



Generation means analysis for seed yield and its components in soybean [*Glycine max* (L.) Merrill]

S. R. Maloo and Sandeep Nair

Department of Plant Breeding and Genetics, Maharana Pratap Univ. of Agril. and Technology, Udaipur 313 001

(Received: October 2004; Revised: June 2005; Accepted: June 2005)

Generation means analysis of three crosses, Monetta \times PK 472, JS 80-21 \times MACS 58 and PK 416 \times NRC 12 involving six parents of diverse pedigree, origin and agro-climatic adaptations of soybean [*Glycine max* (L.) Merrill] was carried out for seed yield and its components characters. Six generations viz., P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 of three crosses were grown in randomized block design with three replications during *khari*, 2000 under rainfed conditions at the Instructional Research Farm, Maharana Pratap University of Agriculture and Technology, Udaipur. Seeds were dibbled in 5m long rows with spacing of 60 \times 20cm between rows and plants, respectively. Parents and F_1 s were planted in single row plot while F_2 and backcross generations were grown in 2 rows. Fertilizers were applied @ 40:20:0 N, P_2O_5 and K_2O Kg/ha. Recommended agricultural practices and plant protection measures were followed to raise healthy crop. Observations on days to flower, days to maturity, plant height, braches/plant, pods/plant, pods/cluster, pod length, seeds/pod, 100-seed weight, seed: pod weight ratio, height of pod insertion, biological yield/plant, seed yield/plant and harvest index were recorded on 10 randomly selected competitive plants in non-segregating generations while 20 plants in F_2 and backcross generations in each replication. The scaling tests A, B, C and D [1] and joint scaling test [2] were computed for all the fourteen characters in three crosses to test the adequacy of the additive-dominance model. The gene effects and interactions for each character were estimated after Hayman [3].

Out of four scaling test at least one or two scale were found significant in all the three crosses for most of the characters. This indicated the presence of digenic/epistatic interactions [4,5].

The estimates of means (m) was highly significant for all the characters in all the crosses. The dominance component (h) was significant and greater in magnitude than additive effect (d) for pods/plants, pods/cluster, seeds/pod 100-seed weight, seed yield/plant and biological yield/plant in all the crosses, while it was

recorded significant for plant height in the crosses JS 80-21 \times MACS 58 and PK 416 \times NRC 12, seed: pod weight ratio in Monetta \times PK 472 and PK 416 \times NRC 12 and for days to maturity and harvest index in Monetta \times PK 472 and JS 80-21 \times MACS 58. However, for the traits days to flowering and height of pod insertion dominance component was significant only in the cross JS 80-21 \times MACS 58. This indicated predominant role of dominance gene action in controlling these above traits. Importance of the dominance gene effects in soybean has been reported in the inheritance of days to flowering and 100- seed weight [4], plant height and seed yield/plant [5], pods/plant, seeds/pod and harvest index [6].

Among the digenic interaction effects, both additive \times additive (i) and dominance \times dominance (l) were significant for pods/cluster in the cross JS 80-21 \times MACS 58 and PK 416 \times NRC 12, for height of pod insertion in Monetta \times PK 422 and PK 416 \times NRC 12. Estimates of gene effects recorded in three crosses for important characters are presented in Table 1. Additive \times additive (i) interaction was observed significant for plant height and seeds/pod in the crosses Monetta \times PK 472 and PK 416 \times NRC 12 and seed: pod weight ratio in the cross Monetta \times PK 472 only. Dominance \times dominance (l) type of interaction was found to be significant for pods/plant in the crosses Monetta \times PK 472 and JS 80-21 \times MACS 58. While it was observed to be significant for seeds/pod in the cross JS 80-21 \times MACS 58 only.

Additive \times dominance (i) non-allelic type of interaction was found significant for pod length in the crosses Monetta \times PK 472 and JS 80-21 \times MACS 58, for seed: pod weight ratio in the crosses JS 80-21 \times MACS 58 and PK 416 \times NRC 12. While it was observed significant for the traits like pods/cluster, seeds/pod and height of pod insertion in the cross PK 416 \times NRC 12 and for 100-seed weight in the cross JS 80-21 \times MACS 58.

