

## Generation mean analysis for yield and yield components in mungbean (*Vigna radiata* L. Wilczek)

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### SUMMARY

Using the means of  $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$  and  $F_3$  generations in each cross, estimates of various gene effects were obtained by partitioning method of weighted least square analysis of three parameter model fitted to the five generation means of each cross for twelve characters. Additive-dominance model failed in all the cases, hence five parameter model was applied which gave the information about digenic interactions between genes at different loci. The nature of gene action for seed yield and yield attributing traits were assessed in four sets of crosses involving four parents through generation mean analysis. An experiment was conducted to fulfill the objective of estimation of heterosis and to understand the genetic nature of seed yield and its contributing traits have been carried out by growing the parents,  $P_1$  and  $P_2$  along with  $F_1$ ,  $F_2$  and  $F_3$  during *Kharif*, 2006 on July 10<sup>th</sup>, 2006 in Randomized Complete Block Design (RCBD) replicated four times. A total of 4 populations (4 crosses) and 5 generations of each cross were grown. The mean data of population were subjected to joint scaling test. The results of generation mean analysis indicated varying nature of genes under different genetic backgrounds. Significant inbreeding depression also gave an indication of prevalence of dominance genetic variance along with duplicate type of epistasis for most of the characters under study. Intermating or recurrent selection would be followed for genetic enhancement of grain yield in mungbean

**Key words :** Generation mean analysis, Five parameter model, Yield, Mungbean

*Vigna*, a pantropical genus comprises about 150 species, most of which are found in Asia and Africa. Only seven species of *Vigna* are cultivated as pulse crop, of which two are African and five are of Asiatic origin, in which Mungbean (*Vigna radiata* L. Wilczek) is an ancient and well known crop in Asia particularly in the Indian subcontinent and now becoming popular in other continents (Rahman *et al.*, 2003).

Likewise other pulse crops mungbean is a short duration grain legume crops with wide adoptability, low input requirements and helps in increasing soil fertility through its nitrogen fixation and deep root system, and proved an ideal for different crop rotations, intercropping, relay cropping and as catch crop. Virtually green gram and black gram being short duration and photo-thermo insensitive can help in increasing pulse production in India. Besides, it is widely grown as food legume, over a wide range of Agro-climatic conditions like rainy, winter and summer seasons but maximum area is under *Kharif* crop. India is the largest producer of mungbean, contributing 65 per cent by area and 54 per cent by production towards global mungbean production. In India, it is cultivated in

about 2.75 million hectares with the production of 0.98 million tonnes. However, the national productivity remains low 425 kg ha<sup>-1</sup> (Pandiyan *et al.*, 2006). Low yield and poor stability remains one of the most important constraints facing in its expansion.

In Chhattisgarh, mungbean occupies approximately an area of 46.42 thousand hectares, with total production of 16.30 thousand tonnes and productivity of 351 kg ha<sup>-1</sup> (Anonymous, 2006). The low yield levels are due to several biotic and abiotic factors. The primary yield components in mungbean are pod plant<sup>-1</sup>, seed pod<sup>-1</sup> and 100 seed weight. The importance of these components mainly depends on the suitable breeding method and proper generation in the segregating population. The estimates of genetic components of variation would be very useful to adopt suitable breeding method and to find the best selection stage (generation) for the improvement of these traits (Khattak *et al.*, 2001).

### MATERIALS AND METHODS

#### Genetics of yield and its component traits:

To understand the genetic nature of seed yield and its contributing traits have been carried out by growing the parents,  $P_1$  and  $P_2$  along with  $F_1$ ,  $F_2$  and  $F_3$  during *Kharif*, 2006 on July 10<sup>th</sup>, 2006 in Randomized Complete Block Design (RCBD) replicated four times. A total of 4 population (4 crosses) and 5 generations of each cross were grown. Within each replicate, cross populations were

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