Kmetijski inštitut Slovenije

Emaravirusi na robidah, malinah in gozdnih vrstah

Irena Mavrič Pleško (irena.mavric@kis.si)

8. Seminar in delavnica iz varstva gozdov Pokljuka, 12.9.2017

Kdo/kaj so emaravirusi?

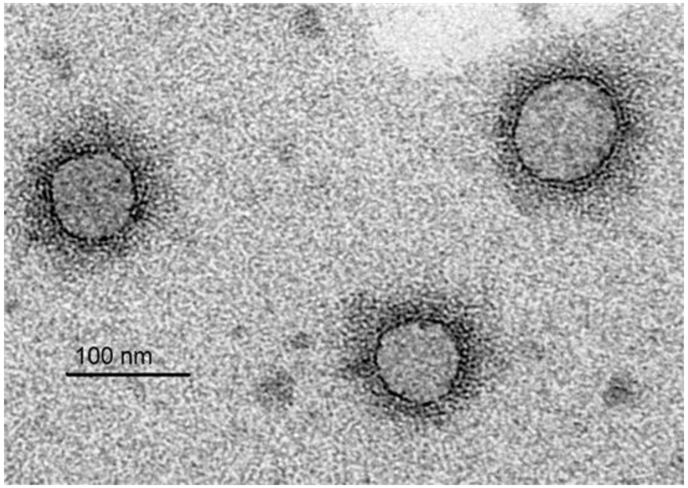
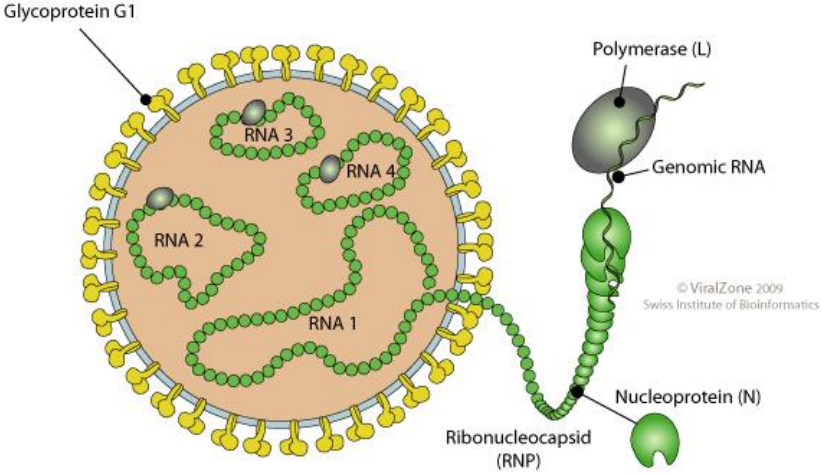
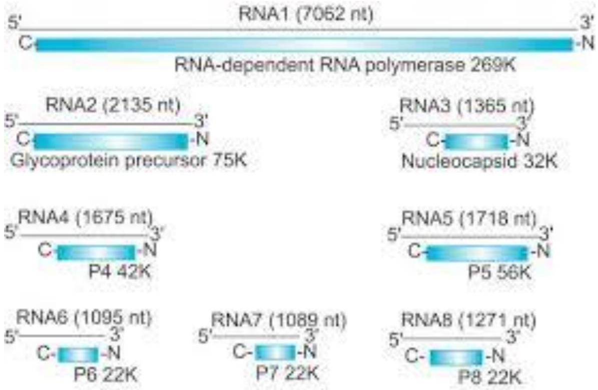


Foto: Inga Ludenberg, University of Hamburg



Vir: https://viralzone.expasy.org/771?outline=all_by_species



Vir: ICTV 2013.001aP, S. MacFarlane

Kmetijski inštitut Slovenije

malina

Raspberry leaf blotch virus – virus packavosti listov malinjaka (RLBV)

