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IDENTIFICATION OF RESISTANCE IN URDBEAN (*VIGNA MUNGO*) AGAINST TWO DIFFERENT VIRAL DISEASES

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Abstract

In order to identify sources of resistance in urdbean (*Vigna mungo*), 132 breeding lines cultivars were evaluated against mungbean yellow mosaic virus (MYMV) and urdbean leaf crinkle virus (ULCV) under field conditions. Fifty three urdbean genotypes were found highly resistant to MYMV and 26 to ULCV. More than 60% lines expressed multiple disease resistance to both the viral diseases.

Introduction

Mungbean yellow mosaic (MYMV) and urdbean leaf crinkle (ULCV) are two important viral diseases of urdbean (*Vigna mungo*) in Pakistan. The ULCV has been reported to decrease grain yield from 35 to 81% in urdbean depending upon host genotype and time of infection (Bashir *et al.*, 1991), whereas the yield losses due to MYMV may be as high as 100% (Ghafoor *et al.*, 2000). The MYMV is a whitefly transmitted geminivirus with wide host range, whereas ULCV is transmitted by *Henosepilachna dodecastigma* the leaf feeding beetles (Beniwal & Bharathan, 1980) with restricted host range. ULCV is also transmitted through urdbean seeds at the rate of 2.7 to 46% (Ahmad *et al.*, 1997). For the control of viral diseases like MYMV and ULCV, the use of host plant resistance is the most ideal and practical approach. Therefore, the present study was undertaken to evaluate urdbean breeding material developed under Pulses Programme at the National Agricultural Research Centre (NARC), Islamabad, to identify sources of resistance against MYMV and ULCV.

Materials and Methods

During 1999, 132 urdbean (Mash) breeding lines were evaluated against MYMV and ULCV in a screening nursery under field conditions with natural infection. The nursery was planted at NARC, Islamabad during first week of July, 1999. Each line was planted in a 4m row length with 30 cm row to row distance. One row of a spreader line (9042) the most susceptible to both viruses was planted after every two test rows with two rows of check all around the nursery to facilitate the spread of the diseases. Environmental conditions were also conducive for spread of both the diseases and heavy infections were observed on spreader rows during the season. The disease severity on each line was assessed by following 0-5 rating scale (Singh *et al.*, 1988). The identity of ULCV was confirmed by direct enzyme-linked immunosorbent assay (DAS-ELISA) and that of MYMV by polymersae chain reaction (PCR).

Results and Discussion

Out of 132 urdbean lines, 53, 32 and 11 genotypes were highly resistant, resistant and moderately resistant respectively against MYMV, whereas the others were moderately susceptible to highly susceptible. In case of ULCV, 26, 59, and 15 were highly resistant, resistant and moderately resistant respectively, the others were moderately susceptible to highly susceptible. More than 60% lines expressed multiple disease resistant response to both the diseases. Only 6 lines viz., 9014, 9018, 9042, 9065, 9104 and 9106 were found highly susceptible to both the viruses. Complete genetic resistance to MYMV has not been reported from the local as well as exotic mungbean and urdbean germplasm evaluated at national and international research institutes (Ahmad, 1979). However, during the last two decades a number of mungbean and urdbean genotypes have been identified as resistant and moderately resistant to MYMV (Ghafoor *et al.*, 1992; Bashir *et al.*, 1988).

Due to continuous use of susceptible varieties, the seed-borne nature of the virus ULCV and secondary spread through insect vectors, a critical situation has developed and the crop is seriously suffering from this disease (Bashir *et al.*, 1991). Although there are no reports on the greenhouse evaluation of mash germplasm by artificial inoculation for resistance to ULCV in Pakistan, but some genotypes such as AARI M-13, ARRI M-26, AARI M-27, AARI M-196 and AARI M-202 have been reported to possess moderately field resistance to ULCV (Haq, 1991). Since ULCV is seed-borne in nature, the initial source of infection under field conditions could come from seed. It is therefore, essential to evaluate the present mash germplasm for resistance to seed transmission also. The sources of resistance to MYMV and ULCV identified in this study could be used to breed virus resistant mash cultivars to improve crop production in the country.

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