

## Molecular Characterization, Host Plant Resistance and Epidemiology of Bean Common Mosaic Virus Infecting Cowpea (*Vigna unguiculata* L. Walp)

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**Abstract :** The identification of virus in cowpea especially potyviruses is confusing. Even though there are several studies on viruses causing diseases in cowpea, difficult to distinguish based on symptoms and serological detection. The differentiation of potyviruses considering as a constraint, the present study is initiated for molecular characterization, host plant resistance and epidemiology of the BCMV infecting cowpea. The etiological agent causing cowpea mosaic was identified as Bean Common Mosaic Virus (BCMV) on the basis of RT-PCR and electron microscopy. An approximately 750bp PCR product corresponding to coat protein (CP) region of the virus and the presence of long flexuous filamentous particles measuring about 952 nm in size typical to genus potyvirus were observed under electron microscope. The characterized virus isolate genome had 10054 nucleotides, excluding the 3' terminal poly (A) tail. Comparison of polyprotein of the virus with other potyviruses showed similar genome organization with 9 cleavage sites resulted in 10 functional proteins. The pairwise sequence comparison of individual genes, P1 showed most divergent, but CP gene was less divergent at nucleotide and amino acid level. A phylogenetic tree constructed based on multiple sequence alignments of the polyprotein nucleotide and amino acid sequences of cowpea BCMV and potyviruses showed virus is closely related to BCMV-HB. Whereas, Soybean variant of china (KJ807806) and NL1 isolate (AY112735) showed 93.8 % (5'UTR) and 94.9 % (3'UTR) homology respectively with other BCMV isolates. This virus transmitted to different leguminous plant species and produced systemic symptoms under greenhouse conditions. Out of 100 cowpea genotypes screened, three genotypes viz., IC 8966, V 5 and IC 202806 showed immune reaction in both field and greenhouse conditions. Single marker analysis (SMA) was revealed out of 4 SSR markers linked to BCMV resistance, M135 marker explains 28.2 % of phenotypic variation (R<sup>2</sup>) and Polymorphic information content (PIC) value of these markers was ranged from 0.23 to 0.37. The correlation and regression analysis showed rainfall, and minimum temperature had significant negative impact and strong relationship with aphid population, whereas weak correlation was observed with disease incidence. Path coefficient analysis revealed most of the weather parameters exerted their indirect contributions to the aphid population and disease incidence except minimum temperature. This study helps to identify specific gaps in knowledge for researchers who may wish to further analyse the science behind complex interactions between vector-virus and host in relation to the environment. The resistant genotypes identified are could be effectively used in resistance breeding programme.

**Keywords :** cowpea, epidemiology, genotypes, virus

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