# GENETIC ANALYSIS OF YIELD, PROTEIN, OIL AND OTHER RELATED TRAITS IN SOYBEAN

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(Received: April 5, 1999; accepted: November 30, 1999)

#### **ABSTRACT**

Combining ability analysis was carried out for yield, protein and oil content and other traits related to productivity in a half diallel set involving seven parents. The estimates of sca variances were higher than gca variances for all the seven characters. Values of the ratio  $\frac{2\sigma_g^2}{2\sigma_g^2 + \sigma_s^2}$  indicated that for traits like protein content, grain yield and days to maturity, non-additive gene effects were predominant. The mean values of parents reflected their combining ability effects in general and genotypes KHSb-2 and DS 74-62 were good general combiners for yield and yield contributing characters. The high performing crosses for yield involved parents with High × Low and Low × Low gca effects. Based on the results, suitable breeding strategies are suggested.

Key Words: Soybean, Glycine max, combining ability

Soybean is becoming popular in different regions of the country and this necessitates evolving of cultivars suited to different agro-climatic conditions. The nature and magnitude of combining ability help in identifying elite parents and desirable cross combinations, which is of immense value in formulation of breeding program. The information on additive and non-additive gene effects associated with yield and other traits in soybean is scanty [1-4]. Further, reports regarding the relationship between combining ability effects and per-se performance of parents and crosses differ. Hence, the present investigation was aimed at studying the combining ability of newly developed and locally adapted lines of soybean.

## MATERIALS AND METHODS

Seven soybean lines were crossed in all possible combinations excluding reciprocals. All the lines and resultant 21 crosses were grown in a randomized

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complete block design using three replications at the college of Agriculture Farm, Dharwad, Karnataka. Each entry was grown in one-row plot of 4 m length with 50 × 15 cm spacing. The observations were recorded on ten random plants in each entry for seven quantitative characters (Table 1). Protein content was estimated based on total Nitrogen content of seeds by micro-kjelahl method [5], by multiplying percentage N by 6.25. Oil content was estimated by using Nuclear Magnetic Resonance (NMR) technique. The data were analyzed by using Model 1 Method 2 of Griffing [6].

### RESULTS AND DISCUSSION

Analysis of variance for combining ability revealed that variances due to gca and sca were significant for all characters except oil content, for which mean square due to sca was not significant (Table 1). This indicates existence of genetic variability

Table 1.	Analysis of	variance	(mean	squares)	for	combining	ability	for	seven
	characters in	soybean							

Source	d.f.	Days to flowering	Days to maturity	Plant height	Pods per plant	Grain yield per plant	Protein content	Oil content
Gca	6	81.3**	61.4**	689.9**	2175.0**	87.2**	4.29**	3.06**
Sca	21	14.7**	21.2**	91.6**	448.7**	30.3**	3.07**	1.06
Error	54	0.5	0.4	0.9	3.0	0.3	0.26	0.80
$\frac{2\sigma_g^2}{2\sigma_g^2 + \sigma_s^2}$		0.5	0.3	0.6	0.5	0.3	0.09	0.63

<sup>\*, \*\*</sup> Significant at 5 and 1% levels, respectively.

in the soybean lines included in the present study and the importance of both additive and non-additive gene effects in the inheritance of these traits. Significant gca and sca variances have been reported for days to maturity, plant height, number of pods per plant and grain yield per plant [4, 5]. Kaw and Menon [6] reported significant gca variance for days to flowering also in addition to above characters. These are in conformity with the present results. Chauhan and Singh [7] found highly significant gca and sca variances for both protein and oil contents, while the mean square due to sca for oil content was non-significant in the present study.

In the combining ability analysis, if both gca and sca effects are significant, it is useful to know how important the interactions are in determining the single cross

performance is better assessed by the ratio  $\frac{2\sigma_g^2}{2\sigma_g^2+\sigma_s^2}$  [8]. Lower value of the ratio for protein content, grain yield per plant and days to maturity indicated the predominant role of non-additive gene effects in the expression of these characters. For other traits viz., oil content, pods per plant, plant height and days to flowering, nearly equal importance of both additive and non-additive gene effects was observed. Though none of the parents was a good general combiner for all the traits, KHSb-2 and DS74-62 posses high gca for grain yield per plant, pods per plant, height and oil content plant. Monetta and SL 96 showed good gca effects for other traits like days to flowering, days to maturity, as also protein content (Monetta). These parents can be used in crossing program depending upon the specific objective like improvement of yield per se or evolving early genotypes to suit particular inter-cropping patterns. Alternatively desirable multiple parents can be put into a central gene pool to generate useful segregants [9].

