RUSH, C.M.*[1], G.B. HEIDEL[1], R.C. FRENCH[2], and M.D. LAZAR[1], Texas Agricultural Experiment Station, Bushland, TX 79012, and USDA-ARS, University of Nebraska, Lincoln, NE 68583. - Relationship between BNYVV and an unnamed soilborne sugar beet virus from Texas.

A study was conducted using PCR technology to determine similarities between BNYVV and an uncharacterized furovirus of sugar beet designated TX7. Published sequence data of an European BNYVV isolate were used to design synthetic primers for each of the four BNYVV genomic RNAs. Specific primers and reverse transcriptase were used to synthesize cDNA from extracts from BNYVV- or TX7-infected *Chenopodium quinoa* which was then amplified by PCR. Most primer sets generated specific PCR products from BNYVV-infected samples but not from healthy plants or those infected with TX7. However, one set of primers specific for BNYVV RNA1 amplified cDNA from both BNYVV and TX7. The PCR products were ca. 950 base pairs (bp) for TX7 vs. 1056 bp for BNYVV. The apparent deletion in TX7 is located near the 3' end (near base 6200 of BNYVV RNA1). Restriction analysis of the TX7 product using Dra I, Tha I, Nhe I, and Spe I gave RFLP patterns similar to those predicted for BNYVV. In fact, Tha I and Nhe I digestion patterns of TX7 PCR products were more consistent with the published BNYVV sequence than those of our BNYVV isolate. This suggests a high degree of sequence homology between these two viruses in the region of RNA1 defined by these PCR primers. The results of this and other work in our laboratory, including RNA and coat protein analysis, indicate that TX7 and BNYVV are closely related. We speculate that TX7 may be a mild strain of BNYVV.