

Cherry leaf roll virus – an emerging virus in Finland affecting several birch species



S. von Bargaen¹, L. Dierker¹, R. Jalkanen² & C. Büttner¹

1) Humboldt-Universität zu Berlin, Berlin, Germany, susanne.von.bargaen@agrar.hu-berlin.de
2) The Finnish Forest Research Institute METLA, Rovaniemi, Finland

METLA

STATE OF THE ART

Virus-related symptoms such as vein banding, leaf roll, chlorosis, and subsequent necrosis (Fig. 2) were found on birch leaves throughout Finland, northern Norway and Sweden. Disease symptoms occurring on downy birch, silver birch, dwarf birch, Kiilopää birch, mountain birch and curly birch could be associated with an infection of *Cherry leaf roll virus* (CLRV, Jalkanen et al. 2007, von Bargaen et al. 2009). CLRV is a positive stranded plant RNA virus (*Secoviridae* family, genus *Nepovirus*) infecting primarily deciduous trees and shrubs. In Finland disease symptoms in birch trees are spreading since their first record in 2002 and a countrywide incidence of CLRV could be shown in affected-birch trees tested since 2006 (Fig. 3).

DISTRIBUTION OF CLRV-INFECTED BETULA SPP. TREES IN FINLAND

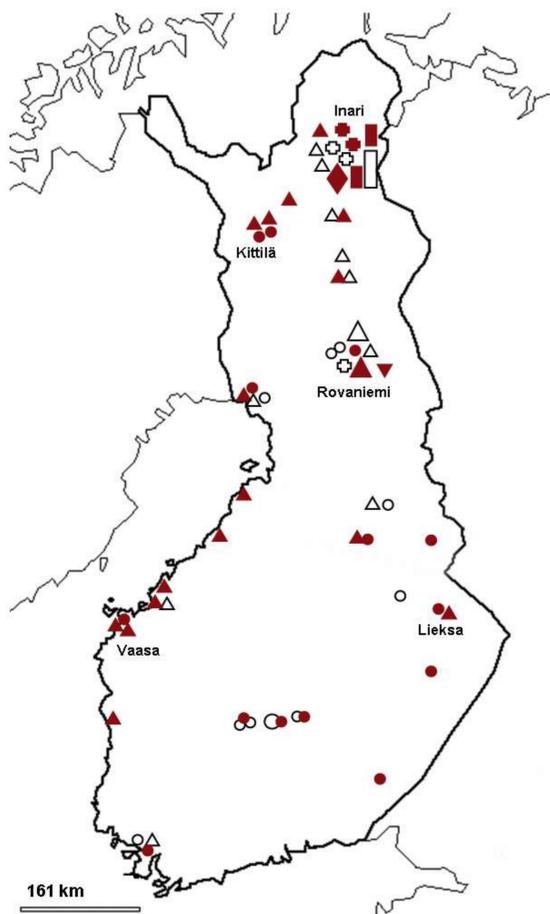


Fig. 3: Locations of sampled trees expressing virus-like symptoms. Species are indicated by following symbols: downy birch (Δ), silver birch (O), curly birch (▽), mountain birch (◻), Kiilopää birch (◊), dwarf birch (+). CLRV infected trees confirmed by IC-RT-PCR are indicated by red colored symbols. Small symbols represent one individual tree, middle sized symbols 4-5 trees, large symbols 10 or more trees.

LITERATURE

von Bargaen, S., Grubits, E., Jalkanen, R., Büttner, C. (2009). *Silva Fennica* 43, 727–738.
Jalkanen, R., Büttner, C., von Bargaen, S. (2007). *Silva Fennica* 41, 755–762.
Rebenstorf, K., Candresse, T., Dulucq, M.J., Büttner, C., Obermeier, C. 2006. *Journal of Virology*, 2453–2462.

ACKNOWLEDGEMENTS

This work was supported by funding through the DFG (BU 890/14-1). We gratefully acknowledge the Julius Kühn-Institute in Dahlem for provision of laboratory and office space during the renovation of our building.

