

First report of begomovirus infecting two ornamental plants: *Ocimum Sanctum* and *Alternanthera Variegata* in India

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Abstract

Background: *Ocimum sanctum* is an ornamental herb that belongs to the family of Lamiaceae. It is an aromatic plant, refined for its medicinal properties (Sethi et al., 2004). *O. sanctum* is established widely across tropical regions and fully fringed in homes and temples across India meant for its religious belief. *Alternanthera variegata* belonging to family Amaranthaceae have variegated leaves, perennial, is low sprawling or prostrate plants, with weak stems and simple leaves arranged in opposite pairs. *Ocimum* and *Alternanthera* plants exhibiting disease symptoms, having curling of leaves were collected from the gardens of Lakshmangarh, Rajasthan, India region in order to identify the begomovirus infection prevailing in them. PCR was carried out using universal coat protein primer (Hallan, 1998). Forward primer sequence was GGRTTDGARGCATGHGTACATG (AC 1048) and reverse primer sequence was GCCYATRTAYAGRAAGCCMAG (AV 494). PCR product of expected size ~ 550 bp was obtained from both samples. PCR product of ~ 550 bp of *O. sanctum* and *A. variegata* samples was cloned and partially sequenced and has been deposited in NCBI GenBank Accession No. JF968443 and JN009666 respectively. BLASTn analysis was conducted with other begomovirus isolates in GenBank database at NCBI (Altschul et al., 1997). In the case of *O. sanctum* the alignment process of begomovirus sequence reveals 98% identity each with Tomato leaf curl virus AV1 gene for coat protein, isolate 4 (AJ810343) and Tomato leaf curl Gujarat virus - [Nepal] segment DNA-A, complete sequence (AY234383). Whereas in the case of *A. variegata* BLASTn analysis of begomovirus sequence showed 93% identity with Tomato leaf curl Kerala virus isolate ToLCV-K5 segment DNA A, complete sequence (EU910140) and 86% identity with Tomato leaf curl virus AV1 gene for coat protein, isolate 21(AJ810360). By means of the results mentioned above this is the first ever report of Begomoviruses infecting *Ocimum sanctum* and *Alternanthera variegata* in India.

Keywords

Begomovirus, *Jasminum sambac*, *Millingtonia hortensis*, PCR

Background

There are reports of begomovirus disease in elaborate plants around the world (He et al. 2009; Ilyas et al. 2013). With respect to the Indian setting, various reports on begomovirus contamination in weeds and harvests are accessible (Chatterjee et al. 2007; Das et al. 2008; Ghosh et al. 2007; Jyothsna et al. 2011; Khan et al. 2002) yet there is significantly less data with respect to begomovirus diseases in decorative plants (Marwal et al. 2013b). This is on the grounds that ornamentals are here and there dismissed or are not contemplated while doing review and begomovirus considers. We had discovered *Chrysanthemum indicum* plants with indications of leaf yellow vein sickness run of the mill to begomovirus contamination; enhanced and sequenced parts of begomovirus coat protein quality, which indicated the same degree of nucleotide personality with *Clerodendron yellow mosaic infection* and *Clerodendron brilliant mosaic China infection*. In any case, *Clerodendron yellow mosaic infection* and *Clerodendron brilliant mosaic China infection* have not been endorsed as species. Hence, in light of the contaminated host, noticed manifestations and spot of gathered examples, we propose to this segregate name *Chrysanthemum indicum yellow vein Delhi infection*. Accordingly, this distinguishing proof addresses the chance of a genuine danger to other financially significant elaborate and cultivation crop plants. There is a requirement for a more extensive investigation, which will be centered on the sequencing of the total genome of the infection and recombination investigation. This can illuminate its root and can be used to recognize conceivable further begomovirus contaminations in the country to evaluate their commitment in misfortunes and to create instruments material in control procedures. Additionally, progressed atomic methods, for example, RNAi will be utilized for the improvement of transgenic plant protection from begomovirus. This will shape the premise of our future examinations.

Arrangement investigation was done utilizing Impact, which uncovered that the secluded begomovirus (JN998441) tainting *Chrysanthemum indicum* indicated 99% succession character with *Clerodendron yellow mosaic infection* (EF408037) and *Clerodendron brilliant mosaic China infection* (FN645907). Moreover, the begomovirus demonstrated most reduced succession personality of 81%, with Tomato leaf twist Pakistan infection (FM164938), Cotton leaf twist Burewala infection (FR750324) and Cotton leaf twist Shadadpur infection (FN552005) being accounted for from Pakistan. The begomovirus sequenced have a putative preserved area of the Geminiviridae family which encodes for coat protein of 154 amino acids having an atomic load of 18.08 kDa (protein id = "AEY68274.1"). The ORF is assigned as AV1, which dwells on the positive sense strand of first outline, having nucleotide facilitates in which the start codon starts at position 1 and the stop codon at 461. Indeed, even with protein arrangements, the begomovirus secluded from *Chrysanthemum indicum* indicated most elevated amino corrosive arrangement characters of 98% with *Clerodendron yellow mosaic infection* (EF408037) announced from India and *Clerodendron yellow mosaic infection* (HE863667) revealed from adjoining nation Pakistan. Phylogenetic investigation dependent on the coat protein

arrangement of begomovirus and other chose successions demonstrates that the segregate bunches with the secludes of Clerodendron yellow mosaic infection (EF408037) and Clerodendron brilliant mosaic China infection (FN645907), which were accounted for from India. The positive PCR response indicated the presence of begomovirus, which was additionally affirmed by Southern blot hybridization utilizing Cotton leaf twist infection as a general and control test for begomoviruses. Every one of the 14 examples from indicative plants hybridized with the test, while tests removed from non-suggestive plants didn't show positive outcomes. Biotest contemplates uncovered that all the 15 precisely immunized seedlings at two-leaf stage appeared comparative side effects as those saw on the field-tainted plants, while the seed transmission biotest contemplates indicated that the infection isn't seed borne in nature. The build created to test for Koch's proposes caused regular yellow vein indications when immunized into *N. benthamiana*. For each examination, 20 *N. benthamiana* plants developed on creepy crawly free nursery were taken. This brought about the improvement of similar sort of indications as seen in *Chrysanthemum indicum*. The genuineness of infectivity test was affirmed by utilizing begomovirus

coat protein quality preliminaries in PCR.

The positive outcomes acquired from sub-atomic what's more, biotest examines affirmed the presence of begomovirus in *Chrysanthemum indicum* named *Chrysanthemum indicum* yellow vein Delhi infection. Results got above uncover that the infection isn't seed borne in nature yet is vector borne. Data will be adequately applied for infection the executives, crop security and advancement of isolate techniques at the state and public level in India. Additionally, the conceivable relationship of a begomovirus with *Chrysanthemum indicum* had not been explored beforehand. In this manner, to the best of our insight, this is the primary report on begomovirus related with yellow vein infection of an fancy plant *Chrysanthemum indicum*.

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