

Emergence of Recombinant Curtoviruses Involved in the Curly Top Disease Outbreak in the Central Valley of California in 2013

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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.