Foto: Darko Jevremović, Čačak

Divja robida

Virus soroden RLBV

Divja robida

Virus soroden RLBV

Divja robida

Virus soroden RLBV

Divja robida

Virus soroden RLBV

Divja robida – pršice šiškarice

Divja robida – pršice šiškarice

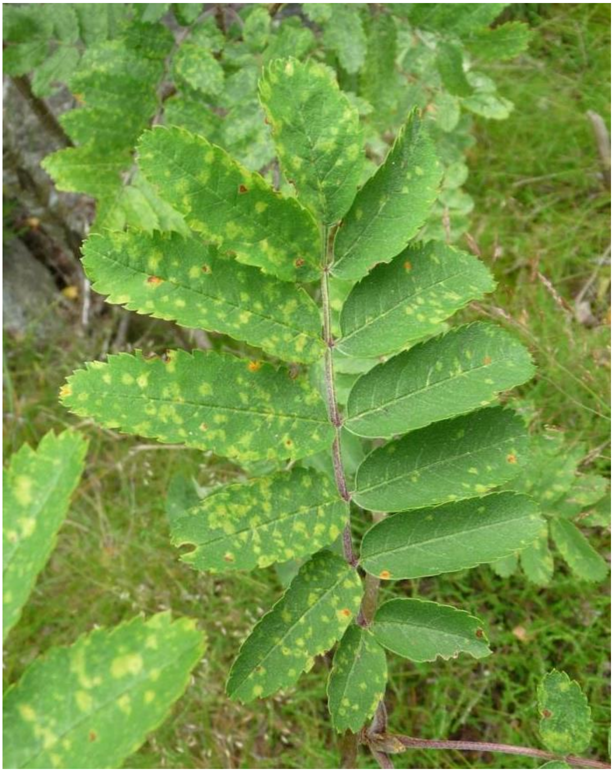
Divja robida – rja

Symptoms – *Sorbus* sp.

EMARaV

1) *S. aucuparia*, European mountain ash, jerebika – Berlin
2) *S. intermedia*, Swedish whitebeam, švedski mokovec – Västeras

