Emergence of Recombinant Curtoviruses Involved in the Curly Top Disease

Outbreak in the Central Valley of California in 2013

Li-Fang Chen a and Robert L. Gilbertson a

a Department of Plant Pathology, University of California-Davis, One Shields Ave., Davis, U.S.A.
lfchen@ucdavis.edu

The curtoviruses (genus Curtovirus) have a monopartite genome, infect dicotyledonous plants and are transmitted by the beet leafhopper (Circulifer tenellus). In the western United States, a complex of curtoviruses causes curly top disease in economically important crops, including beans, pepper, tomatoes and sugar beet. In 2013, a major outbreak caused substantial losses to processing tomato production in California. The predominant curtoviruses causing curly top disease in tomato in California are Beet curly top virus-Wor (BCTV-Wor; previously named Beet mild curly top virus) and BCTV-Svr (previously named Beet severe curly top virus). In 2009, 2010 and 2013, three isolates (BV3, LH71 and CO) with recombinant genomes were identified from infected-tomato and leafhopper samples collected in California. Sequence analyses showed that both BV3 and LH71 with a partial genome shared high similarity with corresponding region of BCTV-Svr, and CO shared high similarity with another region of BCTV-Svr. In addition, both LH71 and CO has a recombinant genome composed of BCTV-Wor (major parent, 89%) and BCTV-Svr (minor parent, 11%).

Inoculation and transmission experiments confirmed BV3 and LH71 induce severe symptom phenotypes, reveals that a key symptom determinant(s) maps to the recombinant region. In 2013, the outbreak of curly top disease had devastated processing tomato, melons, peppers, squash and watermelon, and more than 90% of collected samples were identified as LH71, CO or mixed-infections. Together, these recombinant viruses played major roles in the 2013 disease outbreak, and these results suggest the importance of recombination in evolution and emergence of new curtoviruses than previously recognized.