Table 1. Estimates of gene effects for important characters in soybean

Cross	Parameters	Characters						
		Days to flowering	Plant height (cm)	Pods/plant	100-seed weight (g)	Seed yield/plant (g)	Biological yield/plant(g)	Harvest index (%)
Monetta × PK 472	m	43.33±0.33**	44.67±1.76**	80.33±1.45**	9.33±0.33**	16.83±0.31**	51.00±1.00**	-
	d	-1.00±0.57	-3.00±3.03	-0.67±2.62	-0.67±0.47	-0.69±0.30	-1.67±1.79	-0.26±0.44
	h	2.33±1.82	9.50±9.69	31.49±8.07**	4.00±1.69*	7.08±1.45**	16.67±5.55**	3.10±0.89**
	i	4.67±1.76*	2.00±9.30	18.67±7.83**	2.67±1.63	4.46±1.41**	10.00±5.37	2.17±0.89*
	j	-1.67±0.66*	-1.83±3.34	3.16±2.75	-0.33±0.57	-0.18±0.37	-	-0.27±0.44
	l	-8.67±2.82*	25.00±15.06	26.34±12.62*	-2.67±2.49	-7.36±1.90**	-6.67±8.89	-9.70±1.79**
JS80-21 × MACS 58	m	43.67±0.33**	38.33±1.85**	76.33±4.09**	9.33±0.33**	16.70±0.30**	51.67±1.67**	32.32±0.05**
	d	-0.67±0.67	-1.34±2.40	-4.00±2.21	0.67±0.47	-0.70±0.43	-1.67±1.56	-0.25±0.44
	h	4.67±1.97*	40.67±9.40**	57.34±17.10**	3.83±1.66*	8.67±1.57**	16.67±7.48*	6.10±0.98**
	i	6.67±1.88*	33.33±8.84**	33.34±16.97**	2.67±10.63	6.20±1.47**	9.99±7.36	5.47±0.92**
	j	-1.67±0.88*	0.67±2.68	1.00±2.65	1.17±0.47*	-1.00±0.43	-	-0.14±0.47
	l	-12.00±3.19*	-17.33±13.72	48.00±19.09	-2.34±2.40	-7.47±2.37**	-6.67±9.52	-9.89±1.91**
PK 416 × NRC 12	m	44.67±0.33**	40.00±1.73**	72.33±2.60**	9.67±0.33**	16.40±0.35**	52.33±1.20**	31.33±0.51**
	d	1.00±0.75	-2.67±2.26	-7.67±3.01	0.33±0.33	0.60±0.46	-2.00±2.05	2.22±0.05**
	h	-0.67±2.05	37.50±8.43**	74.33±12.5**	3.33±1.56*	5.31±1.69**	19.17±6.44*	-1.14±2.16
	i	0.67±2.00	25.33±8.27**	54.00±12.03**	1.99±1.49	3.47±1.67	12.00±6.32	-0.44±2.08
	j	-1.33±0.81	-0.50±2.67	-8.67±6.52	0.67±0.47	0.08±0.51	-0.17±2.08	0.14±0.49
	l	-3.99±3.39	-4.33±11.86	10.00±16.29	-2.67±2.10	-4.10±2.36	-10.33±9.84	-1.48±2.41

*Significant at 5% level, ** Significant at 1% level, and - Indicate absence of estimates

The magnitude of additive × additive (i) and dominance × dominance (l) interaction was more than that of additive × dominance (j) for most of the characters in all the three crosses. Complementary epistasis was observed for pods/plant and pod length which appeared to be desirable and would be helpful in further improvement of these traits [5]. Duplicate gene action was observed for most of the characters which indicated hindrance in selection improvement. In this situation reciprocal recurrent selection is likely to be useful for the effective utilization of both types of additive and non-additive gene effects simultaneously [7].

References

1. **Mather K.** 1949. Biometrical Genetics. Dover Publication Inc. New York, USA.
2. **Cavalli L. L.** 1952. Analysis of linkage in quantitative inheritance. In: Quantitative inheritance (eds. E.C.R. Rieve and C.H. Waddington) HMSO, London: PP 135-144.
3. **Hyman B. I.** 1958. The separation of epistasis from additive and dominance variation in generation mean, *Heredity*, **12**: 371-391.
4. **Choukan R.** 1996. Genetical analysis of different characters in segregating populations in soybean [*Glycine max* (L.) Merrill]. *Seed and Plant*, **12**: 7-11.
5. **Raut V. M., Taware S. P. and Halvankar G. B.** 2000. Gene effects for some quantitative characters in soybean (*Glycine max*) crosses. *Indian J. agric. Sci.*, **70**: 334-335.
6. **Srivastava A. N. and Jain J. K.** 1994. Variability and coheritability estimates for physiological and economic attributes in soybean. *Indian J. Genet.*, **54**: 179-183.
7. **Comstock R. E., Robinson H. F. and Harvey H. H.** 1949. A breeding procedure designed to make maximum use of both general and specific combining ability. *Agron. J.*, **41**: 360-367.