S. aucuparia



S. intermedia, NGS 2015

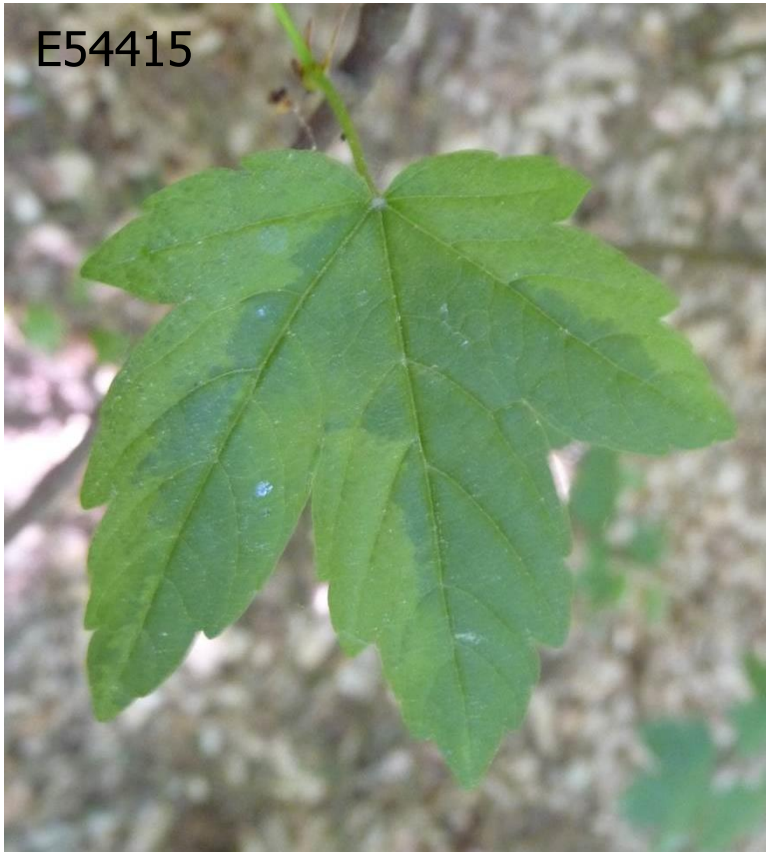
Symptoms – Quercus robur – dob

Emaravirus in common oak

Acer pseudoplatanus – beli javor

Emaravirus in maple

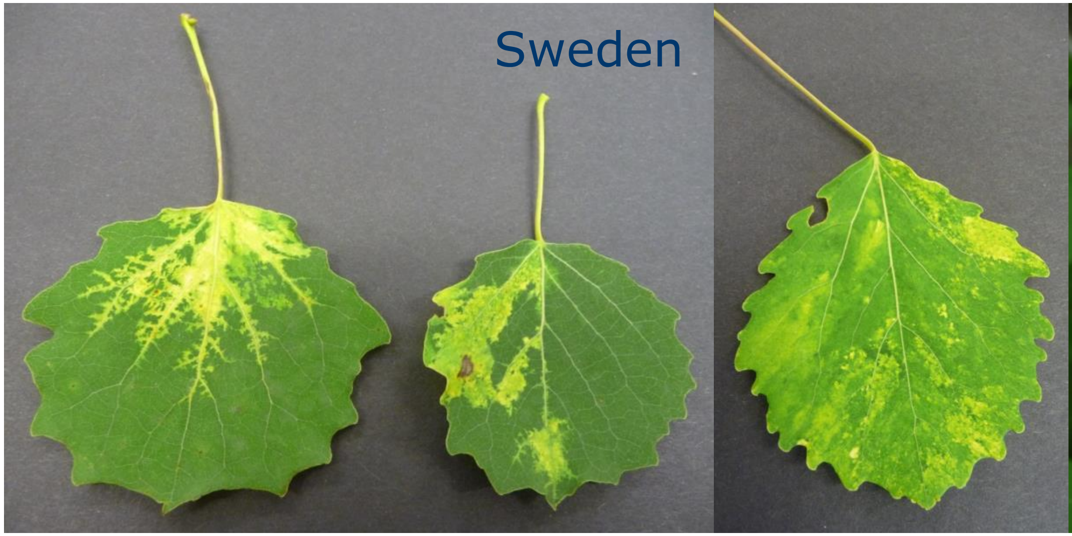
4) maple – Berlin, (Grunewald)



S. von Bargen
Division Phytomedicine

March 2017

Populus tremula – trepetlika



S. von Bargen
Division Phytomedicine

March 2017

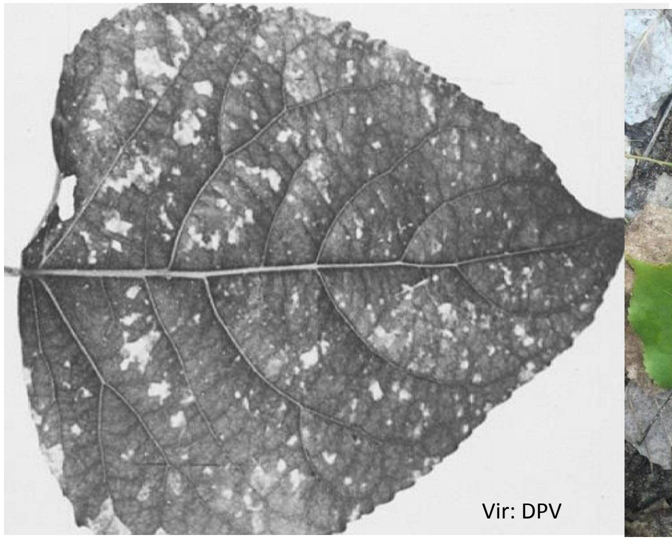
Fraxinus excelsior – veliki jesen

S. von Bargen
Division Phytomedicine

March 2017

Ostale virusne bolezni – mozaiki

topol (poplar mosaic)



Vir: DPV

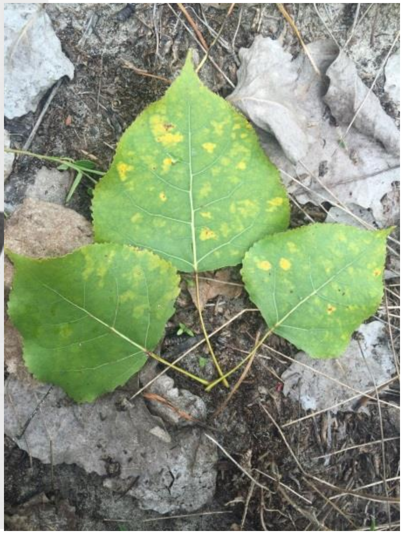


Foto: Jason Smith

jesen(ash mosaic)

