

## ***Epidemiological investigations on Cherry leaf roll virus***

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*Cherry leaf roll virus* (CLRV) is globally distributed in woody and herbaceous plant species including 17 genera. The wide host range and geographical distribution of CLRV indicate a fast adaptability to different hosts and therefore a genetic heterogeneity among CLRV-isolates of different origins. This was confirmed by molecular and serological analyses, which also revealed that phylogenetic affiliations are strongly correlated with the host plant species. This reflects the natural mode of transmission by pollen and seeds which require a high degree of host specificity of CLRV-isolates. However, transmission barriers are not absolute, as some CLRV isolates were found in phylogenetic groups not accordingly to their host plant species. Conclusively, further efficient modes of transmission must be relevant for CLRV distribution in natural habitats. In order to prove whether molecular properties reflect biological characteristics, the mechanical transmissibility of genetically diverse *Cherry leaf roll virus* (CLRV) isolates to different woody host plant species was tested. In an outdoor study three CLRV isolates from elderberry, walnut and sweet cherry were inoculated by stem slashing on *Sambucus nigra*, *Juglans regia*, *Prunus avium*, *Sorbus aucuparia*, *Betula pendula*. CLRV infected trees were detected by IC-RT-PCR, but molecular analysis could not identify the inoculated CLRV isolates as the causal agents. Thus indications towards varying capabilities of genetically diverse CLRV isolates to adapt to different hosts were not gained. As uninoculated control trees were found to be infected, we conclude that CLRV infection of trees was due to transmission from natural sources. This is supported by our findings of CLRV contaminated aphids sampled from elderberry (*Sambucus nigra*) seedlings of the experimental plot. It is shown that CLRV is a pathogen that may easily be disseminated by natural ways of transmission to healthy woody hosts.