

Does the high genetic variation found in *Cherry leaf roll virus* variants from Finland explain the epidemics of the "birch leaf-roll disease"?

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The "birch leaf-roll disease" is currently causing extensive epidemics in Fennoscandia strongly reducing the birch forest vigor. *Cherry leaf roll virus* has been often detected in diseased birch trees. First results on CLRV characterization from Finland showed that the virus variants from Finnish birches differ genetically from the ones described until now in birches from other regions. To further characterize Finnish CLRV strains we assessed samples from 14 birch trees from the area of Rovaniemi reported to be heavily infected (leaf discoloration and deformation as well as tree decline). PCR fragments from three genomic regions, the coat protein region (CP), the untranslated region (UTR) and the RNA-dependent-RNA polymerase region (RdRp) were amplified, cloned and sequenced. The data obtained from the genomic analysis revealed high CLRV variability within each tree and among trees. In the samples from the 14 trees examined, 5 to 6 different virus variants were found in each genomic region. Interestingly, almost all of the trees were infected with two or more CLRV variants. One genotype in each genomic region appeared predominantly (present in the 9-11 of the samples, depending on the genomic region). Maximal diversity at the nucleotide level between variants was 23.5 %. The diversity at the amino acid level was 16% and 11.2% in the CP and the RdRp region, respectively. The high genotypic and genetic diversity found in limited number of samples all originating from the city of Rovaniemi and covering a restricted geographic area suggests that the CLRV population related to the "birch leaf-roll disease" contains high levels of genetic variation. It is however questionable if this variability is the main reason of the wide disease occurrence or if more pathogenic factors contribute to the disease.