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 lead to the classification as a subgroup c nepovirus.

Sequences of the RNA1 of two CLRV isolates from different host plants (CLRV-395 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 (ORF₁₂₋₆₃₅₀ 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. The region coding for the 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 (Q₁₁₂₁/S₁₁₂₂ and Q₁₁₅₀/S₁₁₅₁) also corresponded to ToRSV.