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VARIABILITY IN COWPEA GERMPLASM FOR REACTION TO VIRUS INFECTION UNDER FIELD CONDITIONS

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Abstract

Ninety four cowpea germplasm accessions were evaluated under field conditions for viral infection. Virus disease incidence ranged from 0 to 66.6%. Based on ELISA and PCR results the following five viruses viz., cucumber mosaic cucumovirus (CMV), bean common mosaic (BCMV), blackeye cowpea mosaic (BlCMV) and cowpea aphid-borne mosaic potyviruses (CABMV) and mungbean yellow mosaic geminivirus (MYMV) were detected. Eighteen (19%), 45 (47.8%), 49 (52.1%) and 55 (58.5%) lines out of 94 tested were found infected with CMV, BlCMV, BCMV and CABMV, respectively. The natural occurrence of BCMV, CMV and MYMV on cowpea are being reported for the first time in Pakistan. Ten accessions 27005, 29154, 27181, 27196, 27197, IT97K-89235, IT94K-556-6, IT96K-113-6, IT85F-1380 and IT95K-1985 were found resistant to viral infection.

Introduction

Cowpea {*Vigna unguiculata* (L.) Walp.}is an important protein-rich crop and is utilized as fresh vegetable pods, dry grains and fodder. In Pakistan, in addition to cowpea yellow mosaic virus, five other seed-borne viruses infecting cowpea have been reported (Bashir & Hampton, 1993). Cowpea germplasm is being maintained in Plant Genetic Resources Institute (PGRI), at National Agricultural Research Centre (NARC), Islamabad. The identification of host resistance to pests and diseases is an important component for the genetic improvement of crop germplasm. During summer season of the year 2000, 94 cowpea germplasm accessions (81 local and 13 exotic) maintained in PGRI were evaluated with the objective to observe variation among genotypes to natural virus infection and selection of genotypes showing resistance under field conditions to provide sources of resistance for breeding programme.

Material and Methods

Ninety four cowpea germplasm accessions were planted at NARC, Islamabad under field conditions. Each accession was planted in a 4 meter row length with 50 cm row to row distance. Plants in each accession showing virus-like symptoms were counted at 15 days interval to determine the disease incidence. Eighty days after planting, five plants from each accession with or without virus symptoms were selected at random for sampling. Leaf samples were collected and processed for virus detection using direct antigen coated enzyme-linked immunosorbent assay (DAC-ELISA). Six antisera to the following cowpea viruses were used in DAC-ELISA tests: cucumber mosaic virus (CMV), cowpea aphid-borne mosaic virus (CABMV), blackeye cowpea mosaic virus (BlCMV), bean common mosaic virus (BCMV), cowpea severe mosaic virus (CSMV), and southern bean mosaic virus (SBMV). The samples showing bright yellow mosaic symptoms for geminivirus were tested by polymerase chain reaction (PCR).

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Results and Discussion

The virus disease incidence under natural infection conditions ranged from 0 to 66.6%. Fourteen accessions were observed with bright yellow mosaic suspecting geminivirus symptoms. From these accessions mungbean yellow mosaic virus (MYMV) was detected. A whitefly transmitted yellow mosaic disease has been reported on cowpea in Pakistan (Ahmad, 1978), but there was no confirmation of the identity of the causal virus by reliable test. We confirmed the identity of MYMV by PCR and this is the first report of MYMV on cowpea in Pakistan. Eighteen lines (19.1%) out of 94 were found with latent virus infection.

Based on ELISA results, four viruses viz., BlCMV, BCMV, CABMV and CMV were detected from samples showing symptoms other than bright yellowing. All these four viruses are reported as seed-borne in cowpea (Hampton *et. al.*, 1992). Eighteen (19%), 45 (47.8%), 49 (52.1%) and 55 (58.5%) lines out of 94 tested were found infected with CMV, BlCMV, BCMV and CABMV, respectively. Although BlCMV and CABMV have been reported previously on cowpea in Pakistan (Bashir & Hampton, 1993), but natural infection of cowpea germplasm by CMV and BCMV seems to be the first report in Pakistan. All the four viruses viz., CMV, CABMV, BCMV, BlCMV were detected from local material except two exotic lines (IT95D-286-4 and IT 95K-222-14) from IITA, Ibadan, Nigeria which were found infected with CABMV and BlCMV, respectively. Since BlCMV and CABMV are seed-borne in cowpea and wide spread in Nigeria (Thottappilly & Rossel, 1992), it is not surprising that these two viruses possibly came through infected seeds, as earlier reported by Bashir *et. al.*, (1999).

Only 10 accessions (five local: 27005, 29154, 27181, 27196 and 27197 and five exotic: IT97K-89235, IT94K-556-6, IT96K-113-6, IT85F-1380, and IT95K-1985) were found free of visible symptoms and no virus was detected in these lines by ELISA. These lines may serve as resistant sources for breeding programme provided their resistance is confirmed by artificial virus inoculation.

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