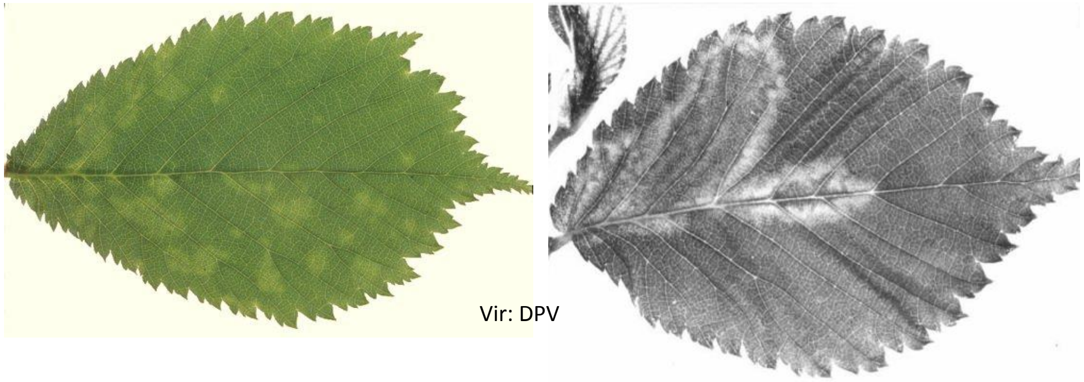
https://www.plantmanagementnetwork.org/pub/php/research/2013/ash/

Ostale virusne bolezni

Breza CLRV

Vir: http://dpg.phytomedizin.org/de/symposia/2015/iufro-viruses-in-trees-and-forests-unit-70204/

