

Pathogenesis of begomoviruses in Tomato

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Introduction

Tomato (*Solanum lycopersicum*, Solanaceae) is host of several viral species, according to recent counts in the encyclopedia of plant viruses.¹ More than 50% of these are DNA viruses in the genus Begomovirus of the family Geminiviridae,¹ transmitted through the phloem by feeding of whiteflies *Bemisia tabaci*. In the begomovirus genera, Tomato yellow leaf curl virus (TYLCV), possess the most cause of concern in tomato production due to documented losses reaching 40-100%,²⁻⁴ plus the continuous spread of the vector. Begomovirus infections are a problem common to China, Mexico, the Netherlands, the United States, and Spain, the main producers of tomato in the world.⁵ Also severe cases are appearing in Asia, Israel, the Mediterranean and the Middle East where TYLCV, Tomato leaf curl China virus and Tomato leaf curl New Delhi virus can occur alone mixed or in complexes with beta-satellites.⁶⁻⁸

Begomovirus infection in tomato

Three categories of symptoms, namely yellow leaf curl disease, mosaic/mottle, and leaf deformation can be established; these come with an intensity, distribution and time of appearance depending on the cultivar and the virus. In typical non-mixed infections by monopartite viruses, like TYLCV, the virulence factor is protein C4;⁹ most of the C4 interactors are ribosomal or participate in ubiquitination, but others are key regulators of the plant defenses pathways; the infection induces down-regulation of genes related to basic metabolism and biosynthesis of secondary metabolites, with significative loss of transcripts for photosystem II and up-regulation of anthocyanin biosynthesis.¹⁰⁻¹² Production of cellulose is seriously injured in cultivars susceptible to TYLCV,¹⁰ however rather than deploying a complete antiviral response, infected plants follow a photosynthetically poor life cycle with curled new leaves and reduced growth that reaches senescence 50-60 days post infection.¹³ This is critic if the plants become infected soon after transplanting, hence among recommended management strategies is to avoid planting in seasons with high whitefly populations.² Noteworthy, some evidence suggests that seed transmission of TYLCV might account to a high percentage of early infections.¹⁴

In other pathogenic systems, for example Tomato leaf curl China virus (TYLCCNV) and its satellites, symptoms are modulated by β C1. TYLCCNV itself or with an alpha satellite induces mild symptoms, which turn into severe apical leaf curling if a beta-satellite is added to the complex;^{15,16} overexpression β C1 protein in healthy plants produces leaf curling, vein swelling, and blistering of leaves, indicating that, after all, severity in leaf curl diseases is a result of impaired cell wall biosynthesis. The interactions of β C1 proteins, in general, involve polymerases and RNA methylases that participate in RNA silencing plus proteins in the ubiquitination pathway;^{15,17} their pathogenicity is negatively regulated by the sucrose-nonfermenting kinase 1 (SnRK1),^{15,18} which also phosphorylates proteins Rep and C2, as well, and was linked with resistance to TGMV¹⁹ independent of ty- genes. During interactions of the TYLCCNV with its satellites, expression of genes involved in starch metabolism and glycosaminoglycans synthesis is more often disturbed in presence of the beta-satellite if the

alpha satellite is absent,¹⁶ all together suggesting metabolic changes that might lead to impairments in cell-wall biosynthesis.

Bipartite begomoviruses, particularly those in the clade of Abutilon mosaic virus, trend to produce mild yellowing in which the nuclear shuttle protein (NSP) acts as suppressor of antiviral response. NSP main target is a transmembrane leucine rich protein involved in viral PAMPs identification, named NIK1 for NSP-interacting kinase I;^{20,21} NIK1 has direct interaction with ribosomal protein L10A (rpL10A), in such a way that its over expression results in severe shut down of the translational machinery;²² ectopic expression of NIK1 in tomato delays the infection and reduces manifestations of Tomato yellow spot virus, other bipartite begomovirus in the same clade, whereas in tobacco leaves infected with Tomato golden mosaic virus (TGMV) rpL10A distribution is distorted; additionally, Arabidopsis *nik1* null mutants are more susceptible to Cabbage leaf curl virus (CaLCuV),²³ which belongs to in a different clade of American begomoviruses, all together indicating that NIK1 plays a central role in response to these pathogens.

The transcriptional activity induced by bipartite begomoviruses in tomato is likely to resemble that of Pepper golden mosaic virus in *Capsicum annum* and CaLCuV in *A. thaliana*, characterized by an increased expression of plant defense genes in the ethylene, jasmonic and oxidative stress pathways, but with down-regulation of particular steps in the ethylene pathway.²⁴ Conversely, Navqi and co-workers found that polyubiquitinators, 40S ribosomal proteins, ethylene response proteins, and a cell wall protein precursor are among the genes differentially expressed in infections by the Old World bipartite virus Tomato leaf curl New Delhi virus.²⁵

Conclusion

Begomovirus pathogenicity is determined by a complex interaction between viral and host proteins that together cause general and specific symptomatology. In emergent of plant viral diseases, genetic changes in viral proteins or interaction between proteins of two or more co-infecting viral species, allow new or stronger reactions that favor viral pathogenesis. Under these circumstances, the symptomatology

is no longer modulated by the typical pathogenicity determinants and becomes dependent on genetic changes such as point mutations,^{26,27} recombination events,^{28,29} rearrangements and coinfections.³⁰⁻³⁷

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Conflicts of interest

The authors declare no conflicts of interest regarding the publication of this paper.

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