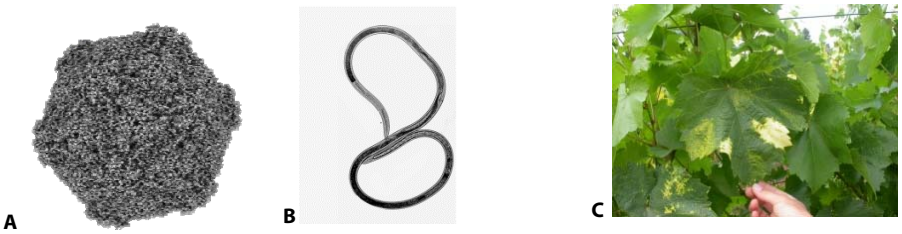


**Abb. 1 Die Reisigkrankheit:** A - Grapevine Fanleaf Virus (GFLV), B - Xiphinema index, C -Symptome an Vitis vinifera ssp. vinifera

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.

Literatur

SCHELLENBERGER, P., SAUTER, C., LORBER, B., BRON, P., TRAPANI, S., BERGDOLL, M., MRMONIER, A., SCHMITT-KEICHINGER, C., LEMAIRE, O., DEMANGEAT, G., RITZENTHALER, C., 2011: Structural insights into viral determinants of nematode mediated grapevine fanleaf virus transmission. PLoS Pathog. **7** (5).

GUTHA, L. R., CASASSA, L. F., HABERTSON, J. F., NAIDU, R. A., 2010: Modulation of flavonoid biosynthetic pathway genes and anthocyanins due to virus infection in grapevine (Vitis vinifera L.) leaves. BMC Plant Biology 10 (187).

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

**Kerstin Lindner, Renate Koenig[2]**

Julius Kühn-Institut, Institut für Pflanzenschutz in Ackerbau und Grünland
[2]Julius Kühn-Institut, Institut für Epidemiologie und Pathogendiagnostik

Tobacco rattle virus (TRV) is a widely distributed soil-borne pathogen which is transmitted by trichodorid 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

related to the originally described TRV Sym and TRV PpK20 RNA 1 molecules (Genbank accession numbers X06172 and AF314165). In central and northern Germany, however, we observed TRV RNA 1 variants which were more closely related to those which we had recently identified in two ornamental plants, i.e. in Alstroemeria and Hosta (Koenig et al., 2012 and 2013). These latter types of RNA 1 molecules have recently also been detected in potatoes in Poland (Yin et al., 2014). A third group of RNA 1 molecules in Northern Germany was found to be more closely related to those of some strains found in The Netherlands and North America. The RNA 1 of the resistance-breaking TRV type PpO85M described by Robinson (2004) has so far not been found in Germany. Investigations on the pathogenic effects of different TRV strains for various potato cultivars are now in progress.

References

KOENIG, R., LESEMANN, D.E., PFEILSTETTER, E., WINTER, S., PLEIJ, C.W., 2011. Deletions and recombinations with the RNA1 3' ends of different tobraviruses have created a multitude of tobacco rattle virus TCM-related RNA2 species in Alstroemeria and tulip. J. Gen. Virol. 92, 988-996.

KOENIG, R., LESEMANN, D.E., PLEIJ, C.W., 2012. Tobacco rattle virus genome alterations in the Hosta hybrid 'Green Fountain' and other plants: reassortments, recombinations and deletions. Arch. Virol. 157, 2005-2008.

ROBINSON, D.J., 2004. Identification and nucleotide sequence of a *tobacco rattle virus* RNA-1 variant that causes spraing disease in potato cv. Bintje. J**.** Phytopathology **152, 286-290.**

YIN, Z., PAWEŁKOWICZ, M., MICHALAK, K., CHRZANOWSKA, M., ZIMNOCH-GUZOWSKA, E., 2014. The genomic RNA1 and RNA2 sequences of the tobacco rattle virus isolates found in Polish potato fields. Virus Res. 185, 110-113.

## 150 - Detektion und Diversität des *European mountain ash ringspot-associated virus* (EMARaV) in Ebereschen (*Sorbus aucuparia* L.) in Norwegen

*Detection and variability of European mountain ash ringspot-associated virus (EMARaV) in Sorbus aucuparia L. in Norway*

**Theresa Büttner, Jenny Robel, Hans-Peter Mühlbach[2], Susanne von Bargen, Carmen Büttner**

Humboldt-Universität zu Berlin, Lebenswissenschaftliche Fakultät, Albrecht Daniel Thaer-Institut für Agrar- und Gartenbauwissenschaften, Fachgebiet Phytomedizin; Lentzeallee 55/57, 14195 Berlin, Deutschland
[2] Universität Hamburg, Biozentrum Klein Flottbek; Ohnhorststr. 18, 22609 Hamburg, Deutschland, phytomedizin@agrar.hu-berlin.de

Das *European mountain ash ringspot-associated virus* (EMARaV) ist ein negativ-orientiertes einzelsträngiges RNA Virus, welches 4 Genomsegmente enthält (Mielke und Mühlbach 2007). Das Virus ist in weiten Teilen Europas in Ebereschen (*Sorbus aucuparia*) verbreitet (Robel et al. 2013). In dieser Studie wurden erstmals 31 Blattproben von Ebereschen mit Symptomen wie chlorotischen Ringflecken und Scheckungen von verschiedenen Standorten in Norwegen auf eine EMARaV-Infektion untersucht. Zur Detektion des Virus wurden zwei unabhängige Fragmente innerhalb des kodierenden Bereichs der viralen RNA2 (300 bp) bzw. der 3´ nicht-translatierten Region der RNA3 (204 bp) mittels RT-PCR amplifiziert. Das Virus konnte in 9 Bäumen aus Mittelnorwegen nachgewiesen werden. Anhand des Sequenzvergleichs der RNA2 und RNA3 Fragmente wurde zum einen die Infektion der Ebereschen mit EMARaV bestätigt und zum anderen konnte die Variabilität der EMARaV Varianten miteinander verglichen werden. Die Identitäten der Aminosäuresequenzen der RNA2 Fragmente der norwegischen Varianten untereinander und im Vergleich mit EMARaV Sequenzen aus der Datenbank lagen zwischen 96,5-100%. Die RNA3 Fragmente zeigten auf Nukleotidebene Identitäten von 67,2-100% untereinander bzw. zu den bereits veröffentlichten Sequenzen. Es konnte gezeigt werden, dass es 2 Gruppen von Sequenzvarianten innerhalb der norwegischen viralen RNA3 Fragmente gab, die nicht mit der geografischen Distanz korrelierten.

Literatur

MIELKE, N., H.-P. MÜHLBACH, 2007: A novel, multipartite, negative-strand RNA virus is associated with the ringspot disease of European mountain ash (Sorbus aucuparia L.), J. Gen. Virol. **88**, 1337-1346.