Occurrence of EMARAV and CLRV in tree species native to Finland

N. Arndt¹, S. von Bargen¹, E. Grubits¹, R. Jalkanen², C. Büttner¹

¹Institute of Horticultural Sciences, Humboldt -Universität zu Berlin, Lentzeallee 55/57, D-14195 Berlin
phytomedizin@agrar.hu-berlin.de

²Metla, Finnish Forest Research Institute, Rovaniemi, Finland

Since the first report of accumulation of virus-like symptoms in downy birch (Betula pubescens) and silver birch (B. pendula) in Fennoscandia in 2007 by Jalkanen et al., Cherry leaf roll virus (CLRV) could be associated with the disease symptoms. Samples from symptomatic birch species showing leaf roll and proliferation, chlorosis, vein banding and mottling of leaves were collected in the following years from different regions in the country and assessed for a CLRV infection by RT-PCR. Furthermore, mountain ash trees (Sorbus aucuparia) with ringspot and mottling symptoms characteristic for an infection with the European mountain ash ringspot-associated virus (EMARAV) were included in the study as well as singular trees of other woody host species native to Finland. It was found that red elderberry (Sambucus racemosa) as well as six different Betula species which are typical deciduous tree species of the boreal forests were infected by CLRV; besides many virus affected silver and downy birches from locations all over the country, an individual sampled curly birch (B. pendula var. carelica) as well as several dwarf (B. nana), mountain (B. pubescens subsp. czerepanovii), and Kiilopää birches (B. pubescens subsp. appressa) growing in the northern part of the country up to the alpine tree line were CLRV affected. As expected symptomatic S. aucuparia trees were found to be infected by EMARAV; however an infection with CLRV of mountain ash could also be confirmed in two sampled trees revealing a mixed infection with the two viruses in a single case.

Sequence analysis of CLRV samples originating from birches in Finland based on short fragments of the coat protein (112 bp) and 3’ non-coding region (375 bp) revealed unique phylogenetic relationships of the virus isolates.

Jalkanen, R. et al. (2007) Silva Fennica 41, 755-762