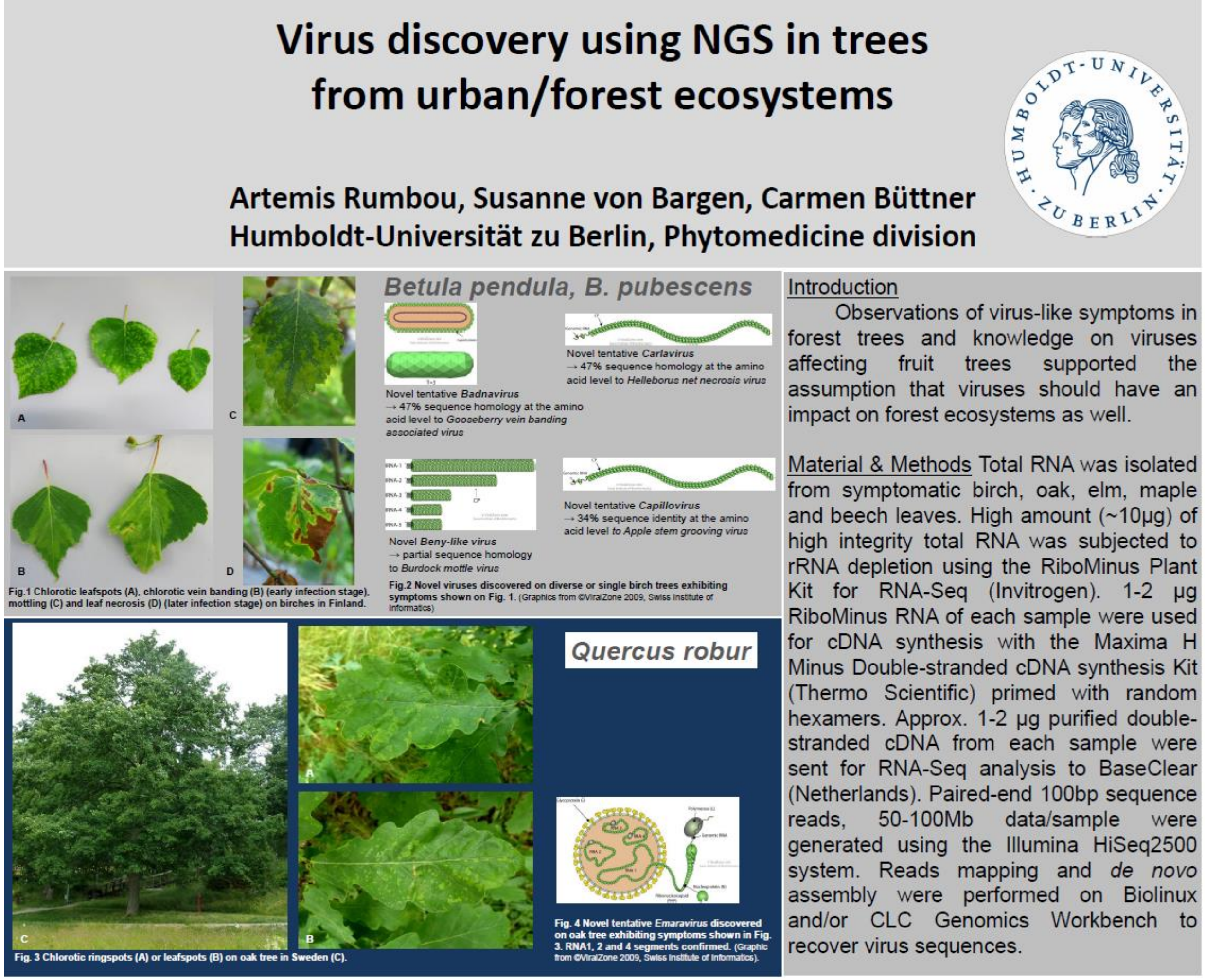
Brest – Elm mottle virus



Vir: DPV

Dren – več nepovirusov

Ostale virusne bolezni



Virus discovery using NGS in trees from urban/forest ecosystems

Artemis Rumbou, Susanne von Bargen, Carmen Büttner
Humboldt-Universität zu Berlin, Phytomedicine division

Fig.1 Chlorotic leafspots (A), chlorotic vein banding (B) (early infection stage), mottling (C) and leaf necrosis (D) (later infection stage) on birches in Finland.

Novel tentative *Badnavirus*
→ 47% sequence homology at the amino acid level to *Gooseberry vein banding associated virus*

Novel tentative *Carlavirus*
→ 47% sequence homology at the amino acid level to *Helleborus net necrosis virus*

Novel *Beny-like virus*
→ partial sequence homology to *Burdock mottle virus*

Novel tentative *Capillovirus*
→ 34% sequence identity at the amino acid level *to Apple stem grooving virus*

Fig.2 Novel viruses discovered on diverse or single birch trees exhibiting symptoms shown on Fig. 1. (Graphics from ©ViralZone 2009, Swiss Institute of Informatics)

Fig. 3 Chlorotic ringspots (A) or leafspots (B) on oak tree in Sweden (C).

Fig. 4 Novel tentative *Emaravirus* discovered on oak tree exhibiting symptoms shown in Fig. 3. RNA1, 2 and 4 segments confirmed. (Graphic from ©ViralZone 2009, Swiss Institute of Informatics).

Introduction

Observations of virus-like symptoms in forest trees and knowledge on viruses affecting fruit trees supported the assumption that viruses should have an impact on forest ecosystems as well.

Material & Methods Total RNA was isolated from symptomatic birch, oak, elm, maple and beech leaves. High amount (~10μg) of high integrity total RNA was subjected to rRNA depletion using the RiboMinus Plant Kit for RNA-Seq (Invitrogen). 1-2 μg RiboMinus RNA of each sample were used for cDNA synthesis with the Maxima H Minus Double-stranded cDNA synthesis Kit (Thermo Scientific) primed with random hexamers. Approx. 1-2 μg purified double-stranded cDNA from each sample were sent for RNA-Seq analysis to BaseClear (Netherlands). Paired-end 100bp sequence reads, 50-100Mb data/sample were generated using the Illumina HiSeq2500 system. Reads mapping and *de novo* assembly were performed on Biolinux and/or CLC Genomics Workbench to recover virus sequences.

Ostale virusne bolezni

cost EUROPEAN COOPERATION IN SCIENCE AND TECHNOLOGY

1st conference of the COST Action FA1407 – D.I.V.A.S. 16th – 18th November 2015 - Ljubljana – Slovenia

