

**Research Paper :**

# Combining ability analysis for quantitative traits and yellow mosaic virus in mungbean [*Vigna radiata* (L.) Wilczek]

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## SUMMARY

Combining ability analysis was carried out involving diverse genotypes in one-way diallel in mungbean. Both additive and non-additive genetic variances were found important for inheritance of seed yield and its components. The parents, PDM-11, GM-4 and GM-9918 were good general combiners for seed yield and two and more yield attributing traits. The highest sca effect for seed yield was observed in cross PDM-11 x GM-4 followed by PDM-143 x GM9918. These cross combinations also had sca effect in the desire direction for branches per plant, pods per plant, harvest index, 100-seed weight and YMV incidence. In case of MYMV resistance, the parental lines PDM-143, PDM-11 and PDM-14 have potentiality to donate resistant gene. The crosses PDM-143 x GM-9918, PDM87 x GM-4 and PDM-87 x GM-4 were superior combinations for MYMV incidence. These promising crosses gave superior trasgressive segregants in advance generation.

**Key words :**  
Mungbean,  
Quantitative  
traits, YMV

India is one of the major pulses growing countries in the world, but average productivity level, 397 kg /ha is the lowest in the world of the mungbean [*Vigna radiata* (L.) Wilczek]. Several reasons have been suggested for low productivity of this crop, which include inheritent low productivity of yield, damages caused by several diseases like yellow mosaic virus (YMV), pests, abiotic stress factors and poor management. It is generally felt that there is an urgent need to break the bottlenecks for increasing productivity of this crop. To breed resistant variety, it is necessary to know mechanism of resistance and its genetic control. However, very scanty information is available on this aspect of yellow mosaic virus in mungbean (MYMV). Identification of suitable parents for hybridization is an important means to meet the objectives of breeding programme. It helps to identify parents and crosses which are likely to give the maximum improvement for the trait under consideration but also provide means of understanding regarding gene action involved in it. An attempt was, therefore, made to identify the best general combiners and specific cross combinations for seed yield, YMV incidence and its components in mungbean.

## MATERIALS AND METHODS

A set of 36 genotypes comprising of 8

genotypes and 28  $F_1$  crosses were sown in randomized block design with three replication during *summer* season of 2004 at Main Pulses Research Station, Gujarat Agricultural University, Sardarkrushinagar. Each genotype consisted of single row of two meter length. The infector row of GM-3 variety (susceptible to YMV) was grown in alternate rows, so as increase the incidence of yellow mosaic virus. The hybrid cotton and okra were also sown around the plot for increasing the incidence of the whitefly (*Bamisia tabaci*), which acts as a vector of the YMV. Five random plants were selected from each parents and crosses in each replication. The observations were recorded for eight important characters. The important character YMV incidence recorded prior to leave senession on standard scale 0-5. International mungbean breeding nursery follows 5 point scale system for YMV incidence. Data were subjected to analysis of variance for mean performance (Panse and Sukhatme, 1967) and combining ability analysis as per Model-I and Method -2 of Griffing (1956).

## RESULTS AND DISCUSSION

The mean squares for combining ability for different traits are presented Table 1. It indicated that both gca and sca variances were highly significant for all the characters. This

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