Characterisation of Cherry leaf roll virus (CLRV) isolates from different host plants

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Cherry leaf roll virus (CLRV) is a widespread pathogen of woody plants in Germany and throughout the European community. It has been detected also in a limited number of herbaceous plants, e.g. rhubarb (Rheum rhabarbarum L.). CLRV has been reported to be of economical importance in European walnut plantations. In recent years it has been causing reduced yields in cherry trees in the United States, if occurring in mixed infections with Prunus necrotic ringspot virus or Prune dwarf virus. Sixty-three CLRV isolates from seventeen different host plant species were characterized on molecular and serological level. Phylogenetic analysis of a 280 bp fragment in the 3' non-coding region of the viral genomic RNA revealed six different isolate groups corresponding to their original host plant species. Also coat protein sequences of CLRV strains were compared leading to similar groupings. Furthermore clustering of CLRV variants based on viral sequence parts, resembled arrangement, based upon serological reactivity of isolates using a set of polyclonal and monoclonal antibodies. Results suggest, that the significant variability of CLRV strains and their association with certain host plant species is due to the natural mode of transmission of the virus by pollen and seed which presumably limits efficient cross-species transmission, leading to rapid genetic isolation and adaptation of CLRV variants to particular host species.

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