In general, the order of ranking of soybean genotypes based on mean values was similar to that based on the estimates of gca effects for all traits except for oil content. Thus, in the present study, the per-se performances of the parents were indications of their gca effects. Positive association between the two was also reported by many researchers [2, 3, 10]. In contrast, Chauhan [4] and Leffel and Weiss [11] did not find significant correlation between gca effects and mean values for seed yield and pods per plant. Mean values of the crosses and their sca effects (Table 2) were not as close in order as observed for gca and per-se performance of parents.

Though the performances of parents and crosses themselves give some indication regarding their usefulness, long term potentialities of them are least known at the initiation of the breeding program. If there is a general agreement between combining ability values and per-se performance, it will not be difficult to make the right choice for selection of parents. However, in the absence of correlation between the two, the question regarding relative importance to be attached to each needs to be addressed. In such cases, much reliance can not be placed on parental mean values as an index of their superiority for inclusion in the hybridization program aimed at yield improvement [7]. On the other hand, if the objective is to produce commercial hybrid (F1), more weightage is to be given to mean values of crosses [12]. Thus when a character mean is of desirable status, still due weightage is to be given to gca/sca scored in F1, depending upon the objective and nature of the crop.

A persual of top five crosses showing desirable sca effects for grain yield per plant (Table 2) indicates High  $\times$  Løw and Low  $\times$  Low combinations with respect to

Ranking of parent varieties of soybean and elite crosses based on character means and estimates of gca and sca effects. Table 2.

A Parental varieties

Rank		Days to flowering	ring	Days	to maturity	rity	Plant	Plant height (cm)	(m)	Pods	Pods per plant	#	Grain y	Grain yield/plant (g)	t (g)	Protein	Protein content (%)	(%)	Oil co	Oil content (%)	
1	parent mean	mean	gca	parent	mean	gca	parent	mean	gca	parent	mean	gca	parent	mean	gca	parent	mean	gca	parent r	mean	gca
_	96-TS	39.9	-3.58**	-3.58** Monetta	93.8	*64.4°	LBS	68.7	15.50** KHSb-2	KHSb-2	8.8	17.45** KHSb-2	KHSb-2	27.6	4.72** [	LBS	43.54	0.60** KHSb-2	HSb-2	20.95	0.45
п	Monetta	41.0	2.38** Bragg	Bragg	9.66	0.03	KHSb-2	47.6	6.57** LBS	LBS	94.0	16.80** DS74-62	DS74-62	20.6	3.47** Monetta	fonetta	41.68	1.02** DS74-62	S74-62	20.90	0.64*
Ħ	Bragg	41.9	2.06** SL-96	%-7S	101.3	-1.05**	-1.05** DS74-62	45.6	2.86**	2.86** DS 74-62	82.6	13.63** LBS	TBS	15.5	0.05	Bragg	41.03	-0.10 Hardee	ardee	20.85	0.24
2	Hardee	52.6	0.09 LBS	LBS	102.8	±86:0-	Bragg	33.3	33.3	33.3 -4.35**	Hardee	58.1	58.1 -6.00**	Hardee	14.7 -0.88**	0.88**	96-TS	39.33 0.20		%TS	20.17
>	LBS	53.6		0.70** Hardee	102.9	0.21	Hardee	32.7	4.65**	Bragg	38.3	-13.00**	96-TS	12.6	-2.62** Hardee	lardee	39.22	-0.08 Bragg	388	19.53	0.29
I I	DS74-62	55.7	1.91**	1.91** DS74-62	109.8	2.63**	SL-96	25.0	36** ]	36** Monetta	35.1	-9.20** Bragg	Bragg	10.8	-0.76** KHSb-2	HSb-2	39.09	-0.65** Monetta	onetta	- 82.61	-1.02**
NI I	KHSb-2	9:09	5.22**	5.22** KHSb-2	114.1	3.43**	3.43** Monetta	23.4	-8.58** 5	96-TS	34.4	-19.69** Monetta	Monetta	6.9	-3.89** DS 74-62	S 74-62	38.55	-0.99** LBS	8	17.72	-0.50
RQ OT	B. Top five crosses	T06865		Í																	
Rank Cross	Cross	F1	<b>8</b> 09	Cross	F1 mean	sca	Cross	F1	) scs	Cross	F1	S.	Cross	F1	ss.	Cross	F1 mean	2	Cross	F1	sca
-	ľχľ		-5.88** V×VI	V×VI	98.0	-5.52**	3	89.5	29.29** 1	<u>*</u>	149.9	41.03** VIXVII	VIXVII	24.0	VIXV **87.6	ΣX	44.12	3.60** VXII		23.27	2.19**
п	IV×V	42.5	42.5 -5.84** II×VII	II×VII	98.8	-5.27** V×VI	V×VI	34.8	8.73** IIXIII		139.8	34.74™ VI×IV	VIXIV	27.2	9.64** IIxVI	κΝΙ	43.90	3.13** III×VI	I <sub>X</sub>	20.42	1.05
Ħ	ПхИП	45.5	-5.13** VIIXIII	VIIVIII	98.6	-4.44** IV×VII	IV×VII	30.5	5.24** V×IV	V×IV	8.68	34.20** I×VIII	IXVIII	33.4	9.43** VIIXIV	NIXIV	41.72	2.10** IxVII	II.	21.08	86:0
≥	IV×VI	44.5	-5.01** VXIII	N×III	95.7	4.14** VII×VI	VIIXVI	27.3	5.16** VIxVII	VI×VII	73.8	28.13** IIIXII	IIXII	29.8	70.06** III×VI	Ι×Ν	41.22	1.57** IXIV	2	21.35	0.85
>	Π×VI	43.3	-4.07** VIIXIV	VIIXIV	100.2	-2.90**	I×VI	61.6	5.16** IXIII	ШХ	124.1	18.37** VIIXV	VIIxV	18.5	5.82** []	пхип	41.47	1.03 <b>⁺⁺ VII</b> ×II		21.03	0.74
SE (gi)			0.21			0.19			0.29			0.53			0.17			0.16			0.28
SE (sij)	(1		0.63			0.57			0.85			1.55			0.49			0.46			0.80

