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## Determination of gene action for yield and its related traits in soybean under North-Western Himalayas conditions of India

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### Abstract

**Aim :** To understand the nature and magnitude of gene action for yield and its related traits in soybean.

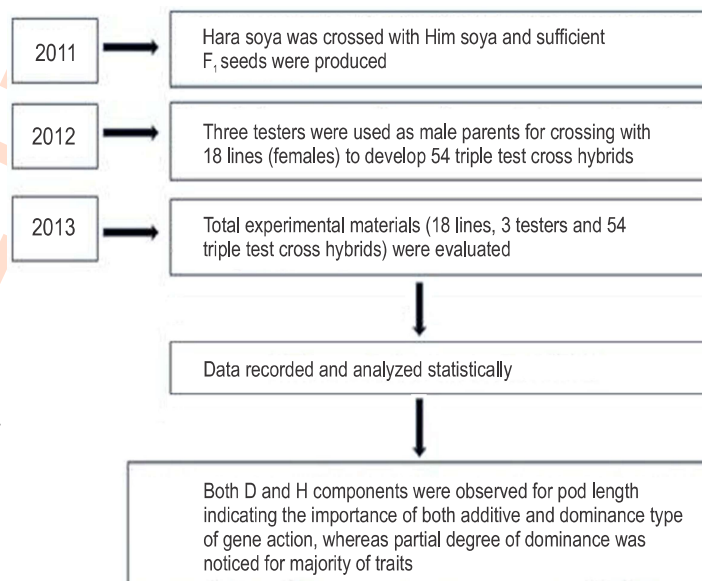
**Methodology :** Fifty four triple test cross progenies developed by crossing 18 lines with three testers Him soya and Hara soya ( $P_1$  and  $P_2$ ) and their  $F_1$ s were used as testers 'L<sub>1</sub>', 'L<sub>2</sub>' and 'L<sub>3</sub>'.  $F_1$  seeds were produced by crossing Him soya with Hara soya during kharif 2011. By crossing these three testers with 18 lines (females), 54 triple test cross hybrids were developed during kharif 2012. The fifty four  $F_1$  hybrids along with 18 lines and 3 testers were sown during kharif 2013 in a randomized block design with three replications.

**Results :** In the triple test cross progenies, sufficient genetic variations were found for all the traits, except petiole length. Epistasis was observed to be an integral part of genetic variations for traits like plant height, branches per plant, nodes on main stem, internode length, pods per plant, pod length, biological yield per plant, seed yield per plant, oil content, crude protein content. Epistatic interaction for most traits was additive x dominance and dominance x dominance (j+l) type. In addition to additive x dominance and dominance x dominance (j+l), additive x additive (i) type epistasis was observed for plant height, internode length, pods per plant and biological yield per plant. For the inheritance of most traits, fixable type of gene action was found as additive component (D), was more pronounced than dominance component (H), except pod length.

**Interpretation :** For improvement of traits, selection in the early generations will be useful as additive gene action was observed.

The importance of additive x dominance (j) and dominance x dominance (l) type of epistasis in the inheritance of seed yield and other related traits signifying the importance of recurrent selection in order to develop high yielding varieties. For pod length, both additive and dominant components were observed. Thus genetic improvement in seed yield would be easier through indirect selection for pod length.

**Key words:** Epistasis, Gene action, Modified triple test cross, Soybean



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## Introduction

Soybean [*Glycine max* (L.) Merrill, 2n= 40] belongs to family Leguminosae is known as "Miracle crop" of the world, which is well adapted to various agro-ecological zones. North-Eastern China is considered as the centre of origin (Vavilov, 1951 and Leppik, 1971). This crop is also known as 'King of American Agriculture' (Kuehn, 1972). Throughout the world, including India, soybean is most popular because of its oil used for cooking and a base for margarine and other consumer products. It contains about 40% high quality protein and 20% oil. The fatty acid composition of soybean ranges from 27.02-34.09% for oleic acid, 10.59-12.09% for palmitic acid, 3.11-4.52% for stearic acid, 44.51-51.80% for linoleic and 4.44-5.61% for linolenic acid (Gulluoglu *et al.*, 2018). Soybean is popularly known as "Miracle Bean" due to its versatile use in Indian food (Mahesh *et al.*, 2017). This crop fixes atmospheric nitrogen and thus, serves as natural soil fertilizer (Ito *et al.*, 2006). Soybean is grown on small scale in Himachal Pradesh, parts of Central India covering Madhya Pradesh, Eastern Bengal, the Khasi Hills, the Naga Hills and the Kumaon Hills of Uttarakhand. Locally, this crop is known as *bhat*, *bhatman*, *bhatmas*, *ramkulthi*, *garakalay* and *kalitur* (Singh, 2006). The total contribution of this crop to the foreign exchange is Rs 7000 crores through the export of de-oiled cake, in addition it also fulfills approximately 20% of the total edible oil requirement of the country (Mishra *et al.*, 2018).

