Geminivirus Coat Protein Gene Replacement Changes Tripartite Interaction between Virus Vector and Host.

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INTRODUCTION:

Agriculture is of immense importance all over the world whereas, viruses always have sound effect on the growth of plants, besides interacts with host defence mechanism, leads to the alteration of crop physiology. The geminivirus Coat protein (Cp) is multifunctional and is involved in systemic infection, virion formation and insect transmission; but it is not required for viral DNA replication. Furthermore, the role of Cp in systemic infection depends on the specific geminivirus-host combination. However, in some host plant species, Cp of some whitefly-transmitted bipartite begomoviruses is not required for systemic infection (i.e., cell-to-cell and long-distance movement) or symptom development. In contrast, Cp is required for systemic infection of monopartite begomoviruses, curtoviruses and mastreviruses. It is worth investigating, that alteration in Cp gene constitutes a novel epidemiological adaptation for a geminivirus. Coinfection is also a prerequisite for recombination occurring between viruses, and it is suggested from the available evidence that due to intergenic recombinations, present taxonomic structure of the family *Geminiviridae* has established. Recent evidence indicates that dicot-infecting mastreviruses are particularly prone to inter-specific recombination (trans-encapsidation). Irrespective of the type of geminivirus examined, the Cp is essential for insect transmission, and it is the determinant of vector specificity. Hence, this article will help scientific community to better understand the coinfection with different Geminiviruses especially due to vector inspecificity thus lead to the occurrence of revolutionary recombination events occurring with the potential to yield new viruses that could adversely affect agriculture.

Keywords: Geminiviruses, Coat Protein gene, Replacement, tripartite interaction.

GENOME ORGANIZATION OF MASTREVIRUS.

1. Monopartite, circular, ssDNA genome (+) genome of about 2.6-2.8 kb. 3' terminus has no poly(A) tract.
2. There are coding regions in both the virion (positive) and complementary (negative) sense strands..

DICOT INFECTING MASTREVIRUSES

❖Tobacco yellow dwarf virus (TYDV) (Morris *et al*., 1992).
❖chickpea chlorotic dwarf virus (CpCDV) (Horn *et al*., 1993).
❖BeYDV- Bean yellow dwarf virus (BeYDV) (Liu *et al*., 1999)
❖Chickpea chlorosis virus (CpCV-A, CpCV-B) and chickpea redleaf virus (CpRLV) (Thomas *et al*., 2010).

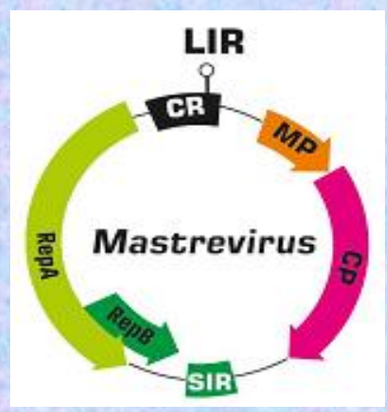
DICOT INFECTING MASTREVIRUSES HOST RANGE

- Chickpea
- Lentils
- Faba beans
- Field pea
- French bean
- Sugar beet
- Pepper
- Cotton Squash
- Tomato

1. Host DNA polymerase being used.
2.Trans-activation of late (virion-sense) genes.
3.Establish a cellular environment conducive for virus replication.

1. Translated from alternatively spliced sense transcripts and required for replication, initiating and terminating rolling circle DNA replication.
2. Interfere with cell cycle.

1. Potential stem-loop structure.
2. Conserved Nona-nucleotide sequence (TAATATTAC) where ssDNA synthesis Is initiated.



contains bidirectional polyadenylation signals.

Cell to cell movement.

1.Transmission by Insect (Insect specificity).
2.Encapsidation (Virus assembly).
3.Systemic infection (cell to cell movement).

COINFECTION OF BEGOMOVIRUS WITH MASTREVIRUS

•The prerequisite of coinfection between begomovirus-dicot infecting mastrevirus intergenic recombination was shown first time by Mubin *et al*. (2012) in a weed (*Xanthium strumarium* L.: non-host of CpCDV) in Pakistan.
•The second evidence of coinfection between '*Cotton leaf curl burewala virus*' (CLCuBuV), a begomovirus with dicot infecting mastrevirus;'*Chickpea chlorotic dwarf virus*' (CpCDV) was reported by Manzoor *et al*. (2014) in cotton (non-host of mastrevirus).
•Recently a new study about begomovirus-dicot infecting mastrevirus co-infection in squash plants (non-host species of dicot infecting mastrevirus) has been reported by Fahmy *et al*. (2015) for full length complete genome of the CpCDV infected squash plants by studying its putative recombination events along with its phylogenetic analysis and molecular characterization.

CONCLUSION

In a nutshell it can be concluded that replacement of coat protein gene may help to broaden our understanding about the range and distribution of mastreviruses across world and will provide the necessary information regarding their control.
Coinfection open avenues to find out the potential factors, which made the mastreviruses to evolve from monocotyledonous plants to dicotyledonous and their ability to cause infliction in non-host plants, thus expanding its host range with the passage of time.

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