

COMBINING ABILITY ANALYSIS IN SOYBEAN

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ABSTRACT

Combining ability analysis was conducted for yield components and quality attributes in soybean (*Glycine max* (L.) Merr.). Both additive as well as nonadditive gene effects were present. However, the ratio of nonadditive/additive gene effects showed the preponderance of nonadditive gene action for the expression of all the 14 traits under study. The genotypes viz. PK 416 and Pk 564 were the best general combiners for most of the yield and quality traits. The high performing crosses for important characters like pods per plant, yield per plant, oil content and protein content showed that in general these crosses involved low x low, medium x low and high x low general combiners. The low x low crosses giving high sca values may be due to the genetic diversity of the parents and non allelic interaction.

Key words: Soybean, combining ability, gene effects.

The choice of the parents in the hybridization programme is of immense importance for getting better segregants in crop like soybean where hybridization followed by pedigree method is most commonly used. The information on additive and nonadditive effects associated with yield and quality traits in soybean is scanty [1, 2]. Keeping in view the importance of soybean crop as a rich source of vegetable oil and protein, the present investigation was undertaken to assess the nature of gene action involved in the inheritance of grain yield and its components along with quality traits. One other objective was to identify the best general combiners for different traits and also the best cross combinations having high sca effects which can be exploited by pedigree method of selection for the improvement of various characters in soybean.

MATERIALS AND METHODS

Nine diverse genotypes of soybean viz. SL 96, SL 152, SL 160, PK 416, PK 472, PK 564, DS-75-12-1 of Indian and F 87-3065 and F 87-3095 of USA origin were crossed in a diallel mating pattern. The 36 F₁s were grown to produce F₂ seed. The 36 F₂s along with the 9

parents were grown in a randomized complete block design with three replications. Data were recorded on 14 quantitative traits on ten randomly selected plants (Table 1). Total oil content of dry seeds was determined by nuclear magnetic resonance (NMR) technique [3]. Different fatty acids (palmitic, stearic, oleic, linoleic and linolenic) were determined by gas liquid chromatography after converting different fatty acids into their respective esters [4]. Protein content was estimated by the Kjeldahl's method. The combining ability analysis was conducted following [5].

RESULTS AND DISCUSSION

The analysis of variance showed that the differences among the 45 genotypes were significant for all the 14 traits thereby indicating the presence of genetic variability in the material under study (Table 1). A perusal of Table 2 revealed significant differences due to general and specific combining ability for all the traits under study. This showed that both additive as well as nonadditive gene effects were important for the expression of these traits. However, the ratio of non additive/additive variance showed that the nonadditive type of gene effects were more important in the expression of these traits (Table 2). Similar results have also been reported by [6, 7]. However, [8] reported the importance of additive gene action for protein, oil and its components in F₂ population in soybean.

For grain yield per plant which is the most important economic trait, PK 564 was the best general combiner. It was also a high general combiner for quality traits namely, oil, protein and fatty acid content (Table 3). Moreover, it was a poor general combiner for earliness. PK 416, a popular soybean variety of Punjab was another good general combiner for yield as well as other traits except linolenic acid, an important unsaturated fatty acid which determines oil quality and its stability [9, 10]. The genotypes, viz. F 87-3065 and F 87-3095 were desirable for low linolenic acid. The large number of low x low and low x medium general combiners which resulted in the high specific combining ability effects among the top ranking crosses are of great importance as such combinations could throw desirable transgressive segregants if the additive effects of one parent and complimentary epistatic effects of the other parent act in the same direction for maximum expression of the traits. The results are in agreement with those of [11] in groundnut.

A perusal of sca effects of the promising crosses for important traits viz. pods per plant, yield per plant, oil content and protein content (Table 4) showed that generally low x low, medium x low and high x low general combiners had high sca values. Similarly for grain yield per plant, a cross between F 87-3065 x SL 96 had the positive sca value followed by F 87-3095 x SL 96. In both these crosses indiginous as well as exotic strains are involved. Hence, the highest sca values seem to be the contribution of genetic diversity among the

Table 1. Analysis of variance (mean squares) for different characters in a diallel cross of soybean

Source	d.f.	Plant height	Bran-ches per plant	Pods per plant	100-seed weight	Yield per plant	Days to flower	Days to maturity	Oil content	Protein content	Palm-itic acid	Stearic acid	Oleic acid	Lino-leic acid	Lino-leic acid
Treatments (crosses+parents)	44	136.0**	2.64**	224.6**	1.09**	3.34**	6.75**	30.69**	2.51**	15.37**	1.91**	0.086**	4.11**	5.81**	0.01**
Error	88	0.80	0.14	2.0	0.02	0.06	0.96	1.98	0.14	0.84	0.09	0.004	0.12	0.27	0.01

**Significant at 1% level.

Table 2. Analysis of variance (mean squares) of combining ability for different characters in 9 x 9 diallel cross of soybean

