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Tomato yellow leaf curl disease (TYLCD) is one of the most devastating plant diseases in the world. As a result of its continuing rapid spread, it now afflicts more than 30 tomato growing countries in the Mediterranean basin, southern Asia, Africa, and South, Central and North America. The disease is caused by a group of viral species of the genus *Begomovirus*, family Geminiviridae (geminiviruses), referred to as *Tomato yellow leaf curl virus* (TYLCV). These are transmitted by an insect vector, the whitefly *Bemisia tabaci*, classified in the family Aleyrodidae. The genome of TYLCV generally consists of a single circular single-stranded (ss) DNA molecule, with only one exception in which two components were identified. It encodes six open reading frames, only one of which codes for the coat protein (CP) that represents a building block of the viral particle. TYLCV, like all other

members of the Geminiviridae, has geminate particles, apparently consisting of two incomplete $T = 1$ icosahedra joined together to produce a structure with 22 pentameric capsomers and 110 identical CP subunits. Close to 50 years of intensive research into TYLCV epidemics has been conducted to find solutions to the severe problem caused by this virus. To date, breeding for resistance appears to be the best approach to controlling this disease, although only partially resistant varieties are commercially available. Since the virus consists of a ssDNA that replicates in the host-cell nucleus, the molecular mechanisms involved in its nuclear import have been the focus of our studies in recent years and results, as well as prospects, are discussed in this review. In addition, we describe our recent finding of a suppressor of gene silencing encoded by one of the TYLCV-*lSr* genes. This paper provides an overview of the most outstanding achievements in TYLCV research that may lead to more effective control strategies.

Keywords:

TYLCV; tomato; geminivirus; ssDNA;

whitefly; PTGS

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