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GENE ACTION FOR YIELD AND ITS COMPONENTS IN GRASSPEA

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ABSTRACT

Gene action for yield and its components was studied in three crosses of grasspea using generation mean analysis. Both additive and non-additive gene effects were involved in the expression of number of primary branches, pods per plant and grain yield per plant. Plant height was found to be predominantly under the control of dominance gene effect. Simultaneous utilization of both additive and non-additive genetic effects can be achieved by intermating of segregants in early segregating generation.

Key words: *Lathyrus sativus*, Gene action, generation means, yield components

Although grasspea is considered as a model crop for sustainable agriculture with great future, relatively little efforts have been made in the past to improve it. The main reason has been its neurotoxic potential in human beings and animals which leads to lathyrism. Now, the development of certain low β-N-Oxalyl-L-α β-diamino propionic acid (ODAP) genotypes have opened a new avenue in grasspea research and development.

Yield being a complex character is a sum-total and ultimate result of interaction of several component characters. Knowledge of the relative magnitude of additive and non-additive gene action forms the guidelines for handling the segregating material from crosses. The present investigation was undertaken to study the nature and magnitude of gene effects in respect of grain yield and yield contributing characters, viz., plant height, number of primary branches, pods per plant and seeds per pod in three crosses of grasspea.

MATERIALS AND METHODS

The material comprised three crosses P 24 × Bio R 202; LSD 3 × Bio L 212 and Bio R 202 × P 28 involving five low ODAP parents. The details of parents involved in the crosses alongwith their ODAP content are listed in Table 1. The experiment with six generations (P_1, P_2, F_1, F_2, B_1 and B_2) was conducted at Research farm of Indian Institute of Pulses Research, Kanpur during the *rabi* 1996-97. The experimental material was sown in a completely randomized block design with three replications, each having one row of P_1, P_2 and F_1; two rows of B_1 and B_2 and six rows of F_2. Each row was of 3 m length, 30 cm apart and plant to plant distance of 5 cm. From each replication data for plant height, number of primary branches, pods per plant, seeds per pod and grain yield per plant were recorded on five randomly selected plants from parental and F_1 generation, 15 plants from backcrosses and 30 plants from F_2 generation. Generation mean analysis [1] was adopted to estimate the contributions of gene effects. In the absence of non-allelic interaction, m, d and h components were estimated following Jinks & Jones [2].

Table 1. Pedigree and ODAP content of grasspea genotypes involved in the crosses studied

S. No.	Genotypes	ODAP (%)	Pedigree
1.	P 24	0.277	Selection from Germplasm
2.	LSD 3	0.297	Selection from P 24
3.	P 28	0.191	RED × P 24
4.	Bio R 202	0.077	Somaclone developed from P 24
5.	Bio L 212	0.093	-do-

RESULTS AND DISCUSSION

It is evident from scaling test [3] that all three scales were non-significant (Table 2) for seeds per pod in all the three crosses; for number of primary branches in LSD 3 × Bio L 212 and Bio R 202 × P 28; for pods per plant in P 24 × Bio R 202 and for plant height in LSD 3 × Bio L 212 which do not preclude the absence of higher order interactions. However, atleast two scales were significant in pods per plant in Bio R 202 × P 28 and one of the scales was significant for rest of the cases, indicating inadequacy of simple additive dominance-model and presence of epistasis.

Plant height was predominantly under the control of non-additive gene effects with duplicate type of gene interaction in P 24 × Bio R 202 and Bio R 202 × P 28. The l type of component of gene interaction was positive and highly significant in these crosses suggesting greater role of dominance × dominance effects in the expression of the character. Also, the negative sign of additive × additive (i) component in these two crosses makes it obvious that selection should be deferred to later generations when desirable recombinants become available for this character.