Virus discovery using NGS in trees from urban/forest ecosystems

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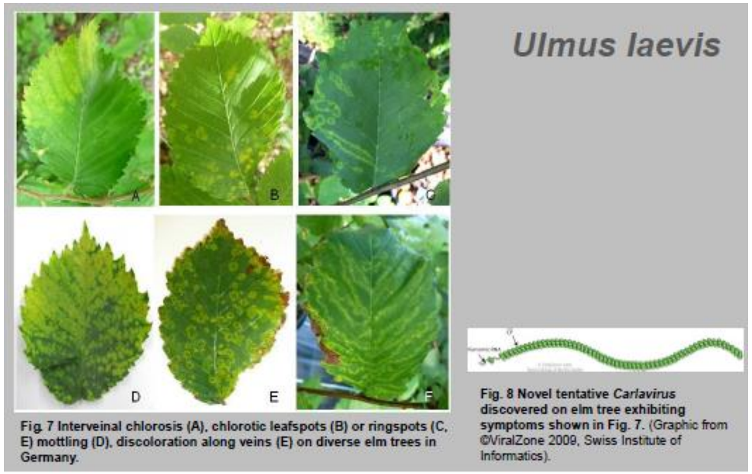
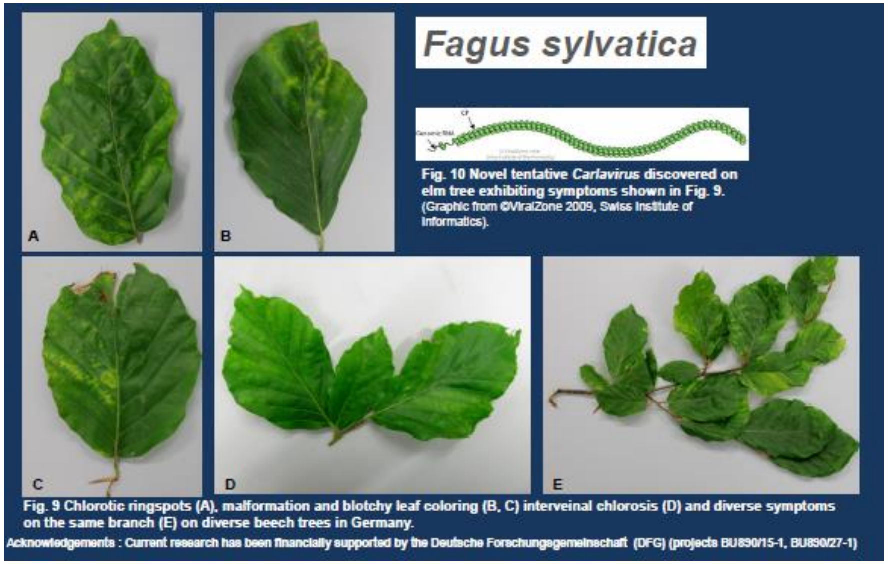


Ulmus laevis

Fig 7 Interveinal chlorosis (A), chlorotic leafspots (B) or ringspots (C, E) mottling (D), discoloration along veins (E) on diverse elm trees in Germany.

Fig. 8 Novel tentative *Carlavirus* discovered on elm tree exhibiting symptoms shown in Fig. 7. (Graphic from ©ViralZone 2009, Swiss Institute of Informatics).



