Click www.researchjournal.co.in/online/subdetail.html to purchase.

International Journal of Agricultural Sciences
Volume 8 |Issue 2| June, 2012 | 400-402

RESEARCH PAPER

Inheritance of quantitative traits and yellow mosaic virus in mungbean [*Vigna radiata* (L.) Wilczek]

M.B. PATEL*, J.H. VACHHANI, L.L. JIVANI, B.N. PATEL AND D.S. KELAIYA
Main Oilseeds Research Station, Junagadh Agricultural University, JUNAGADH (GUJARAT) INDIA

Abstract : This study comprised of five families to study gene action. For days to flowering, all three types of gene effects were observed in five families, this indicated that both additive as well as non-additive gene effects had a major contribution in inheritance of this trait. In plant height, all the type of gene effect were registered in five significant crosses but the magnitude of non-additive gene effect was much higher than additive component except in PDM 14 x GM 4, this cross expressed additive x additive (i) type of gene action. In seed yield, it was concluded that epistatic components additive x additive (i) and dominance x dominance (l) effect was significant in cross GM 4 x GM 3 and PDM 143 x GM9918, PDM 11 x K 851 and PDM 87 x GM 3, respectively. In general, the magnitude of dominance x dominance type of gene action was very higher magnitude for yield per plant. In this trait, none of the family observed significant in desire direction for intra- allelic interaction gene action for YMV incidence. For improvement of such crosses, *inter-se* mating, multiple crossing and recurrent selection would be more fruitful as dominance could be diluted due to inbreeding and additive gene could be fixed.

Key Words : Inheritance, Mungbean, Quantitative traits, YMV

View Point Article : Patel, M.B., Vachhani, J.H., Jivani, L.L., Patel, B.N. and Kelaiya, D.S. (2012). Inheritance of quantitative traits and yellow mosaic virus in mungbean [*Vigna radiata* (L.) Wilczek]. *Internat. J. agric. Sci.*, **8**(2): 400-402.

Article History : Received : 19.11.2011**; Revised :** 25.02.2012**; Accepted :** 08.04.2012

INTRODUCTION

India has done remarkable progress in enhancing the productivity of cereals but the production of pulses to the level of self-sufficiency has been a cause of worry in the past and even today. Every year country suffers from gross deficit of pulses and shortfall in requirement is to meet through import from various countries. The yield levels of this crop could be increase by way of genetic improvement. 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 not only 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 made to identity specific cross combinations for YMV incidence, seed yield and its components in mungbean.

The analysis of generation means (Hayman and Mather, 1995 and Hayman, 1958) is useful in testing the adequacy of different types genetic models and then estimating the genetic parameters in the form of components of means. The parameters obtained are useful to the breeder in understanding the genetic structure of populations, their variation and response to various breeding approaches. The grain yield is a very complex trait controlled by polygene with small effects. The information of genetic architecture of yield and its various components is therefore, the prerequisite for adopting a sound breeding programmme with the above in view, the present investigation was conducted to study genetic parameters for yield components, including resistance to yellow mosaic virus(YMV).

MATERIALS AND METHODS

This study comprised of five families to study gene action. Five families were *viz*., PDM 143 x GM 9918, PDM 11 x K 851, PDM 14 x GM 4, PDM 87 x GM 3 and GM 4 x GM 3. From

* Author for correspondence.