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GENETIC ANALYSIS OF PROTEIN CONTENT IN MUNGBEAN (*VIGNA RADIATA* L. WILCZEK)

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ABSTRACT

Mungbean is an excellent source of high quality and easily digestible protein. However, its seed productivity and percentage of protein are rather low in India. Hence detailed genetic analysis of protein content was undertaken on four selected high yielding crosses of mungbean. Protein percentage in seed being a polygenic trait coupled with the fact that maternal genetic constitution by itself or along with filial constitution determine the seed protein, presence of large nonadditive gene action makes the task of improving this trait very difficult.

Key words: *Vigna radiata*, protein percentage, genetic analysis.

Mungbean is an excellent and cheap source of high quality and easily digestible protein. However its seed productivity (5q/ha) and protein percentage (18% - 22%) are rather low in India. In developing countries inadequate protein availability has been identified as the major cause of widespread malnutrition among the less privilaged classes of society. Genetic improvement of protein content in pulses becomes very important in view of predominantly vegetarian habit of Indian people. Genetic analysis of protein content therefore was undertaken in four crosses of mungbean selected on the basis of their high yield productivity out of a 7 × 7 half, diallel cross.

MATERIAL AND METHODS

The pedigree of the parents involved in selected crosses is given below :

Parent line	Pedigree
PS-16	An IARI, New Delhi selection from Iran germplasm
Pusa-105	An IARI selection from a double cross.
Hyb. 12-4-2	Selection made from a land race of Orrisa
ML-267	PAU, Ludhiana selection.
11/395	Selection from RAU, Dholi, Bihar.

The crosses with high mean performance were selected for detailed genetic analysis. Half of the bulk seed from F_2 of the selected crosses was advanced upto F_3 generation following random bulk procedure. The parents, F_1, F_2 and F_3 generations were raised together in a compact family block design with three replications at IARI field in New Delhi to record data for generation mean analysis [1]. Protein analysis of these crosses in F_1, F_2, F_3 and parental generations was done by Micro kjeldahl method as described by Tewari [2]. The samples for protein analysis were taken from grinded bulk seed of five plants per replication in the parents and F_1 generations and of 200 plants per replication in F_2 and F_3 generations.

RESULTS AND DISCUSSION

The generation mean data (table 1) for the four crosses of mungbean for protein content was analysed for gene action (table 2) following Hayman (1958) model [1].

Table 1. Generation means for protein content (%) in four selected crosses of mungbean.

Cross / Generation	PS-16 × Hyb. 12-4-2	Pusa-105 × ML-267	11/395 × ML-267	Hyb. 12-4-2 × ML267
P_1	27.43	26.58	26.63	26.79
P_2	26.79	27.40	27.40	27.40
F_1	29.33	25.28	31.98	28.00
F_2	26.40	27.12	28.15	25.00
F_3	26.42	26.58	28.07	30.47
S.E.	0.37	0.57	0.25	0.57

PS-16 × Hyb. 12-4-2 : For this cross only dominance effect was highly significant and positive. Among interactions, additive × additive component (i) was highly significant.

Pusa-105 × ML-267 : Inspite of absence of significant differences among means of different genertions, the additive effect — (d), the dominance effect (h) and the additive × additive interactions (i) were highly significant.

11/395 × ML-267 : Here all the main effects and digenic interactions were significant. The dominance effect was negative, while the additive × additive and dominance × dominance interactions were positive.

Hyb. 12-4-2 × ML-267 : For this cross additive effect (d), dominance effect (h) and additive × additive interaction (i) were highly significant.

Table 2. Generation mean analysis for protein content in four selected crosses of mungbean (Five parameter model, Hayman., 1958)

Cross / Parameter	PS-16 × Hyb. 12-4-2	Pusa-105 × ML- 267	11/395 × ML-267	HYb. 12-4-2 × ML-267
$\hat{m}$	90.30 ± 0.70	52.80 ± 0.95	19.80 ± 0.44	80.00 ± 1.00
$\bar{d}$	-2.60 ± 1.95	28.10** ± 2.81	3.05* ± 1.23	-33.00* ± 2.83
$\hat{h}$	169.00** ± 2.38	60.13** ± 3.39	-8.47** ± 1.48	120.13** ± 3.40
$\hat{i}$	119.80** ± 3.06	74.53** ± 4.35	19.12** ± 1.91	139.63** ± 4.37
$\hat{j}$	-8.09 ± 6.98	-1.73 ± 9.93	98.93** ± 4.35	-4.01 + 9.98

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

It will be pertinent to discuss here some aspects specific to determination of protein in seed before discussing the results of its genetic analysis. The main consideration arises from the fact that the F_1 embryo is actually borne on the mother plant belonging to the parental generation and seeds on F_1 plants carry F_2 embryo and the same holds true for the subsequent generations. There is also the possibility of cytoplasmic effects being involved in the trait. Being a polygenic trait coupled with the fact that maternal genetic constitution by itself or along with filial constitution determines the protein percentage in the seed [3-6], the presence of large non-additive genetic effects in the four crosses masking the selection process will make the task for genetic improvement in this trait very difficult.

The analysis of variance for protein content had indicated that generation mean differed significantly except in the cross Pusa- 105 × ML-267. It was interesting, however, to note that even in this cross the three genetic components namley d, h and i were highly significant. The anamolous behaviour can be explained if we presume that the polygenes carried in the two parents Pusa- 105 and ML-267 may be in a dispersed state, and although the mean of the parents did not differ, the genetic backgrounds of the parents for protein content may be divergent.

The measure of additive component (d), was significant in all the crosses except in the cross PS-16 × Hyb. 12-4-2, while the additive × additive component ($\bar{i}$) was significant in all the four crosses. $\bar{d}$, being a joint estimate of d, the additive effect, and j, the additive × dominance interaction in absence of backcross generations is therefore, an overestimate of d, when d and j have the opposit signs, while it is an underestimate when they have the same sign. Viewed from this angle the significant value of $\bar{d}$ must be studied in conjunction with the fixable interaction component

(i). The dominent component ($\bar{h}$) was significant in all the four crosses. In case of PS-16 × Hyb. 12-4-2, (h) was negative while in cross Pusa 105 × ML-267 and Hyb. 12-4-2 × ML-267 (h) was positive. The component 1 was found nonsignificant in three of the four crosses except in cross 11/395 × ML-267. In all the four crosses h and 1 have opposit signs indicating presence of duplicate epistasis. Generation mean analysis clearly showed the importance of fixable as well as non fixable genetic action for protein content. Similar findings were also reported earlier [4]. The nonadditive gene action can be exploited by breaking the repulsion phase linkages in segregating populations through biparental crossings and advancing the selection process to later generations. This could give a change to utilize additive × additive epistasis in favourable direction and may permit detection of superior near homozygous progenies.

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