To keep pace with increasing population, there is a need to further increase the productivity potential of this crop. In order to increase the production of a crop, developing high yielding varieties through appropriate breeding programme is a prerequisite. The knowledge of genetic basis underlying the trait of interest is required for developing superior genotypes (Karikari *et al.*, 2019). In self pollinated crops, recombinant breeding approach can be followed to combine various desirable traits like high yield, quality traits as well as other yield contributing attributes. Moreover, seed yield is a complex quantitative character resulting from the action and interaction of large number of yield contributing traits. For improving these traits, knowledge of genetics of yield and its related traits is important for breeding programme to be effective for further selection and management of breeding material (Jalata *et al.*, 2019). The type of gene action present in particular trait of interest is required for plant breeder for selecting suitable breeding method (Cockerham, 1961).

Therefore, for rational choice of suitable breeding method, partitioning of total genetic variance into additive, dominance and epistasis components is important. For any breeder, a good genetic model should provide precise and unbiased estimates for all the components of genetic variations. Though there are different breeding methods, however, in this study we followed modified triple test cross technique of Kearsley and Jinks (1968) that check epistasis and in addition to this provide estimates of additive and dominance components even when epistasis is not present. This technique does not depend on

gene frequencies, gene correlations and mating systems. By this approach, large number of parents can be evaluated as only three testers are used in this technique as compared to other mating designs like diallel mating design. In soybean, little is known about the genetics of quantitative traits; therefore, this study was planned to check the nature and magnitude of genetic variances or to understand gene action for yield and related traits.

## Materials and Methods

The present study was carried out at the experimental farm of Chaudhary Sarwan Kumar Himachal Pradesh Krishi Vishvavidyalaya, Palampur, Himachal Pradesh, India. Two contrasting parents viz., Hara soya L<sub>1</sub> and Him soya L<sub>2</sub> were used as testers. The F<sub>1</sub> progeny developed from crossing between Hara soya and Him soya was used as third tester (L<sub>3</sub>). Eighteen true breeding genotypes/lines viz., SL-682, SL-679, SL-795, P6-1, P9-2-2, P2-2, DS-1213, PK-472, Hardee, Bragg, Shivalik, PS-1466, PS-1469, H-330, VLS-59, JS-335, P169-3 and P13-4 were crossed with three testers (L<sub>1</sub>, L<sub>2</sub> and L<sub>3</sub>). The experimental material consisted of 18 fixed lines, 3 testers, 54 triple test crosses was sown in a randomized block design (RBD) with three replications during 2013-14.

The experimental plot consisted of a single row of 2m length for each treatment. The plant to plant and row to row spacing were 20 and 50 cm, respectively. Five plants were tagged randomly from each entry and replication to record observations for 17 traits viz., days to 50% flowering, days to 75% maturity, reproductive phase, plant height (cm), branches per plant, nodes on main stem, internode length (cm), petiole length (cm), pods per plant, pod length (cm), seeds per pod, biological yield per plant (g), seed yield per plant (g), harvest index (%), 100-seed weight (g), crude protein (micro-Kjeldhal method, AOAC, 1970) and oil content (Sudar *et al.*, 2007). The average of individual five plants in each replication was used for analysis. Statistical analyses for all triple test-cross calculations were performed with the computer software Indostat.

