Cherry leaf roll virus (CLRV) - genome organisation of the RNA1

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The complete organisation of the *Cherry leaf roll virus* genome, a virus which affects many fruit trees and other woody hosts, has not been determined to date. However, partial sequence information of the bipartite virus which is available of the 3´ proximal portion including the complete 3´ non-coding region (NCR) of the genomic RNA1 and RNA2 has led to the classification as a subgroup c nepovirus.
Sequences of the RNA1 of two CLRV isolates from different host plants (CLRV-E395 originating from *Rheum rhabarbarum* and CLRV-E326 from *Juglans regia*) were obtained and compared with other nepoviruses. The genomic structure of the CLRV-RNA1 coding for a polyprotein corresponds with other established subgroup c nepoviruses like *Tomato ringspot virus* (ToRSV), *Blackcurrant reversion virus* (BRV) and *Peach rosette mosaic virus* (PRMV). The polyprotein of the rhubarb isolate ($ORF_{12\text{-}6350\ nt}$; 2112 amino acids) contains a N-terminal protease cofactor (PCo), adjacent is a nucleotide-binding protein-domain (NTB), followed by the sequences coding for the genome-linked viral protein (VPg), a protease (Pro) and the viral replicase (RdRp). Putative protein functions were predicted by identification of characteristic sequence motifs (Argos 1988; Gorbalenya et al. 1989a and 1989b; Rott et al. 1995, Wang et al. 1999). The region coding for the putative CLRV-VPg protein was identified with the computer programs NetPicoRNA V1.0 and. NetCorona V1.0., and exhibited highest similarities to the corresponding ToRSV-VPg. Predicted specific protease recognition sequences in the CLRV isolates (Q_{1121}/S_{1122} and Q_{1150}/S_{1151}) also corresponded to ToRSV.

References

Argos, P. (1988). A sequence motif in many polymerases. Nucleic Acids Res 16, 9909–9919.

Gorbalenya, A.E., Blinov, V.M., Donchenko, A.P., Koonin, E.V. (1998a). A NTP-binding motif is the most conserved sequence in a highly diverged monophyletic group of proteins involved in positive strand RNA viral replication. Journal of Molecular Evolution 28, 256–268.

Gorbalenya, A.E., Donchenko, A.P., Blinov V.M., Koonin E.V. (1989b). Cysteine proteases of positive strand RNA viruses and chymotrypsin-like serine proteases. FEBS Letters 243, 103–114.

Rott, M.E., Gilchrist, A., Lee, L., Rochon D.M. (1995). Nucleotide sequence of tomato ringspot virus RNA1. Journal of General Virology 76, 465–473.

Wang, A., Carrier, K., Chisholm, J., Wieczorek, A., Huguenot, C., Sanfaçon, H. (1999). Proteolytic processing of tomato ringspot nepovirus 3C-like protease precursors: definition of the domains for the VPg, protease and putative RNA-dependent RNA polymerase. Journal of General Virology 80, 799-809.