

Analysis of the 3' non-coding region of Cherry leaf roll virus, a nepovirus of subgroup c

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Cherry leaf roll virus (CLRV) is a member of the family *Comoviridae*, genus *Nepovirus*. The bipartite genome consists of RNA1 (7918 nucleotides, nt) and RNA2 approx. 6800 nt in length. Each RNA comprises a single open reading frame encoding one polyprotein being cleaved proteolytically into functional proteins. Both genomic RNAs contain a VPg at the 5' terminus as well as a 3' terminal poly(A) tail. The genome organisation of CLRV is according to other members of the genus; especially the long 3' non-coding region (3' NCR) of about 1600 nt of both RNAs is a typical feature of the *Nepovirus* subgroup c.

Sequence comparisons of coding regions of the RNA1 (a 523 nt fragment of the RNA dependent-RNA polymerase, RdRp), RNA2 (coat protein, CP, 1539-1542 nt) and the complete 3' NCR (1557-1602 nt) revealed that parts of the untranslated region exhibited higher sequence conservation than protein-coding parts of the genome. CLRV isolates analysed originated from different locations and host plants, thus representing various phylogenetic clusters as proposed by Rebenstorf et al. (2006). Protein encoding sequences exhibited a maximal nucleotide diversity of 23 %, whereas it was found that the 5' proximal part of 3' NCR directly adjacent to the stopcodon of the polyprotein showed higher variability (33 %). The middle part of the 3' NCR revealed 25 % nucleotide variability while the 3' terminal region was highly conserved (17 %). These findings of sequence conservation support the role of the 3' NCR involved in translational regulation (Dreher and Miller 2006). Furthermore, 3' NCRs of RNA1 and RNA2 originating from individual CLRV isolates are not identical, although they exhibit only moderate sequence variability of max. 2 %. This is in accordance with the 3' NCR sequences of other nepoviruses exhibiting isolate specific diversity of 3' NCRs of 1 % (*Tomato ringspot virus*) and 7 % (*Blackcurrant reversion virus*).

References

Dreher, T.W., Miller, A. (2006). Translational control in positive strand RNA plant viruses. *Virology* 344, 185 – 197.

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