## Results and Discussion

The two testers (Hara soya and Him soya) used in this study showed considerable genetic diversity and These testers were selected from true breeding lines of soybean by selection generation after generation. Therefore, they fulfilled the basic requirements of triple test cross analysis. Analysis of variance revealed significant differences among them for all the traits, namely, days to 50% flowering, days to 75% maturity, reproductive phase, plant height, branches per plant, internode length, nodes on main stem, pods per plant, seeds per pod, pod length, biological yield per plant, seed yield per plant, harvest index, 100-seed weight, protein content and oil content, except petiole length. Thus, sufficient amount of genetic variations were present for the material as revealed through analysis of variance (Table 1). These genetic variations can be exploited through recombination breeding. Both the testers showed considerable

**Table 1:** Analysis of variance for different traits in soybean

Source of variation	Mean sum of squares		
	Replication	Treatment	Error
Traits	df	74	148
Days to 50% flowering	31.720*	50.890*	4.630
Days to 75% maturity	149.490*	15.290*	3.470
Reproductive phase	0.003*	0.004*	0.001
Plant height	917.520*	102.830*	35.220
Branches/plant	3.620*	2.950*	0.560
Internode length	5.550*	0.730*	0.270
Nodes/main stem	3.240*	3.670*	0.890
Petiole length	4.660*	0.970	1.340
Pods/plant	295.050	1038.030*	132.830
Seeds/pod	1.670*	0.040*	0.020
Pod length	0.040*	0.070*	0.009
Biological yield/plant	102.760*	215.660*	31.430
Seed yield/plant	16.680	56.990*	6.810
Harvest index	0.009	0.008*	0.005
100 seed weight	0.730	22.320*	1.270
Protein content	0.160	2.980*	0.190
Oil content	0.610*	2.800*	0.090

\*Significant at  $P \leq 0.05$ , df= degree of freedom

**Table 2:** Analysis of variance for detection of epistasis for different traits in soybean

Source of variation	Epistasi	i-type interaction	(j+l) type interaction	Epistasis x replication	l type x replication	(j+l) type x replication
Traits	(df=18)	(df=1)	(df=17)	(df=36)	(df=2)	(df=34)
Days to 50% flowering	28.720	44.460*	27.790*	23.440	16.460	23.850
Days to 75% maturity	11.640	8.160*	11.850*	14.20	23.720	13.640
Reproductive phase	0.004	0.00009	0.0043*	0.004	0.007	0.004
Plant height	352.820*	569.070*	340.100*	92.340	0.940	97.720
Branches/plant	13.010*	1.040*	13.710*	3.670	1.640	3.790
Internode length	3.340*	20.730*	2.310*	0.520	0.410	0.530
Nodes/main stem	21.930*	22.560*	21.890*	4.210	3.780	4.230
Petiole length	4.320	16.780	3.580*	8.850	0.170	9.360
Pods/plant	3088.900*	1067.560*	3207.800*	916.720	27.390*	969.03
Seeds/pod	0.140	0.120*	0.140*	0.090	0.030	0.100
Pod length	0.680*	0.20*	0.700*	0.060	0.070	0.060
Biological yield/plant	1111.470*	586.080*	1142.370*	160.660	9.350	169.560
Seed yield/plant	214.760*	50.650*	224.410*	43.400	13.990*	45.130
Harvest index	0.030	0.006*	0.030*	0.020	0.004	0.020
100 seed weight	12.380	9.710*	12.540*	8.710	1.920	9.110
Protein content	6.970*	6.740*	6.980*	0.980	0.390	1.010
Oil content	2.720*	1.610*	2.780*	0.590	0.070	0.630

\*Significant at  $P \leq 0.05$ , df= degree of freedom

differences as they had extreme high vs low relation with the population and would give an estimate of additive and dominance variation with equal accuracy (Datt *et al.*, 2011). In this study, significant influence of non-allelic interaction was found for all the

traits. Epistasis is an important genetic component that underlies phenotypic variation and is also a key mechanism that accounts for missing heritability. Identifying epistatic interactions in genetic association studies can help to understand better genetic manner

**Table 3:** Analysis of variance for sums ( $\bar{L}_{11} + \bar{L}_{22}$ ) and differences ( $\bar{L}_{11} - \bar{L}_{22}$ ) for different traits in soybean

