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etration from lower surface of leaf.

9 Showing the disease incidence found in fields in different months.

10 Mechanically inoculated plants of *Oxalis corymbosa* showing vein clearing and mottling.

11 Inoculated leaf of *Chenopodium amaranticolor* Coste and Reyn. Showing necrotic local lesions.

12 Inoculated leaves of *Vigna unguiculata* L. showing necrotic local lesions.

13 Leaf of *N. tabaccum* L.cv. Jayashree type FCV showing blistering and raised dark green areas (Right) and Healthy (left).

14 Infected leaf showing vein banding, the green of tissue along with the veins is about as dark as green of healthy or somewhat more dark. The area of pale green patches decreases to the base of the leaf.

15 Inoculated plant showing mottling and leaf deformation on newly emerging leaves.

16 Leaves of *Capsicum annum* L. showing severe mottling and reduction in leaf size.

17 Leaves of *Vigna unguiculata* L. showing systemic symptoms in the form of severe leaf deformation.

18 Leaves of *Dahlia pinnata* showing systemic symptoms in the form of severe reduction in leaf size.

19 Leaves of *Aster* showing vein clearing and mild mosaic symptoms.
Showing comparison of local lesions produced on two hosts *C. amaranticolor* and *V. unguicuata*.

Showing effect of temperature on the infectivity of the virus.

Showing effect of dilution of crude sap on the infectivity of virus.

Electron micrograph of virus isolates showing isometric particles with a central core.

Virus band seen after sucrose density gradient centrifugation.

Detection of CMV by ELISA in various samples based on data of absorbance at 405 nm; Antibodies; Antigen, Crude sap from leaf (dilution of 1 : 500) from H1, H2, H3, H4, H5, H6, H7, H8, and H; B= Buffer; H=Sap from uninoculated *N. rustica* plants taken as negative and positive controls. Were as H1, H2, H3, H4, H5, H6, H7, H8= Symptomatic inoculated plants.

Detection of CMV in symptomatic and asymptomatic host plants through DAC-ELISA. Yellow colour - positive; No colour development - Negative.

RNA-3 genome of CMV showing locations of primers used for amplification. Movement protein (MP) ORF, Coat protein (CP) ORF, UTR untranslated region. Arrows indicate location of primers.

Screening of clones by restriction digestion using EcoRI restriction enzyme. Lane 1= Positive control showing CP insert of Lane 2-3= false clone Lane M = λ DNA/EcoRI/HindIII.

Hypothetical RNA-3 genome of CMV showing locations of MP (movement protein) ORF, CP (coat protein) ORF, UTR untranslated region and IR (Intergeneric region in between).

Phylogenetic tree for Cucumber mosaic virus (CMV) CP at nucleotide level generated by MEGA v4.1 showing relationships of a member of CMV under study (JQ779842) with other Cucumber mosaic viruses. The out-group used in this analysis is Tomato aspermy virus.

Phylogenetic tree of Cucumber mosaic virus (CMV) at amino acid level generated by MEGA v4.1 showing relationships of a member of CMV under study (JQ779842) with other CMV isolates. The out-group used in this analysis is Tomato aspermy virus.

Phylogenetic relationship of the virus isolated from the Aligarh India isolate (JQ779842) with strains of Cucumber mosaic virus (CMV) subgroup I (Ia and Ib) and II based on the nucleotide sequence alignment using Mega4.0 neighbour-joining tree method. The tree was rooted on Peanut stunt virus (PSV; Nc_002040) as an out-group. The virus from the present study is highlighted with yellow box.

Amino acid sequence alignment of coat protein gene (amino acid) of Cucumber mosaic virus (CMV) Oxalis isolate with that of CMV strains of subgroups I (A and B), II and Indian isolates using Multalin programme 5.4.1.

Multiple sequence alignment of coat protein gene (nucleotide) of Cucumber mosaic virus (CMV)-Oxalis
isolate with that of CMV strains of subgroups I (A and B), II and Indian isolates using Multalin programme 5.4.1.

36. PCR amplification of Movement protein (MP) gene showing amplification of ~840 bp from naturally infected *Oxalis corymbosa* (1) plants and inoculated samples (2,3,4,5).

37. Screening of clones by restriction digestion using *EcoRI* restriction enzyme. Lanes- 1-2= digested plasmids showing MP insert of ~840 bp. Lane 3= false clone Lane M = λ-DNA/EcoRI/HindIII.

38. Phylogenetic tree *Cucumber mosaic virus* (CMV) MP at amino acid level generated by MEGA v4.1 showing relationships of a member of CMV under study (JX026954) with other CMV isolates. The out-group used in this analysis is *Tomato aspermy virus*.

39. Phylogenetic tree *Cucumber mosaic virus* (CMV) MP at nucleotide level generated by MEGA v4.1 showing relationships of a member of CMV under study (JX02695) with other CMV isolates. The out-group used in this analysis is *Tomato aspermy virus*.

40. Multiple sequence alignment of Movement Protein of CMV-Oxalis isolate at nucleotide level with that of CMV strains of subgroups I (A and B), II isolates using Multalin programme 5.4.1.