

## Molecular characterization of the *Cherry leaf roll virus*

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The *Cherry leaf roll virus* (CLRV) is globally distributed primarily on deciduous and fruit trees from at least 17 genera. Reports about CLRV occurrence are from temperate regions of Europe, the former USSR, North America, Syria, New Zealand, Japan and Chile. In these countries CLRV could be proved consistently in the forest, in public greens, plantations and in nurseries, mainly on birch, English walnut, black elderberry and sweet cherry. In Finland we observe an increasing impact of epidemic-like CLRV-infections within all investigated native *Betula* species.

The exceptionally wide woody host range and geographical distribution of CLRV indicates a genetic heterogeneity among CLRV-isolates of different origins. This was shown by sequence analysis of different genome regions and by serological testing.

The genome organisation of the bipartite RNA virus (family *Comoviridae*) corresponds to the classification as a subgroup c nepovirus. But there are some unique molecular features within the two CLRV-RNAs. One characteristic concerns the CLRV non-coding regions which are the shortest at the 5' ends and the longest at the 3' ends of the RNAs. The screening for translation-associated elements and secondary sequence analysis suggest a different functional regulation of translation as generally known for this virus family.