Traits	Mean squares			
	Sums (df=17)	Sums × replication (df=34)	Differences (df=17)	Differences × replication (df=34)
Days to 50 % flowering	101.880*	9.610	37.060*	11.810
Days to 75% maturity	21.850*	7.180	9.630*	3.520
Reproductive phase	0.008*	0.001	0.002	0.001
Plant height	329.920*	85.070	75.830	51.890
Branches/plant	5.740*	1.050	2.940*	1.020
Internode length	2.700*	0.630	0.510	0.480
Nodes/main stem	11.12*	1.840	4.380*	2.070
Petiole length	1.330	2.350	1.870	3.420
Pods/plant	4183.39*	265.18	718.670*	297.450
Seeds/pod	0.150*	0.070	0.030	0.040
Pod length	0.120*	0.020	0.180*	0.020
Biological yield/plant	825.180*	80.950	162.610*	56.800
Seed yield/plant	280.560*	11.620	28.520	18.870
Harvest index	0.020	0.010	0.010	0.010
100 seed weight	88.420*	3.050	8.890*	3.170
Protein content	9.940*	0.540	2.460*	0.280
Oil content	9.030*	0.200	2.770*	0.160

\*Significant at  $P \leq 0.05$ ; df=degree of freedom

**Table 4:** Estimates of additive (D) and dominance (H) components of genetic variance, average degree of dominance  $(H/D)^{1/2}$ , correlation ( $r_{s,d}$ ) and directional element (F) for different traits in soybean

Traits	D	H	$(H/D)^{1/2}$	$r_{s,d}$	F
Days to 50 % flowering	123.020*	33.670*	0.520	0.540*	-17.400*
Days to 75% maturity	19.560*	8.160*	0.650	-0.070	0.440
Reproductive phase	0.009*	0.002	0.440	0.240*	-0.0004*
Plant height	326.460*	31.920	0.310	0.270*	-13.800*
Branches/plant	6.250*	2.550*	0.640	0.480*	-0.960*
Internode length	2.760*	0.040	0.110	-0.090	0.020
Nodes/main stem	12.370*	3.070*	0.490	0.050*	-0.160*
Petiole length	-	-	-	-0.220	0.200
Pods/plant	5224.290*	561.640*	0.330	-0.450	385.440
Seeds/pod	0.110*	-	-	0.360*	-0.004*
Pod length	0.130*	0.230*	1.310	-0.090	0.008
Biological yield/plant	992.300*	141.080*	0.380	-0.030*	5.600*
Seed yield/plant	358.590*	12.870	0.190	0.180*	-6.120*
Harvest index	0.010	0.002	0.480	0.250*	-0.00004*
100 seed weight	113.82*	7.630*	0.260	0.130*	-1.880*
Protein content	12.540*	2.900*	0.480	-0.100	0.280
Oil content	11.760*	3.490*	0.540	0.490*	-0.390*

of multifaceted traits (Crawford *et al.*, 2017). Due to heterozygous nature of the lines, there is involvement of different alleles which result in significant estimates of epistasis. Barona *et al.* (2012) also observed the presence of epistasis for majority of traits which underlines the importance of both additive and dominance components of variance if

process assuming no epistasis had been engaged, this would have been biased. Epistasis was considered as an essential part of genetic system for all the 17 traits studied (Table 2). As total epistasis is partitioned into additive x additive (*i* type), additive x dominance and dominance x dominance (*j* and *l* type) interactions showed the existence of *i*, *j* and *l* type of epistasis

for all traits, except reproductive phase and petiole length where only *j* and *l* type of epistasis was observed. Therefore, it is important to consider while improving commercially important traits through breeding programme. The information regarding interallelic interactions may be lost if one ignores the epistasis and one may get biased estimates of additive and dominance components which give rise to wrong conclusions (Singh *et al.*, 1997). While breeding self-pollinated crops, where the main aim is to develop inbred lines, *i* type epistasis is of utmost importance because it is fixable in homozygous material and contributes to the superiority of elite lines (Cockerham, 1954; Goldringer *et al.*, 1997). The significance of mean square due to sums and differences provide a direct test of significance of additive and dominance components of variation. The significance of mean squares due to sums (except petiole length and harvest index) and differences (except reproductive phase, plant height, internode length, petiole length, seeds per pod, seed yield per plant and harvest index) for most traits observed in the present study (Table 3) indicates the significance of both additive and dominance variance in controlling the expression of these traits in soybean. The relative magnitude of D and H components revealed that additive genetic component was predominant for days to flowering, days to 75% maturity, reproductive phase, plant height, branches per plant, internode length, nodes on main stem, pods per plant, biological yield per plant, seed yield per plant, harvest index, 100-seed weight, protein content and oil content, whereas dominance was predominant for pod length (Table 4). Use of recurrent selection has been suggested to improve the characters when both additive and non-additive gene effects are involved in expression of the traits.

