

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-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 (ORF_{12-6350 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.