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RESEARCH ARTICLE

GENERATION MEAN ANALYSIS OF SEED PROTEIN ARCHITECT IN MUNGBEAN (*Vigna radiata* (L.) WILCZEK)

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ABSTRACT

The generation mean analysis is commonly employed in studies of inheritance of quantitative traits. In this study, five mungbean (*Vigna radiata* L. Wilczek) hybrids were evaluated at the Plant Breeding Farm, Department of Agricultural Botany, Faculty of Agriculture, Annamalai University to record the data for generation mean analysis during March 2006 to August 2008. Mungbean like other pulse crops contributes the major source of dietary protein for the large section of vegetarian population of the world. It is also an excellent source of high protein and easily digestible protein. In India, mungbean is generally grown on marginal or sub-marginal lands, which have poor fertility status. Hence, line x tester analysis was undertaken to study in detail the genetic analysis of seed protein content among five hybrids of mungbean. It is already known that the seed protein content is a polygenetic trait coupled with the maternal or along with the filial constitution. Secondly, the presence of large number of non-additive gene action also makes the improving this trait very difficult.

INTRODUCTION

Mungbean (*Vigna radiata* (L.) Wilczek) hold an important position among the Vigna or the pulse family. It an ancient and well known crop among Asian countries for its dietary or nutritional value (Shanmugasundaram, 2004). It is also an excellent source of high quality and easily digestible protein with a seed protein content ranging from 18 to 22 percent. In the developing countries, the widespread malnutrition is attributed to the inadequate protein availability among the poor sections of the population. Genetic improvement of protein content is difficult due to the genetic make up of the crop, poor partitioning of assimilates from the source to the sink, cultivation under poor environments, low soil fertility and non-availability of photosynthates particularly during seed filling stage. Seed Protein is an important trait, but its inheritance is extremely complex and very little basic information is available on all types of gene effects/inheritance controlling the seed protein.

Epistatic effects involving genic combinations of fixed and non fixed genes are shown to contribute to the genotypic mean of any population. These effects define specific additive x additive and additive x dominant epistatic components. As such components are not estimable; their relative importance cannot be assessed (Singh Inderjit *et al*., 2006).

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These epistatic effects can cause bias in the estimates of the additive and dominance components to which they are confounded. The magnitude of the bias depends on the relative values of the epistatic effects, comparatively to deviations d and h, type of prevailing epistasis and direction of dominance. Hence, the genetic analysis was studied in five crosses of mungbean selected based on their high yield potential. Out of five lines and four testers crossed in line x tester fashion.

MATERIALS AND METHODS

The experiment was carried out at the Experimental Farm of the Plant Breeding Farm, Department of Agricultural Botany, Faculty of Agriculture, Annamalai University to record data for generation mean analysis during March, 2006 to August, 2008. The best five hybrids namely, VRMGG 1 x VBN 1, EC 30072 x VBN 1, VRMGG Local x PMB 27, LGG 450 x LGG 410 and LGG 460 x PMB 27 genotypes (varieties/lines) of mungbean were used in this experiment and were collected from Faculty of Agriculture, Annamalai University. A Randomized Complete Block Design (RCBD) with three replications was used in the experiment. The individual plot was of 3m long with three rows. The seeds were sown with a spacing 30cm row to row and 10cm plant to plant. N, P and K fertilizers @ 40-60-20kg/ha were applied as a basal dose (Rohman *et al.,* 2003) during final land preparation. The standard agronomic practices were maintained to raise a good crop. From the F_2 generation, F_3 progeny

Table 1. Generation means for seed protein content (percent) in five crosses of mungbean.

Generations Crosses	P_1	P_2	F_1	F_2	F_3
LGG 450 x LGG 410	25.83	19.60	24.80	21.29	20.89
VRMGG Local x PMB 27	21.70	15.50	26.87	21.72	21.29
LGG 460 x PMB 27	19.63	15.50	26.87	23.49	23.03
EC 30072 x VBN 1	22.73	19.63	22.63	21.11	21.42
VRMGG 1 x VBN 1	26.67	19.63	27.90	26.09	25.59

Table 2. Generation means analysis for seed protein content in five selected crosses of mungbean.