Source	d.f.	Plant height	Bran-ches per plant	Pods per plant	100-seed weight	Yield per plant	Days to flower	Days to maturity	Oil content	Protein content	Palm-itic acid	Stearic acid	Oleic acid	Lino-leic acid	Lino-leic acid
Gca	8	1061.7**	26.8**	1691.4**	79.5**	49.0**	1910.6**	9689.8**	288.9**	992.9**	100.1**	3.18**	375.0**	34.7**	1894.1**
Sca	36	934.3**	18.5**	1274.7**	65.8**	30.8**	1803.2**	8593.7**	261.1**	985.5**	90.9**	3.36**	384.1**	32.2**	1729.4**
Error	88	0.83	0.05	0.67	0.01	0.02	0.32	0.70	0.05	0.28	0.02	0.001	0.04	0.004	0.09
σ^2_g		96.44	2.43	153.70	7.22	4.45	173.60	880.80	26.26	90.23	9.09	0.29	34.08	3.15	172.18
σ^2_s		933.47	18.45	1274.03	65.79	30.78	1802.88	85.93	261.05	985.72	90.88	3.36	384.06	32.19	1729.31
σ^2_s/σ^2_g		9.68	7.59	8.29	9.11	6.91	10.38	9.75	9.94	10.91	9.99	11.62	11.26	10.22	10.04

**Significant at 1% level.

Table 3. Estimates of gca for different characters in soybean varieties

Parent	Plant height	Branches per plant	Pods per plant	100 seed weight	Yield per plant	Days to flower	Days to maturity	Oil content	Protein content	Palmitic acid	Stearic acid	Oleic acid	Linoleic acid	Linolenic acid
PK 564	14.26*	2.46*	17.52*	3.88*	3.24*	18.75*	42.37*	6.63*	15.84*	4.62*	0.77*	8.43*	19.98*	-2.48*
PK 416	9.14*	1.29*	14.90*	3.21*	2.59*	14.75*	33.79*	6.15*	8.81*	3.05*	0.64*	5.83*	14.99*	2.01*
PK 472	7.34*	1.44*	7.76*	2.10*	1.16*	10.02*	23.75*	4.41*	5.37*	1.79*	0.36*	3.64*	9.18*	1.32*
SL 160	2.68*	0.85*	8.59*	0.93*	0.93*	4.81*	9.98*	1.84*	3.53*	1.20*	0.19*	3.69*	2.98*	0.72*
SL 152	0.94*	-0.21*	-6.10*	-0.37*	-0.42*	0.32*	-1.05*	-0.05	-0.62*	0.28*	0.01	0.12*	-0.24*	0.05*
DS-75-12-1	-0.05	-0.27*	-6.21*	-1.33*	-1.05*	-5.92*	-11.84*	-2.29*	-2.32*	-0.69*	-0.17*	-2.23*	-4.80*	-0.70*
F 87-3095	-7.50*	-1.28*	-6.75*	-1.92*	-1.33*	-9.10*	-21.33*	-3.60*	-7.10*	-2.52*	-0.44*	-4.27*	-9.23*	-1.36*
F 87-3095	-11.40*	-1.81*	-13.37*	-2.80*	-2.33*	-14.19*	-32.08*	-5.67*	-10.19*	-3.28*	-0.60*	-6.37*	-13.94*	-1.95*
SL 96	-15.40*	-2.17*	-16.34*	-3.71*	-2.79*	-19.43*	-42.99*	-7.43*	-13.89*	-4.45*	-0.75*	-8.76*	-18.91*	2.58*
S.E. (g)	0.26	0.06	0.23	0.02	0.04	0.16	0.23	0.62	0.15	0.05	0.01	0.06	0.08	0.02
CD 5%	0.50	0.11	0.45	0.04	0.08	0.31	0.45	0.12	0.29	0.09	0.02	0.11	0.16	0.003

**Significant at 1% level.

Table 4. Specific combining ability effects of selected crosses for important traits in soybean

Yield per plant	Pods per plant	Oil content	Protein content
F 87-3065 x SL 96 (L x L)	DS 75-12-1 x SL 96 (L x L)	F 87-3065 x SL 96 (L x L)	F 87-3065 x SL 96 (L x L)
F 87-3095 x SL 96 (L x L)	F 87-3065 x SL 96 (L x L)	F 87-3095 x SL 96 (L x L)	DS 75-12-1 x SL 96 (L x L)
DS 75-12-1 x SL 96 (M x L)	F 87-3095 x SL 96 (L x L)	F 87-3095 x F 87-3065 (L x L)	F 87-3095 x SL 96 (L x L)
F 87-3095 x F 87-3065 (L x L)	SL 152 x SL 96 (L x L)	DS 75-12-1 x SL 96 (L x L)	F 87-3095 x F 87-3065 (L x L)
SL 152 x SL 160 (M x L)	PK 472 x F 87-3065 (M x L)	SL 152 x SL 96 (M x L)	DS 75-12-1 x F 87-3065 (L x L)
SL 152 x F 87-3095 (M x L)	PK 416 x F 87-3065 (H x L)	DS 75-12-1 x F 87-3065 (L x L)	SL 152 x SL 96 (M x L)
PK 416 x F 87-3065 (H x L)	SL 160 x SL 152 (M x L)	SL 152 x F 87-3065 (M x L)	DS 75-12-1 x F 87-3095 (L x L)
SL 160 x SL 96 (M x L)	SL 160 x SL 96 (M x L)	SL 160 x SL 96 (M x L)	SL 160 x SL 96 (M x L)

L—low, M—medium, H—high general combiners.

parents. Therefore, the crosses between diverse parents having high sca values may further be exploited through pedigree method of selection to derive the desirable segregants for different traits so as to evolve superior genotypes.

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