SYMPTOM DIVERSITY IN VIRUS-DISEASED BIRCH SPECIES

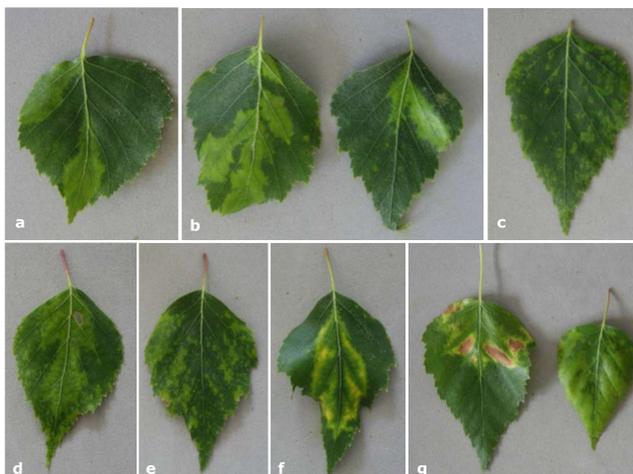


Fig. 1 Germany Symptoms observed in June 2009 in leaves of CLRV-infected silver birch trees in Berlin-Dahlem. Chlorotic vein banding, Schwarzer Grund (a) and Am Vogelsang (M0186, b), ringspots (M0197, c), chlorotic mottle M0255 (d) and M0336 (e), chlorotic line pattern (M0306, f) and chlorotic and necrotic vein banding (M0261, g)

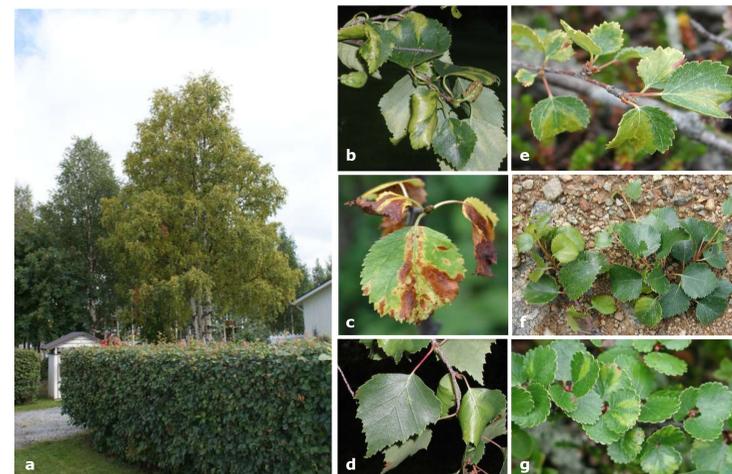


Fig. 2 Finland Symptoms observed in July and Aug. in native birch species. Downy birch, canopy of a symptomatic tree exhibiting chlorotic vein banding and leaf roll symptoms (a), vein banding and leaf roll (b), necrotic lesions (c) of leaves. Silver birch, leaf roll and chlorosis (d). Kiilopää birch, vein banding (e). Mountain birch, vein netting and chlorotic leaf patterns (f). Dwarf birch, intercostal chlorosis of leaves (g).

