

GENETICS OF QUANTITATIVE CHARACTERS IN SUMMER MUNG BEAN
(*VIGNA RADIATA* (L.) WILCZEK VAR. *RADIATA*)

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Yield in mung bean is a complex character and is dependent on its component characters like clusters/plant, pods/plant, seeds/pod and seed weight. Singh and Singh [1] reported nonadditive gene action for yield, pods/plant, clusters/plants; and predominantly additive gene action for seed weight. The experimental material consisting of 7 generations of two summer mung bean crosses, viz. MG 46 × S.M. No. 1 and MG 28 × S. M. No. 1 was sown in RBD with three replications. Both MG 46 and MG 28 are early in maturity with good podding capacity, whereas S.M. No. 1 is late with lesser number of pods per plant. The gene effects were estimated by weighted analysis of generation means. The Cavalli's joint scaling test [2] was significant for all the characters in both crosses, except for branches and pods/plant in cross MG 28 × S. M. No. 1, indicating the inadequacy of additive—demoninance model.

In cross MG 46 × S. M. No. 1, only additive × additive (i) component was significant for clusters/plant, the nonsignificant value of d indicated dispersion of genes in the parents. The negative sign of i makes it obvious that selection should be deferred to later generations when desirable recombinants become available. The preponderance of duplicate type of epistasis was observed for pod length, pods/plant, seed weight and branches/plant. The magnitude and the signs of d and i components suggest that it would be possible to select for/longer main branches, more pods/plant, more seeds/pod and bolder seeds in advanced generations of this cross, but it may not possible to improve number of branches and clusters per plant (d and i with opposite signs). However, it may be possible to select higher yielding lines due to overall compensating mechanism of different component characters of grain yield, whereas it may be possible to select for short duration lines.

In cross MG 28 × S.M. No. 1, the 3-parameter model was adequate for branches and pods per plant only. The additive component d was significant for both the traits, whereas dominance component h was not significant. Duplicate type of epistasis (h and l having opposite signs) was indicated for main branch length and 100-seed weight. Complementary epistasis was observed for days to flowering and pod length. The nonsignificant d and significant i for main branch length, and clusters/plant indicated dispersion of genes among the parents. Component j was positive and significant for pod length and 100-seed weight, indicating that genes

with positive effect were more often dominant. The nonsignificant component j (additive \times dominance) for days to flowering and main branch length with significant h and nonsignificant d for these characters gives an indication of dispersion of genes in the parents. The information provided by the magnitude and direction of components d , j and i indicates that improvement by concentration of desirable genes in a single line was possible for days to flowering, main branch length, clusters/plant, and seeds/pod as transgressive segregates were expected for these traits in the advanced generations of the cross.

The results indicate that improvement for yield could be achieved in the progeny of these two crosses by selecting for component characters, e.g. pod length, seeds/pod, pods/plant, and seed weight. In addition to this, clusters/plant could also be used for yield improvement in cross M. G. 28 \times S. M. No. 1.

REFERENCES

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