Molecular properties of Cherry leaf roll virus

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The *Cherry leaf roll virus* (CLRV) is a globally distributed pathogen occurring primarily on deciduous, fruit and ornamental trees from at least 17 genera, including many economically important trees like walnut, cherry and birches. CLRV is a nepovirus of the *Comoviridae* within the *Picornavirus* superfamily with a bipartite genome organisation and protein expression strategy resembling other members of the genus. Nepoviral RNAs exhibit 3´ non-coding regions (3´ NCR) with extensive sequence identities (80-100 %), exclusively illustrated by the members of the nepovirus subgroup c, including the CLRV, with very large 3´ NCRs of over 1500 nt. Sequence comparisons between the RNA1 and RNA2 specific 3´ NCRs of six different CLRV isolates from different host plant species and phylogenetic groups displayed almost identical 3´ NCRs (97.5-99.5 %) for five CLRV isolates. A raspberry isolate exhibits 3´ NCRs with only 73.8 % sequence identity, raising the question about the prerequisite of sequence identity within the 3´ NCRs of a RNA population of an individual CLRV strain. So far, the question for the benefit of the long 3´ NCRs in any replication or translation mechanism is still unanswered, but the selective 3´ NCR sequence conservation of almost all previously analyzed nepovirus isolates, confirmed a strict necessity of identity for maintaining functional sequences within this region. It is commonly considered that homologous recombination is responsible for the 3´terminal sequence identity. But this is only one of several efficient mechanisms to ensure viability of RNA populations, at least for the CLRV since a raspberry isolate with non-homologous 3´ NCRs was found in this study.
Furthermore, a stable secondary hairpin structure was predicted within the analyzed 3´ NCRs of all six different CLRV isolates. This is located in a region with high sequence variability of up to 34 % and the conservation of this secondary structure suggests that it represents an important functional domain within the 3´terminus of CLRV-RNAs.