Gene effects	LGG 450 x LGG 410	VRMGG Local x PMB 27	LGG 460 x PMB 27	EC 30072 x VBN 1	VRMGG 1 x VBN 1
m	21.29 ± 0.62**	21.72 ± 0.51**	23.49 ± 0.64**	20.11 ± 0.32**	26.09 ± 0.54**
^ (d)	3.10 ± 0.73**	3.12 ± 0.08*	20.7 ± 0.52**	0.55 ± 0.73	0.52 ±0.73
^ (h)	3.45 ± 2.03*	4.58 ± 1.82*	3.48 ± 2.22**	2.40 ± 2.02	2.57 ± 1.77
^ (i)	7.58 ± 2.27**	2.69 ± 1.76	-1.68 ± 2.41	0.86 ± 2.31	-4.15 ± 2.08**
^ (l)	2.13 ± 5.88	11.45 ± 5.61**	2.54 ± 6.71	2.03 ± 6.16	2.08 ± 5.13
Epistasis	C	C	C	C	C

*, ** - Significant at P = 0.05 and P = 0.01 percent, respectively.
C – Complementary gene action

generation was developed following a random bulk procedure. Selfing of parents and the progenies were carried out in a CRBD, replicated thrice at to the record data for generation mean analysis.

Biochemical Analysis

Seed protein content of the parental and the crosses in F_1, F_2 and F_3 generations was done by Micro kjeldahl's method as described by Yoshida *et al*. (1972). 0.5 g seeds from the samples of seed protein content were taken from grinded bulk seeds of five plants per replication in the parents and F_1 and 200 plants per replication in the F_2 and F_3 generations. The protein from the defatted meal were precipitated with 10% trichloroacetic acid and recovered by centrifugation at 5000 rpm for 30 min at 4°C. The protein content was then determined calorimetrically according to the method of Yoshida *et al*. (1972) using bovine serum albumin (BSA) as standard.

RESULT AND DISCUSSION

The generations mean data (Table 1) for the five crosses of mungbean for seed protein content was analysed for gene action (Table 2) following Hayman (1958) model. In general, when quantitative characters are governed by additive or dominance gene action, the selection of hybrid can be achieved easily. However when interaction effects govern these characters, it becomes very difficult to improve the character by simple selection. The system of genetic analysis provides information on the mean effects besides on the additive, dominance and interaction effects. In self-pollinated crops like mungbean, additive component of genetic variation can be utilized for genetic improvement. Among the digenic interactions, additive x dominance (i) type is more fixable and more useful for plant breeders. Between the two types of epistatic interactions, complementary gene action could be successfully exploited in the selection programme (Sunil Kumar, 2005).

LGG 450 x LGG 410

For this cross, significant differences were observed among the means of different generations. the additive effect (d), the dominance effect (h) and the additive x additive interaction (i) were highly significant.

VRMGG Local x PMB 27

Here in this cross, all the main effects and among the digenic interactions. Dominance x dominance effect (l) was positive and significant.

LGG 460 x PMB 27

In this cross, only the main effects *viz.*, additive and dominance gene effects were significant and positive. Among the digenic interactions, additive x additive was negative and dominance x dominance was negative in nature.

EC 30072 x VBN 1 :

For this cross, all the main effects and digenic interactions were positive and non-significant.

VRMGG 1 x VBN 1 :

Among the main effects, the additive and gene effect and dominance gene effect showed positive and non-significant gene effects whereas, among the digenic interactions additive x additive (i) was negative and highly significant.

All the five crosses showed unidirectional sign for 'h' and 'l' effects indicating the presence of complementary type of gene interaction for seed protein content. Naresh Chandra and Tickoo (1998) recorded duplicated epistasis for seed protein in mungbean. As discussed above that seed protein content to be a polygenic trait governed by maternal genetic constitution and large number of non-

additive gene effects in the crosses mask the selection process as evidenced by Patil *et al*. (2001), Naresh Chandra (1989) and Jain (1978) were found to be wrong in the case of the present investigation. The present study proves that the seed protein content can be selected as all the five hybrids showed complementary gene action. The measure of additive component (d) was significant in all the crosses except EC 30072 x VBN 1 and VRMGG 1 x VBN 1 while, the additive x additive component (i) was positive and significant only in the cross LGG 450 x LGG 410 and negatively significant in the cross VRMGG 1 x VBN 1. Tiwari (1993) and Sandhu *et al*. (1994) recorded additive gene effects for protein content. The dominant component (h) was significant in LGG 450 x LGG 410, VRMGG Local x PMB 27 and LGG 460 x PMB 27. The component 'l' was found to be non-significant in all the crosses except VRMGG Local x PMB 27. Similar findings were reported by Naresh Chandra and Tickoo (1998). From the above discussions it can be concluded that the above crosses can be exploited for increasing the seed protein content in mungbean.

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