GENOME ORGANIZATION OF CLRV AND PHYLOGENETIC RELATIONS OF VIRUS VARIANTS OCCURRING IN FINNISH BIRCH SPECIES

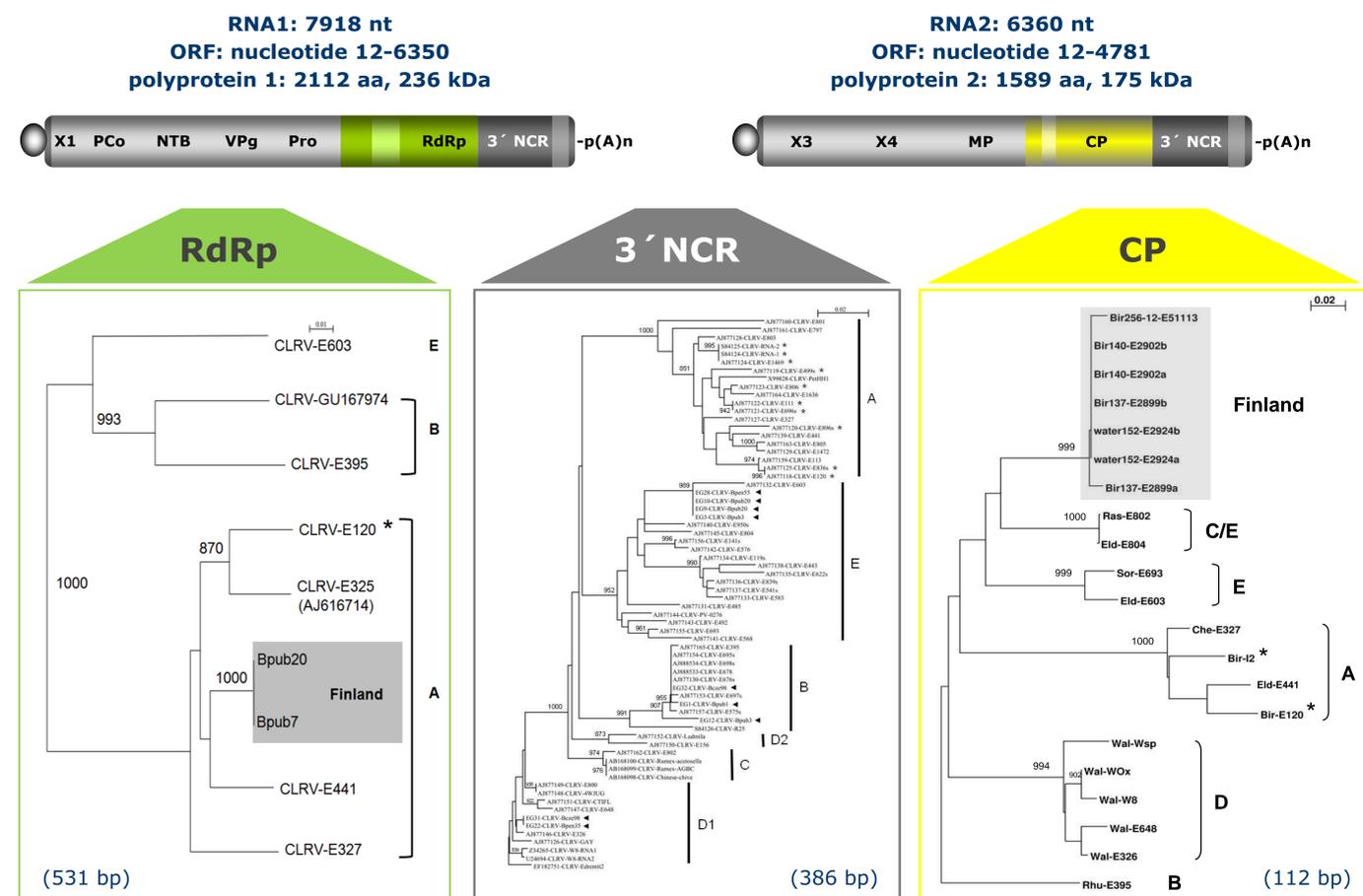


Fig. 4 Neighbor-joining phylogenetic trees calculated with ClustalX 2.0 using nucleotide alignments of fragments of the RNA1-encoded RNA-dependent-RNA polymerase (531 bp, RdRp), the 3' non-coding region (386 bp, 3' NCR), and the RNA2-encoded coat protein (112 bp, CP). Bootstrap analyses were performed with 1000 replications and values above 800 are indicated on branches. Phylogenetic clusters (A to E) as established by Rebenstorf et al. (2006) by analysis of the 3' NCR fragments of CLRV are indicated on the right side of the trees. Samples derived from Finnish locations are in grey boxes or are indicated by an arrow (<). CLRV isolates obtained from birches in Germany and Great Britain are representing phylogenetic group A and are indicated by an asterisk (*). Positions of the analyzed genomic regions are indicated by light colored columns within the model of the CLRV genome.

RESULTS AND CONCLUSION

- Symptoms observed in CLRV-infected birches in Finland are more prominent and differ from virus-affected birches from Germany (Fig. 1 and Fig. 2).
- Phylogenetic analyses of a conserved RNA1-encoded replicase- (RdRp) sequence fragment showed that grouping of CLRV variants obtained from Finnish birches correspond with host-dependent classification determined by Rebenstorf et al. (2006) (Fig. 4).
- Partial sequences obtained from the RNA2-encoded viral coat protein- (CP) as well as the 3' non-coding region (3' NCR) indicate towards the presence of a unique population of CLRV-sequence variants in Finnish birches (Fig. 4).