\*,\*\* Significant at 5 and 1% levels, respectively.

Note: Parental lines involved in the top five crosses are indicated by their specific ranking numbers under respective traits as above in A.

parental gca effects. The crosses KHSb-2  $\times$  LBS and LBS  $\times$  DS74-62 (High  $\times$  Low combinations) exhibited high and desirable sca effect for pods per plant also, a direct yield contributing character. Therefore, sca of yield may be influenced by the sca of yield component and combining ability of the parents may serve as a reliable guide in assessing the yield potential of a cross. Kaw and Menon [3] also observed that superior hybrids (high sca) had at least one parent with high gca. For the other three crosses for grain yield per plant, significant sca effects were associated with Low  $\times$  Low gca effects of parents reflecting a non-additive type of gene action.

Crosses involving High × Low and Low × Low general combiners in the present study which resulted in the high sca effects are of considerable interest as such combinations may give desirable transgressive segregants if the additive effects of one parent and complementary effects of the other parent act in the same direction for maximum expression of the traits. Similar results have been reported in soybean [13] and ground nut [14]. The predominance of non-additive variance leads to bias in favor of heterozygotes in early segregating generations. Therefore, the main aim must be to get homozygosity fast, while reserving selection pressure for later generations in such crosses. The single seed descent breeding method [15] in which populations could be fast advanced to homozygosity by raising 2-3 generations per year seems more appropriate.

It is interesting to note that the local collection of soybean LBS (Local Black Soybean), though not showing significant gca effect for yield, gave high and significant positive sca effects for yield and yield contributing characters in combination with parents KHSb-2 and DS74-62, exhibiting high gca effects for these traits. Hence, it is not necessary that parents having higher estimates of gca effects would also give higher sca effects.

The results also show that different crosses are promising for different characters. In order to utilize them effectively, an inter-se crossing of desirable F1s in all possible combinations may be an alternative strategy. Such multiple parent input into a central gene pool will effect speedy recombination and will also help in breaking strong genetic barriers if present. At F5 or F6, selection should be applied to whole populations across environments for extracting superior lines.

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