

Emergence of “birch-leafroll disease” in Fennoscandia correlated with significant changes in *Cherry leaf roll virus* population

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A viral epidemic associated with the *Cherry leaf roll virus* has emerged in *Betula* species in Fennoscandia exhibiting quick and effective dispersal. A population genetics approach is chosen in order to characterize the virus's diversity and the sources of genetic variation aiming to investigate factors that may affect this disease's emergence. Two CLRV populations are analyzed, one natural population originating from urban trees in Rovaniemi, Finland and one population that occurred after infecting young *Betula* seedlings with scions from the original trees based on RT-PCR data in the coat protein (CP), the RNA-dependent RNA polymerase (RdRp) and the 3'- untranslated region (UTR). Both populations are characterized by remarkably high genetic diversity. The CLRV variants detected in each genomic region are clustered into five-six different haplotypes, one of which was predominant in each population. Single trees are mixed infected by highly variable CLRV haplotypes that cluster into different phylogenetic groups. As an additional source of genetic variation, recombination events in the CP region are evidenced. Clustering of CLRV variants from birch to phylogenetic groups from other hosts implies potential virus's spillover from diverse hosts to *Betula* sp. We suggest that increased genetic diversity and the coexistence of a complex of highly variable strains in the same host constitute signs of a significant change in the pathogen population presumably leading to the disease's emergence.