The magnitude of additive component is increased in the testers due to the existence of common alleles, by adding up the dominance effect of common alleles in testers along with the cross product effects of dominance and additive effects. Moreover, the dominance effect will be calculated for non-common loci only results in reducing the magnitude of dominance variance. Epistasis and genetic variance heterogeneity are two non-additive genetic inheritance patterns that are often but not always, related. Additive variance is a type of gene action whereby each of two alleles contributes equally to the production of qualitative phenotypes; neither allele is dominant. The heterozygous genotype produces a phenotype that is intermediate between those produced by the homozygous genotypes. Therefore go for direct selection when additive variance is present. Dominance variance refers to the phenotype deviation caused by the interactions between alternative alleles that control one trait at one specific locus. In dominance variance one allele is dominant over other, so in this case we go for hybridization rather than direct selection. The occurrence of higher extent of additive gene action for seeds per pod and plant height has also been observed in peas (Sharma *et al.*, 2008), for plant height and protein content in barley (Verma *et al.*, 2007), for days to 50% flowering, days to 75% maturity, pods per plant, 100-seed weight and grain yield per plant (Agrawal *et al.*, 2005), for 100-seed weight and yield per plant (Adsul *et al.*, 2016) and for days to 50% flowering (Thakare *et al.*, 2017).

The magnitude of dominant variance was higher for pod length signifying thereby the relative importance of dominance type of gene action. The significant positive correlation between sums and differences was observed for most traits. The remaining traits showed non-significant correlation representing that these traits did not provide any indication for directional dominance in soybean, and alleles with increasing and decreasing effects appeared to be dominant and recessive, respectively. The prevalence of additive genetic variance for most traits viz., days to 50% flowering, days to maturity, plant height, branches per plant, internode length, nodes on main stem, pods per plant, biological yield per plant, seed yield per plant, harvest index, 100-seed weight, protein content and oil content indicates the possibility of improvement of these traits through pedigree method of selection procedure. Hakim and Suyamto (2017) also reported that pods per plant, seed yield and harvest index were found to be primarily controlled by additive gene action. Dominant gene action was found predominant in inheritance of yield and yield contributing characters viz., branches per plant, pods per plant and seed yield per plant (Bhor *et al.*, 2014). Dominant gene action was important for determining seed yield and oil content. The existence of significant amount of dominance components for other traits showed the use of diallel selective mating/biparental mating designs or recurrent selection method for their improvement as reported in linseed (Sood *et al.*, 2007) and soybean (Rose *et al.*, 1992).

The average degree of dominance  $(H/D)^{1/2}$  was in the range of partial dominance for majority of traits showing the importance of additive gene action for these particular traits. High amount of additive gene action has also been observed for many target traits in soybean (Tawar *et al.*, 1989). However, the non-additive variance has been noticed for yield and plant height. The additive and dominance variances were significant for pods per plant and harvest index (Kunta *et al.*, 1985). As pod length showed complete dominance, therefore both additive and non-additive types of gene actions were important for inheritance of this trait. The significance of additive and non-additive type of gene action has also been reported by Singh (1983) and Wahyu *et al.* (2014).

In the present study, the occurrence of additive gene action for majority of traits including seed yield implies that early generation selection may be useful for improving these traits. For traits showing dominance components of variance and '*j*' and '*l*' types of epistasis, heterosis breeding may be useful by developing high yielding hybrids/varieties. Therefore, recurrent selection followed by pedigree method of selection and diallel selective mating/biparental mating might give fruitful results by exploiting both additive and dominant components of variation along with epistasis. The information obtained through present study would help in understanding the genetic basis of traits studied and making breeding strategy for the development of high yielding cultivar (s) or valuable germplasm in soybean.

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