LIU, HSING-YEH, GAIL C. WISLER, WILLIAM M. WINTERMANTEL, and JOHN L. SEARS, USDA-Agricultural Research Service, 1636 East Alisal Street, Salinas, CA 93905. Differentiation of Poleroviruses in sugarbeet.

ABSTRACT

Recent changes to the nomenclature of the *Luteoviridae* family has shown that it is composed of 3 genera: *Polerovirus, Luteovirus*, and *Enamovirus*. This group of viruses has small spherical particles about 26 nm in diameter, is phloem limited, and is aphid-transmitted in persistent manner. Polerovirus induces yellowing symptoms and causes severe losses in sugarbeet, as well as other economically important crops grown throughout the world. Three poleroviruses infect sugarbeet including *Beet chlorosis virus* (BChV), *Beet western yellows virus* (BWYV), and *Beet mild yellowing virus* (BMYV). BMYV has, to date, not been found in the USA.

BChV induces a disease of sugarbeet exhibiting severe foliage yellowing and necrosis. This disease had been occurring with increasing frequency in California, Colorado, Nebraska, and Texas during recent years. Symptoms of this disease resemble those induced by BWYV. Serologically, beet poleroviruses can not be distinguished from one another by using either polyclonal antisera or most monoclonal antibodies. The only way to identify BChV from BWYV was based on host specificity. BWYV isolates from beet have a wide host range and are distinguished by systemic infection of shepherd's purse (*Capsella bursa-pastoris*) and lack of infection of *Chenopodium capitatum*. BChV has a narrow host range and shows interveinal reddening on *C. capitatum* but does not infect shepherd's purse.

One of the objectives of our research is to develop efficient and accurate methods to identify poleroviruses in sugarbeet that are essential for resistance breeding. In order to develop RNA probes we have purified BChV. Viral RNA were extracted from BChV virions. The DNA fragments corresponding to different portions of the viral RNA were produced by reverse transcription followed by the polymerase chain reaction (RT-PCR). Purified RT-PCR products were cloned into pGEM-T Easy plasmid. The clones were sequenced. Analyses of the sequencing data revealed that BChV consists of 6 major open reading frames (ORFs) in the plus strand. The gene organization is very similar to those of BMYV and BWYV. ORF-3, which encodes the viral coat protein, displayed a strong similarity to BMYV (92%) and the European BWYV FL1 isolate (BWYV-FL1) (91%). In contrast, the 5'- penultimate ORF-0 has only 21% similarity to BMYV and 24% to BWYV-FL1. Development of specific primer pairs or probes derived from ORF-0 that can be used for discrimination of different poleroviruses is in progress.

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