Both fixable and non-fixable gene effects were important for the expression of primary branches in the cross P 24 × Bio R 202 predominantly with duplicate type of gene interaction, however, magnitude of 'h' and 'l' component was higher indicating

Table 2. **Estimates of six parameters of five characters in three crosses of grasspea**

Cross	Scale			Genetic components						Type of epistasis
	A	B	C	m	d	h	i	j	l	
Plant height										
C1	-9.78	-21.30**	-1.76	47.83	3.86	-34.98**	-29.32**	5.76	60.44**	Duplicate
C2	-9.17	-9.63	20.62	77.52	-0.90	-92.61**	-	-	-	-
C3	-12.80*	-25.68	-24.28	40.93	5.84	-27.40*	-14.2	6.44	52.68**	Duplicate
No. of primary branches										
C1	1.76**	0.58	1.12	2.30	0.79**	2.06*	1.22	0.59	-3.56**	Duplicate
C2	1.26	1.53	0.38	1.20	0.05	7.72**	-	-	-	-
C3	0.71	-0.71	-1.30	1.20	-1.20**	3.05	-	-	-	-
Pods per plant										
C1	8.20	-0.09	2.57	21.89	9.83*	21.39	-	-	-	-
C2	-3.65	19.95	-26.78*	18.73	-9.00	58.73**	43.08**	-11.8	-59.38*	Duplicate
C3	26.37*	-20.03	-50.22**	25.03	6.80	63.73**	56.56**	23.20*	-62.89	Duplicate
Seeds per pod										
C1	0.67	-0.08	0.08	2.28	-0.12	1.89	-	-	-	-
C2	0.46	0.41	-0.06	2.05	-0.06	5.86**	-	-	-	-
C3	0.01	-0.29	-0.46	2.85	-0.11	0.41	-	-	-	-
Yield per plant										
C1	3.32	-1.24	-9.98**	3.53	3.65*	12.29**	12.06**	2.28	-14.14	Duplicate
C2	-1.83	0.64	-8.69**	3.23	-1.65	10.15**	7.50**	-1.23	-6.31	Duplicate
C3	-3.47	-4.87	-12.70**	4.76	-1.20	7.35*	4.36	0.70	3.98	Complementary

*,*Significant at P = 0.05 and = 0.01, respectively

C1 - P 24 × Bio R 202; C2 - LSD 3 × Bio L 212; C3 - Bio R 202 × P 28 predominance of non-additive gene effects. In LSD 3 × Bio L 212, the expression of this character was under the control of dominant type of gene effect while in Bio R202 × P 28, the additive component was pronounced. Pods per plant was predominantly under the control of dominance effect in LSD 3 × Bio L 212 and Bio R 202 × P 28 crosses. The signs of (h) and (l) estimates were opposite in these crosses which indicates prevalence of duplicate type of gene action which would hinder progress in selection. The additive gene effect was found important in P 24 × Bio R 202 and the additive × additive (i) component was significant with higher magnitude in the crosses LSD 3 × Bio L 212 and Bio R 202 × P 28. Selection for pod number would, therefore, be effective in early segregating generation in cross P 24 × Bio R 202 whereas for the other two crosses selection should be delayed to later generations till the fixation of sufficient epistatic interactions. Of the three crosses studied, seeds per pod was under the influence of dominant type of gene effect in cross LSD 3 × Bio L 212, whereas in other two crosses, none of the parameters was found significant.

Dominance (h) gene effect was significant for grain yield per plant in all the three crosses. However, additive (d) and additive × additive (i) components were observed to be important in two crosses. This suggests that selection for yield per plant would be more fruitful if the selection is delayed till dominance and epistatic components are reduced due to selfing. The gene effect worked out for yield and its components by various workers indicated predominance of non-additive gene action [4, 5].

Among the three crosses, duplicate type of non-allelic gene action was prevalent in two crosses, so the concerned crosses would not prove to have heterosis and new lines need to be introduced for hybridization. The cross Bio R 202 × P 28 may show considerable amount of heterosis for yield per plant as it showed complementary gene action.

The presence of non-additive gene interactions other than additive × additive type seems to be a limiting factor when the main objective is to evolve purelines. In such a situation, maximum gain could be attained by maintaining considerable heterozygosity through mating of selected plants in early segregating generations or if some form of recurrent selection is practiced [6-7]. Intermating of segregants in early segregating generations would certainly enhance the possibility of various recombinants which may result in the accumulation of favourable genes in the ultimate homozygous line with higher grain yield. Therefore, few cycles of recurrent selection followed by pedigree breeding or population improvement approach will be effective in the improvement of yield in grasspea.

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