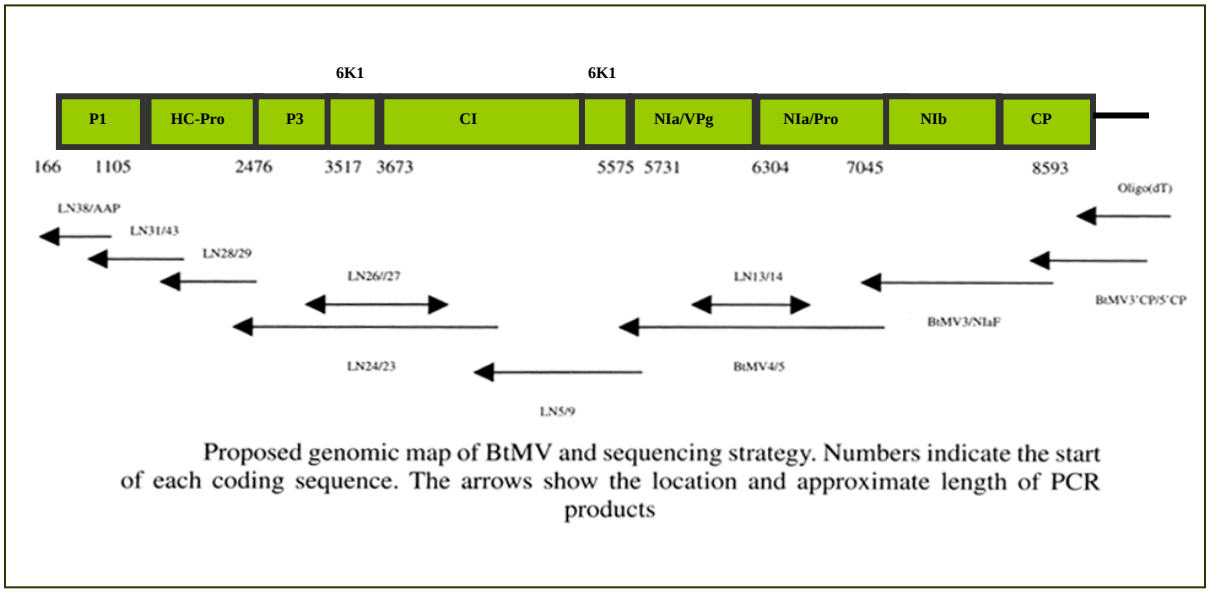
Beet Mosaic Virus

BtMV is a member of the economically important *Potyvirus* group of plant viruses and infects sugar beet and its close relatives. It is distributed world-wide in all major beet-growing areas and in mixed infections with certain other viruses causes severe stunting and yield losses on susceptible sugar beet varieties. We have determined for the first time the complete nucleotide sequence of *Beet Mosaic Virus* (BtMV) genomic RNA. Based on the sequence, we have developed a BtMV-specific RT-PCR assay for accurate diagnosis and differentiation of the virus. The full-length sequence will allow development of virus-resistant plants and a BtMV virus-based transient gene expression vector. The virus specific detection method will be of practical use in early diagnosis and control of BtMV in single and mixed infections.

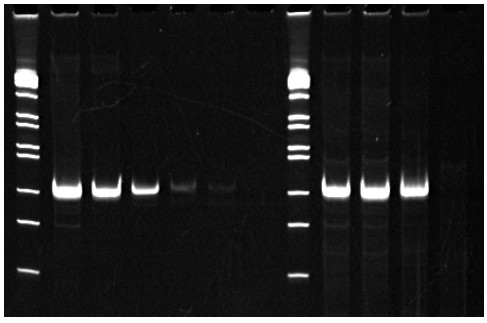


Proposed genomic map of BtMV and sequencing strategy. Numbers indicate the start of each coding sequence. The arrows show the location and approximate length of PCR products

A

B

C



D

A, Proposed genomic map of BtMV and sequencing strategy. **B** and **C** Uninfected and BtMV-infected sugar beet plants, respectively. **D**, RT-PCR products, amplified with BtMV-specific primers from infected leaf and root tissues of sugar beet.

Nemchinov, L.G., Hammond, J., Jordan, R., Hammond, R.W. 2004. The complete nucleotide sequence, genome organization, and specific detection of Beet mosaic virus. Archives of Virology. 149(6):1201-14. Epub 2004 Feb 12.