## EFFECT OF CURTOVIRUS SPECIES COMPETITIVENESS IN HOST PLANTS ON TRANSMISSION AND INCIDENCE OF BEET SEVERE CURLY TOP VIRUS AND BEET MILD CURLY TOP VIRUS

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Curly top disease, caused by viruses in the genus Curtovirus, causes significant economic losses for sugarbeet and other crops throughout the western United States. Recent studies demonstrated the two most abundant curtovirus species in the US are Beet severe curly top virus (BSCTV) and Beet mild curly top virus (BMCTV), but other less prevalent curtoviruses have been found affecting sugarbeet, pepper, tomato and pumpkin with several new species characterized within the past decade. Studies were undertaken to examine virus accumulation, competition and transmission among common weed and crop curtovirus hosts. Examination of virus titers in plants clearly demonstrated BMCTV accumulates preferentially to BSCTV in bean, shepherds purse, and to a lesser degree, tomato. In contrast, BSCTV accumulates preferentially to BMCTV in sugarbeet. Each virus has at least one host plant from our study in which it accumulates more efficiently than the competing curtovirus. Accumulation patterns can shift during mixed infection due to the impact of a competing virus; however, the efficiency of transmission for an individual curtovirus is directly related to its relative titer compared to the competing virus. A corresponding study examined the prevalence of individual curtovirus species in weed and crop host plants in the San Joaquin Valley of California. DNA was isolated from a wide array of curtovirus host plants, including sugarbeet, and analyzed by PCR. A select region of the genome exhibiting DNA sequence divergence among species within the genus Curtovirus was amplified by PCR. DNA sequence analysis of amplified viral genomic segments demonstrated both viruses were prevalent in the valley, and confirmed lab results that particular host species support BMCTV accumulation preferentially to BSCTV and vice versa. Some rare and recombinant curtovirus isolates were also recovered, indicating the virus population in California remains dynamic.