

regions (untranslated (UTR), coat protein (CP) and RNA-dependent RNA polymerase (RdRp) regions) were cloned and sequenced. In each region five to six genotypes were identified. Based on their abundance the genotypes were clustered in three groups: a. one predominant genotype that was present in the majority of the trees, b. a few genotypes common among 3-4 trees and c. rare genotypes detected only once. Concerning the within tree virus variability, a mixture of CLRV variants was found in each individual birch. This outcome is in accordance with the quasispecies evolution theory and elevated mutation rates in RNA viruses. The phylogenetic analysis showed that CLRV variants from the Finnish birches are highly variable belonging to 4 out of the 5 phylogenetic groups defined to date from a different hosts worldwide (REBENSTORF *et al.*, 2006). CLRV genetic diversity among trees was up to 16% for the UTR region - which is the diversity found universally among CLRV strains from all hosts -, and it was even higher in the CP and RdRp regions, reaching 23%. Summarizing, high genotypic and genetic diversity was found in CLRV population from *B. pubescens* from a relatively restricted area in Finland. Still, the CLRV variability is expected to be higher than identified in the analyzed samples, considering strong bottlenecks occurring during cell-to-cell movement and systemic colonization of tissues.

Literatur

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## 148 - Viruserkrankungen im Weinbau

*Viroses in viticulture*

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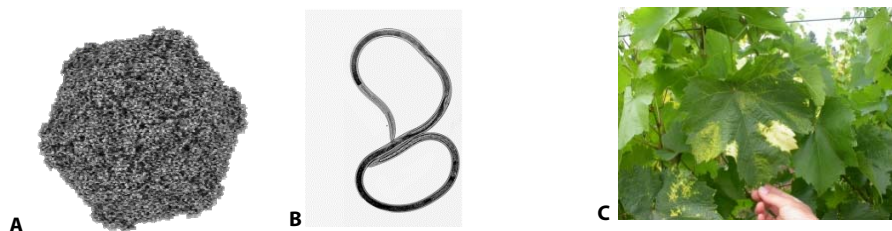
Im Weinbau sind Viruserkrankungen schwer zu identifizieren und momentan nicht behandelbar. Es ist daher unbekannt, wie stark verbreitet Virose tatsächlich sind.

In Europa unterliegen nur Anlagen zur Vermehrung von Rebenpflanzgut einer Kontrolle auf Viruserkrankungen. Die Daten der amtlichen Virustestung (2009-2013) wurden ausgewertet und ermöglichen einen Einblick in Häufigkeit und Verbreitung von Viren in Weinreben.

**Tab. 1** Ergebnisse der amtlichen Virustestung (2009-2013)

Getestete Stöcke insgesamt	Mischproben insgesamt	Virus-positive Mischproben
62.829	8967	371

In älteren Vermehrungsanlagen dominieren die leafroll associated viruses. Aber je jünger die Anlagen, desto höher der Anteil der Nepoviren (nematode transmitted polyhedral viruses). Dazu gehört auch das *Grapevine fanleaf virus*, welches die Reisigkrankheit verursacht und in Deutschland auch durch bodenlebende biotrophe Nematoden (*Xiphinema index*) übertragen wird. Dadurch etabliert sich ein Kreislauf von Infektion und Reinfektion und die Reisigkrankheit bleibt eine permanente Bedrohung im Weinbau.



**Abb. 1 Die Reisigkrankheit:** A - Grapevine Fanleaf Virus (GLFV), B - *Xiphinema index*, C - Symptome an *Vitis vinifera* ssp. *vinifera*

Daher stehen neue nachhaltige Bekämpfungsstrategien im Fokus der aktuellen Forschung. Besonders der frühe Krankheitsverlauf wird untersucht. Es wurde geprüft, ob eine Virusinfektion eine pflanzliche Abwehrantwort auslöst, ähnlich der bei anderen Krankheitserregern.

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## 149 - Molecular analysis of *Tobacco rattle virus* isolates from potatoes in various parts of Germany

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Tobacco rattle virus (TRV) is a widely distributed soil-borne pathogen which is transmitted by trichodoriid nematodes. The genome of TRV consists of two RNA species. TRV RNA 1 contains the genetic information for two replication associated enzymes, for the movement protein and for a silencing suppressor. TRV RNA 2 contains the coat protein gene and further genes for proteins necessary for the nematode transmission of the virus. TRV is able to infect many different plant species. It may cause considerable economic damage by greatly reducing the quality of various agricultural and horticultural products, especially of potatoes and ornamental plants. Infected potato tubers often develop symptoms of 'corky ringspot' or 'Eisenfleckigkeit' which make them unsellable. Some potato cultivars seem to be more susceptible than others, but there are also indications that in certain areas virus strains may occur which are able to overcome the resistance observed with some potato cultivars in other locations. Thus, Robinson (2004) has described a TRV strain which is able to break the normally observed TRV resistance of the cultivar Bintje. The nucleotide composition of the RNA 1 of this TRV strain (Pp085M) was found to differ considerably from that of the RNA1 molecules of other TRV strains.

In recent years we have analyzed the molecular properties of TRV isolates from potatoes in various parts of Germany. Considerable differences were observed not only in the nt compositions of the RNA 2 molecules, but also in those of the RNA 1 molecules which are assumed to be mainly responsible for the pathogenic effects of the virus in potatoes (Robinson, 2004). Three major groups of TRV RNA 1 molecules were distinguished, but the RNA 1 molecules in each individual virus source showed specific differences to the RNA 1 molecules of all other TRV sources from potatoes. The TRV RNA 1 molecules obtained from infected potatoes in Bavaria and in Hessen were closely