Cherry leaf roll virus: genetics and epidemiology

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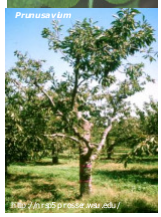
The *Cherry leaf roll virus* is a world-wide pathogen occurring primarily on deciduous and fruit trees from at least 17 genera, but also on ornamental and vegetable plants. Reports are for example from Europe, North America, Syria, New Zealand, Japan and Chile. In these countries CLRV could be proved consistently, and is present in the forest, in public greens, plantations and in nurseries, mainly on birch, elderberry and cherry.

The wide host range and geographical distribution of CLRV indicates a fast adaptability to different hosts and therefore a genetic heterogeneity among CLRV-isolates for different origins.
This was confirmed by sequence analysis of different genome regions and serological testing of many CLRV isolates. These results revealed that phylogenetic affiliations are strongly correlated with the host plant species (Rebenstorf et al., 2006).



Genetic features of CLRV

The 5`non coding region of RNA1 was identified by inverse PCR. Sequence analysis of the 150 bp fragment determines a 11 nt long 5`NCR and the N-terminus of the protease cofactor.

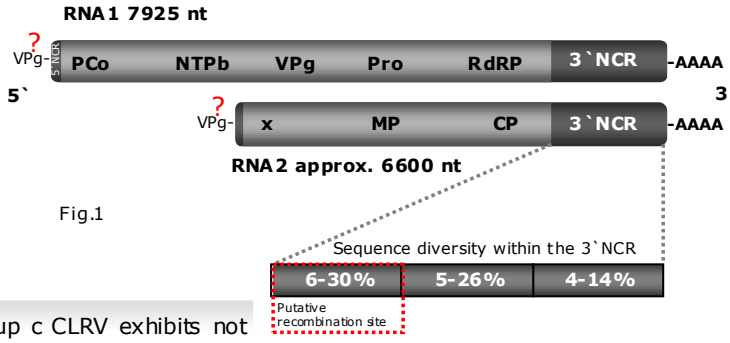


Fig.1

Within the nepovirus subgroup c CLRV exhibits not only the longest 3`NCR but also the shortest 5`NCR.

The CLRV is a subgroup c nepovirus because of its long RNA2 and 3`non coding region on both RNAs.
The extraordinary length of the 3`NCRs up to 1602 nt indicates an important functional role. This is substantiated by high sequence conservation within the 3`NCR of RNA1 and RNA2 (95-99%) as well as between different CLRV isolates (78-96%).

Sequence analyses of the coat protein and a fragment of the 3`NCR revealed grouping of a raspberry isolate into different phylogenetic clusters. This suggests that the raspberry isolate may be a natural CLRV-recombinant. Interestingly, CLRV shows high virulence in *Rubus idaeus* and therefore is treated as a quarantine pathogen in *Rubus*.

Transmissibility of CLRV isolates on different woody host plants

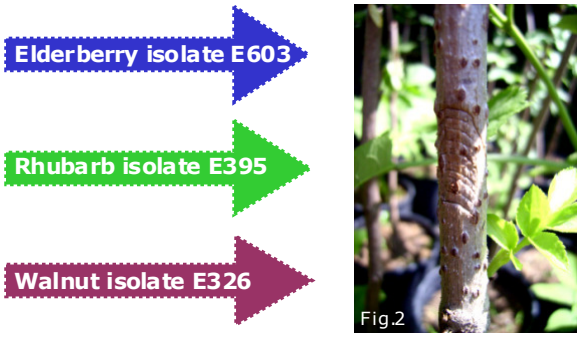


Fig.2

Fig.3

Three selected CLRV-isolates were inoculated on seedlings of five woody host plant species by stem slashing (Fig.2), (50 woody seedlings for every variant). 4 times within 2 years after inoculation the trees were screened for CLRV-infection by IC-RT-PCR. Infection rates of CLRV isolates as well as host range was very limited within this experiment. Conclusively, infectivity could be assessed for the elderberry isolate on *Sambucus nigra* (11 CLRV positive plants), and for the rhubarb and walnut isolates on *Juglans regia* (5/2 CLRV positive plants). There were several more CLRV positive plants of the different species, also among the untreated control plants, but by sequencing of the cloned IC-RT-PCR products the original inoculated isolates could not be reidentified. This suggests occurrence of natural CLRV infection by undetermined modes of transmission in a nursery-like experiment set-up (Fig.3).

Literature: K. Rebenstorf, T. Candresse, MJ. Dulucq, C. Büttner, C. Obermeier (2006): Host Species-Dependent Population Structure of a Pollen-Borne Plant Virus, *Cherry Leaf Roll Virus*. J Virol 80, 2453-2462.