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9-9 Vector transmission of *Cherry leaf roll virus*? Candidate insect species infesting *Betula* spp.

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INTRODUCTION

Natural occurrence of *Cherry leaf roll virus* (CLRV) has been documented worldwide in a multitude of deciduous, fruit, and ornamental trees and shrubs as well as in a variety of herbaceous plants (Büttner *et al.* 2011). The most recorded natural hosts of CLRV are birch species (*Betula* spp.), black elderberry (*Sambucus nigra*), English walnut (*Juglans regia*) and sweet cherry (*Prunus avium*). To date, the host range comprises in total 26 plant genera. Known transmission pathways by seeds, pollen, water, or mechanically for instance, by roots intergrowth are considered as interacting factors for CLRV dispersal. Involvement of biological vectors in the epidemiology of CLRV has not been resolved by previous sporadic studies. So far, evidence of nematode´s attendance in CLRV transmission has not been supported (Jones *et al.* 1981; Wang *et al*. 2002). Also *Myzus persicae* (Sulzer) has been excluded as a vector of a CLRV-elm isolate by transmission experiments in previous studies 40 years ago (Ford *et al.* 1972). Yet, a hypothesis on insect transmission of CLRV was constituted by several proofs of CLRV-contaminated individuals from different insect species in Germany, such as the birch seed-feeding bug *Kleidocerys resedae* and aphids (Werner *et al.* 1997), *Polydrusus* sp. (leaf weevil; Rebenstorf 2005) from CLRV-infected birches, and aphids sampled from CLRV-infected black elderberry in a field study in 2006 (Langer, not published). Therefore, we target on elucidating the putative vector transmission by systematic monitoring of the invertebrate fauna of birches and elderberry in Finland and Germany to find potential CLRV vectors and study them in detail.

MATERIAL AND METHODS

A first case study (Bandte *et al*. 2011) was conducted to comprise the spectrum of potential vector insects in CLRV-infected *B. pendula* in Berlin-Dahlem. As sap sucking insects are the most likely group of potential vectors, aphids, bugs and cicadas (*Hemiptera*) were selected from the vast of arthropods (approx. 2400 individuals) which were captured by tapping the birches. Individuals of potential vector species were analyzed for CLRV contamination by

Immunocapture-RT-PCR using two antibodies (developed against CLRV isolates of two different serogroups) in parallel (Werner *et al.* 1997). Additionally, aphids (*Euceraphis betulae*) were collected in 2008 and 2009 from CLRV-infected *Betula pubescens* in Northern Finland. Since a specific antibody against Finnish CLRV isolates is not available yet, diagnosis was carried out by RT-PCR after total RNA extraction from pooled aphid samples.

RESULTS AND DISCUSSION

The largest group of target insects on *Betula pendula* in Berlin was represented by bugs (*Heteroptera,* 43%) with *Kleidocerys resedae* as the most frequent species. In total, ten bug species, eight cicada species, and nine aphid species were determined in CLRV-infected birches. Positive CLRV detection in *Kleidocerys resedae* (14/122) and the cicada *Kybos lindbergi* (1/6) by IC-RT-PCR substantiated previous findings. CLRV was not detected in any of the 26 tested aphid samples from Finland. The results obtained so far represent only a spot sample of experimental sites that will be systematically monitored for the next three vegetation periods. Insects will be tested for CLRV as described by (IC)-RT-PCR, additionally providing CLRV sequence fragments for phylogenetic profiling of CLRV variants gained from insects and their originating trees.

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