

## GENETIC ARCHITECTURE OF PROTEIN CONTENT IN PEA

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### ABSTRACT

Genetic analysis of generation means was conducted in five crosses of pea for protein content. F1 mean was lower than better parent or near to mid parent value in most of the crosses. Additive gene effects were important and significant for all the crosses. Among epistasis, additive x additive was the most important. The recurrent selection approach was suggested for improvement of this trait.

Pulses play an important role in meeting the quantitative and qualitative protein requirement of humanity. Pulses constitute an important ingredient of Indian vegetarian diet and helps in balancing the nutritive quality of staple grain like rice and wheat. Very limited genetic information is available on protein content in pea. An attempt was made to study the genetic make up of protein content in pea.

### MATERIALS AND METHODS

The material consisted of seven diverse genotypes viz., Bonneville, selection-35, A.F., R-839, R-1038, R-177 and 6587-1 and their five F1s, five F2s and five F3s. The experiment was subdivided in five individual experiments and a set of five experiments was sown in a replicated trial with three replications at Udaipur. Grains of all available selected plants were bulked replication wise and two composite samples were taken from each replication. The protein content was determined by using micro-kjeldahl's method (Anonymous, 1955) The analysis of variance was carried out, separately for each cross under study as suggested by Panse and Sukhame (1985) to test the differences among generations. Hayman (1958) approach was followed for estimation of five genetic components of variation namely, m (mean), d (additive), h (dominance), i (additive x additive) and l (dominance x dominance) from the population means assuming absence of linkage and higher order epistasis.

### RESULTS AND DISCUSSION

An analysis of variance for generation means comprising five generations viz., P1, P2, F1, F2 and F3 was computed for each cross. The mean sum of squares due to treatments were significant in all the crosses except R-839x R-177. The mean values for protein content of all five crosses in different generations are presented in Table 1. The results of generation means analysis indicated that protein content *per se* revealed significant differences between parents in all the crosses under study, suggesting presence of genetic variability in parents. F1 means were lower than better parents or near to mid parent values in most of the crosses and in some crosses even lower than lower protein containing parents. These results were in conformity with those reported by Pandey and Gritton (1975). F2 and F3 population showed comparatively higher protein percentage than hybrid population.

Estimates of gene effects (Table 2) clearly indicated that additive gene effects were more important than dominance deviation. Additive gene actions were significant in all the crosses. Role of additive type of gene action in the inheritance of protein content was also reported by Sandhu (1984). Dominance gene action were significant in crosses A.F. x 6587-1 and 6587-1 x R-1038. Gupta et al. (1984) emphasized role of both additive and non-additive gene action in the inheritance of protein content. The intermediate mean values of F1s between the two

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Table. 1 Mean performance of five generations for protein content in pea.

Cross	Generation					Mid Parent	C.D. at 5%
	P <sub>1</sub>	P <sub>2</sub>	F <sub>1</sub>	F <sub>2</sub>	F <sub>3</sub>		
Bonneville x Selection -35	22.24±0.06	23.14±0.04	21.17±0.07	22.14±0.08	21.79±0.08	22.69	0.38
Bonneville x 6587-1	22.49±0.41	18.46±0.31	20.98±0.29	21.77±0.17	22.02±0.24	20.47	1.73
A.F. x 6587-1	25.13±0.27	20.56±0.42	23.62±0.31	23.80±0.26	22.12±0.20	22.84	2.32
6587-1 x R-1038	19.78±0.29	25.14±0.40	21.49±0.33	23.09±0.22	23.80±0.14	22.31	2.12
R-839 x R-177	19.68±0.29	22.53±0.37	19.12±0.44	20.31±0.26	21.12±0.30	21.10	1.90

Table.2 Estimates of gene effects for protein content in five crosses of pea.

Cross	Gene effect					Type of epistasis
	m	d	h <sub>b</sub>	i <sub>i</sub>	l <sub>i</sub>	
Bonneville x Selection -35	22.14**±0.28	-0.45**±0.15	0.48±0.95	1.20±0.94	-5.25±0.80	D
Bonneville x 6587-1	21.71**±0.41	2.01**±0.42	-1.19±1.58	1.95±1.61	-0.77±4.44	C
A.F. x 6587-1	23.80**±0.51	2.28**±0.41	4.36**±1.61	8.15**±1.69	-9.44±4.95	D
6587-1 x R-1038	23.09**±4.47	-2.68**±0.41	-2.96**±1.42	-7.35**±1.56	-0.48±4.51	C
R-839 x R-177	20.31**±0.51	-1.42**±0.40	-2.95±1.83	-3.82±1.82	1.15±5.31	D

\* Significant at P = 0.05 \*\* Significant at P = 0.01 D = Duplicatory Epistasis C = Complimentary Epistasis

parents also revealed the prevalence of additive genetic control for this trait. Among interaction, only i component (additive x additive) was significant. The prevalence of additive x additive gene effects along with prominent additive effects would imply some scope for selection in segregating generations.

Considering the best procedure to be used in breeding for high protein content, in the present case, it is advisable to use recurrent selection by way of intermating the most desirable segregates alternatively with selection.

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