Abstract

Biological and molecular characteristics of different *Cherry leaf roll virus* (CLRV) isolates

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Cherry leaf roll virus (CLRV) is a pathogen spread throughout the world. Its hosts are mostly woody plants like cherry (*Prunus avium*), walnut (*Juglans regia*) and elderberry (*Sambucus spec.*) but also some herbaceous plants like rhubarb (*Rheum rhabarbarum L*.) can be infected. As CLRV is being spread mainly through seed or pollen, the natural transmission of the virus is presumably restricted to one host plant species in most cases. CLRV is taxonomically classified within the Family *Comoviridae*, Genus *Nepovirus*, Subgroup C due to its non-enveloped, icosahedral shaped virions which are 28 nm in diameter and its bipartite genome organisation of linear positive-sense ssRNA with a 1,5 kb long non-coding region at the 3'-end of RNA2. Ten isolates of CLRV from different host plants were analyzed by serological and molecular methods. For DAS-ELISA and IC-RT-PCR a polyclonal antiserum against purified CLRV particles of an isolate derived from black elderberry was raised. Using this polyclonal antiserum not all tested CLRV isolates were detectable, confirming the serological divergence of CLRV strains from different woody hosts. Purified virus preparations were analyzed by SDS-PAGE revealing no significant differences in coat protein size. Viral nucleic acids were separated by Agarose-gel-electrophoresis. In native RNA gels some of the CLRV isolates showed slight variations in length of both viral genomic RNAs. To evaluate the genome size of CLRV strains some isolates were separated under denaturing conditions and compared with a RNA standard marker. The RNA1 of CLRV isolates are approximately 8,2 kb long whereas the RNA2 are between 6,7-6.9 kb in length.