68**±0.63	Complementary
Number of pods/plants						
C- I: DS-228 × Type-49	137.08**±1.41	-13.58**±0.38	12.72*±5.21	-39.79**±4.70	-10.71±14.41	Duplicate
C-II:DS-228 × MACS-450	97.86**±0.64	-10.28**±0.39	22.91**±2.73	-	-	-
C-III:JS-9305 × Type-49	150.80**±1.07	-37.20**±0.36	21.04**±4.62	-102.90**±4.00	-9.86±12.06	Duplicate
C-IV:JS-9305 × MACS-450	136.78**±1.21	-30.56**±0.42	26.58**±5.61	-79.44**±4.72	-7.77±14.13	Duplicate

Table 3 continued....

Table 3 continued....

100 seed weight (g)						
C- I: DS-228 × Type-49	13.04**±0.23	-1.44**±0.18	3.93**±0.99	0.15±0.90	-0.32±2.64)	Duplicate
C-II:DS-228 × MACS-450	17.53**±0.24	-0.41**±0.14	2.47*±0.97	-	-	-
C-III:JS-9305 × Type-49	14.51**±0.15	-1.49**±0.13	4. 70**±0.51	-0.49**±0.55	-3.86*±1.55	Duplicate
C-IV:JS-9305 × MACS-450	15.67**±0.21	-0.39**±0.14	4.05**±0.78	2.30±0.75	-2.91±2.91	Duplicate
Yield / plant (g)						
C- I: DS-228 × Type-49	39.18**±0.62	-2.61**±0.40	7.21**±2.64	-	-	-
C-II:DS-228 × MACS-450	49.36**±0.84	-7.30**±0.36	9.66**±3.14	-	-	-
C-III:JS-9305 × Type-49	38.23**±0.93	-1.73**±0.44	2.31±3.75	-	-	-
C-IV:JS-9305 × MACS-450	50.70**±1.17	-10.03**±0.48	8.31±4.51	-23.95**±4.06	-3.02±12.27	Duplicate

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

Cross-I : DS-228 (Phule Kalyani) x Type-49

Cross-II: DS-228 (Phule Kalyani) x MACS-450

Cross-III: JS-9305 x Type-49

Cross-IV: JS-9305 x MACS-450

dominance gene action in controlling this trait in soybean. Duplicate type of epistasis observed in all crosses except cross-II and Non-allelic gene interaction was absent in cross DS-228 × MACS-450 indicates internal cancelation of gene effect. Similar results were also reported by Sayad *et al*. (2005), Mallo and Nair (2005), Bhor *et al*. (2014), Thakare *et al*. (2017) and Pawale *et al*. (2020).

100 seed weight (g)

The dominance gene effect (h) was significant and greater in magnitude than the additive gene effect (d) indicating a predominant role of dominance gene action in controlling this trait in soybean. Duplicate type of epistasis observed in all crosses except cross-II and Non-allelic gene interaction was absent in cross DS-228 × MACS-450 indicates internal cancelation of gene effect. Similar results were also reported by Ghassemi and Yazdi-Samadi (1987), Kang *et al.* (1990), Halvankar and Patil (1993), Sharma and Phul (1994) Khattab *et al*. (1998) and Adsul *et al*. (2016).

Yield per plant (g)

As regards gene effects, there is preponderance of dominant gene effect for yield per plant of in cross- I and cross-II. Non-allelic gene interaction was absent in this cross indicates of internal cancelation of gene effect. These results confirm the earlier reports of Jackovic *et al*. (1988), Halvankar and Patil (1993), Triller and Toledo (1996), Khattab *et al*. (1998), Sayad *et al*. (2005), Shinde *et al*. (2010), Adsul *et al.* (2016) and Thakare *et al*. (2017). The yield per plant in cross JS-9305 × Type-49 showed a significant negative additive gene effect, suggesting that early segregating generation selection for

this characteristic may be beneficial. In cross JS-9305 × MACS-450, the additive gene effect was significant in the negative direction and duplicate type of epistasis observed, suggesting that selection for this characteristic would be beneficial to begin with the early segregating generation. Similar results were reported by Lal and Fazlul Haque (1972), Agrawal (1999), Rahangdale and Raut (2002).

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