

## **Cherry leaf roll virus: a threat to Finnish *Betula* spp.**

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*Cherry leaf roll virus*, CLRV, was detected in Finland in several *Betula pubescens* ssp. *pubescens* (downy birch) trees exhibiting symptoms of a viral disease (Jalkanen et al. 2007); the virus could also be confirmed in *B. pendula* (silver birch), both are dominating deciduous tree species in the country. CLRV was found in *B. nana* (dwarf birch), *B. pubescens* ssp. *czerepanovii* (mountain birch) as well as *B. pubescens* ssp. *appressa* (Kiilopää birch) comprising key components of the arctic ecosystem. A single *B. pendula* var. *carelica* (curly birch) an ornamental tree variety used as expensive veneer wood was also found to be CLRV infected.

Fragments of the 3' non-coding region (3' NCR) were amplified by application of CLRV specific IC-RT-PCR.

Testing symptomatic birch trees confirmed CLRV infected birches including 6 different species or subspecies respectively over the country.

CLRV specific fragments from 3 downy birches from Rovaniemi, 2 silver birch trees (Lieksa, Vaasa) and one mountain birch (Inari) were sequenced. Genetic relationships were investigated by PCR-RFLP as well as sequence comparison with CLRV isolates characterised previously by Rebenstorf et al. (2006), who established 5 different phylogenetic groups (A-E) depending on the host plant. Nine individual CLRV clones obtained from 6 different *Betula* trees revealed two different fragment sizes, 404 bp and 412 bp, which were in accordance with grouping of Finnish CLRV isolates by PCR-RFLP (Buchhop et al. 2009). Unlike clustering of CLRV strains from birches growing in the UK and Germany exclusively within group A, Finnish CLRV isolates exhibited highest sequence identities to isolates clustered in phylogenetic group B, D or E. Furthermore, from two trees more than one sequence variant of CLRV was detected indicating a higher sequence variability of the virus not only in the Finnish birch population, but also in individual trees.

### References

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