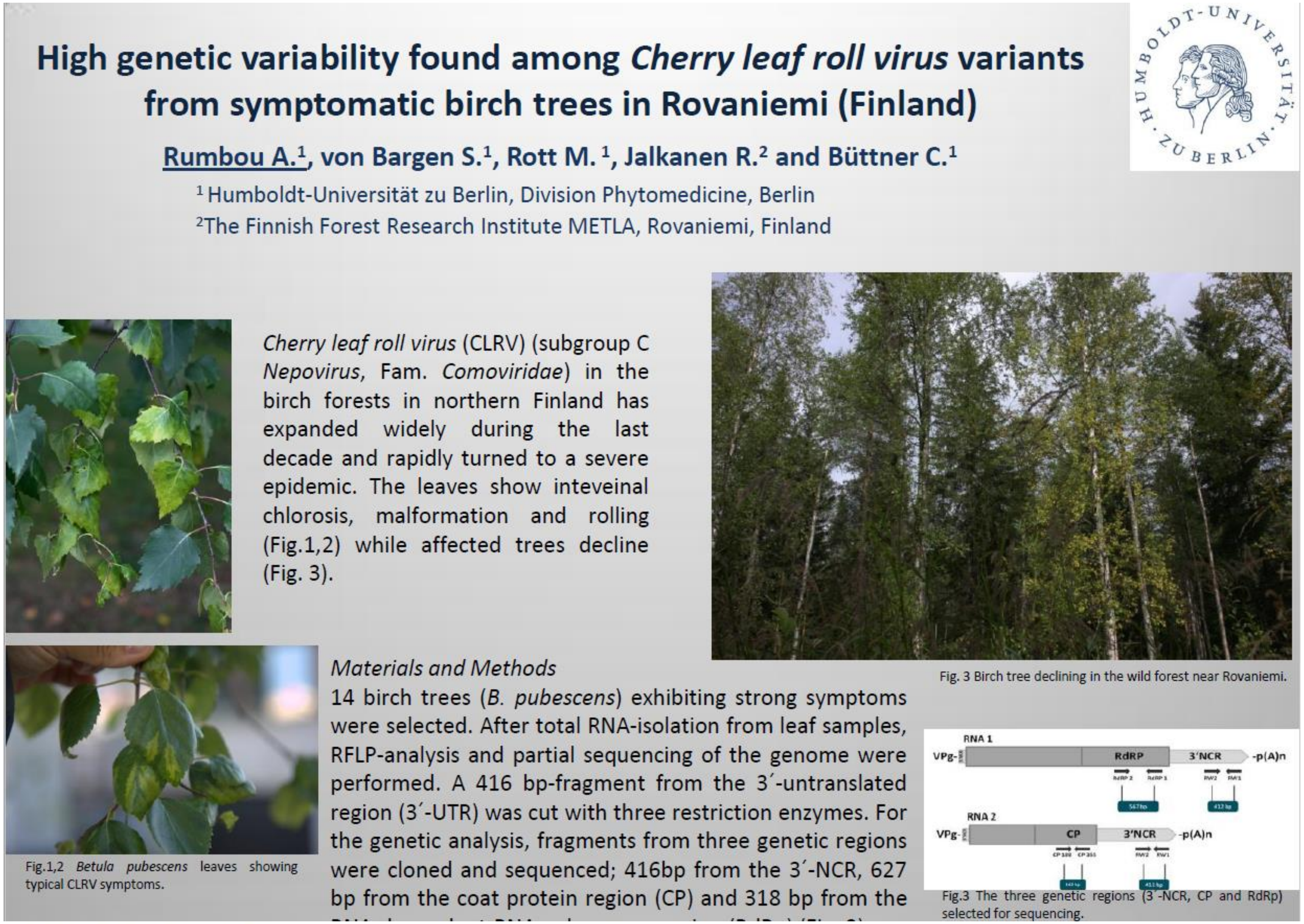
Fagus sylvatica

Fig. 10 Novel tentative *Carlavirus* discovered on elm tree exhibiting symptoms shown in Fig. 9. (Graphic from ©ViralZone 2009, Swiss Institute of Informatics).

Fig. 9 Chlorotic ringspots (A), malformation and blotchy leaf coloring (B, C) interveinal chlorosis (D) and diverse symptoms on the same branch (E) on diverse beech trees in Germany.

Acknowledgements : Current research has been financially supported by the Deutsche Forschungsgemeinschaft (DFG) (projects BU890/15-1, BU890/27-1)

Ostale virusne bolezni



High genetic variability found among *Cherry leaf roll virus* variants from symptomatic birch trees in Rovaniemi (Finland)

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[1] Humboldt-Universität zu Berlin, Division Phytomedicine, Berlin
[2] The Finnish Forest Research Institute METLA, Rovaniemi, Finland

Cherry leaf roll virus (CLRV) (subgroup C *Nepovirus*, Fam. *Comoviridae*) in the birch forests in northern Finland has expanded widely during the last decade and rapidly turned to a severe epidemic. The leaves show inteveinal chlorosis, malformation and rolling (Fig.1,2) while affected trees decline (Fig. 3).

Fig.1,2 *Betula pubescens* leaves showing typical CLRV symptoms.

Fig. 3 Birch tree declining in the wild forest near Rovaniemi.

Materials and Methods

14 birch trees (*B. pubescens*) exhibiting strong symptoms were selected. After total RNA-isolation from leaf samples, RFLP-analysis and partial sequencing of the genome were performed. A 416 bp-fragment from the 3´-untranslated region (3´-UTR) was cut with three restriction enzymes. For the genetic analysis, fragments from three genetic regions were cloned and sequenced; 416bp from the 3´-NCR, 627 bp from the coat protein region (CP) and 318 bp from the

Fig.3 The three genetic regions (3´-NCR, CP and RdRp) selected for sequencing.

Emaravirusi na robidah, malinah in gozdnih vrstah

Hvala
za
pozornost!