

High genetic variability found among *Cherry leaf roll virus* variants from symptomatic birch trees in Rovaniemi (Finland)

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Cherry leaf roll virus in the birch forests in northern Finland has expanded widely during the last decade and rapidly turned to a severe epidemic. To investigate the genetic variability of the virus, 14 birch trees exhibiting heavy symptoms were selected in Rovaniemi. After total RNA-isolation from leaf samples, RFLP-analysis and partial sequencing of the genome were performed. A 420 bp-fragment from the 3'-untranslated region (3'-UTR) was cut with three restriction enzymes revealing at least 8 different genotypes based on the RFLP-patterns. The high variability was confirmed by the sequence analysis. From each RNA isolation fragments from three genetic regions were cloned and sequenced; 420bp from the 3'-UTR, 627 bp from the coat protein region (CP) and 318 bp from the RNA-dependent-RNA polymerase region (RdRp). Genotype variability was found to be high, 3-8 different genotypes were identified in each region. The highest variability was found in the UTR region and the genotypes found were in accordance with the genotypes obtained by RFLP-analysis of the 420 bp UTR-fragment. In the majority of the trees two different genotypes were found in at least one genetic region, suggesting the presence of at least two different virus variants within those trees. The genotypic diversity of the virus among trees is significantly higher than the diversity found earlier in Germany and Great Britain and this may constitute an explanation for the high disease severity in Finland.