Detection of *Elm mottle virus* (EMoV) and a novel putative carlavirus in the genus *Ulmus* in northern Germany

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Introduction

Elm mottle virus (EMoV) is an isometric ssRNA(+) virus belonging to the genus *Ilarvirus* infecting elm trees (*Ulmus* sp.). In European elm (*U. laevis*) with chlorotic ringspots and chloroses, necroses and veinclearing (Fig. 1) approx. 750 nm filamentous particles were observed, indicating towards the infection with an additional virus (Bandte *et al.* 2004). Contigs were identified by high-throughput-sequencing (Illumina RNAseq) of total RNA extracts from symptomatic leaves of a European elm. They showed highest sequence identities to viruses of the carlavirus genus in BlastX. These findings point towards an infection of diseased elms with a putative **novel carlavirus**.

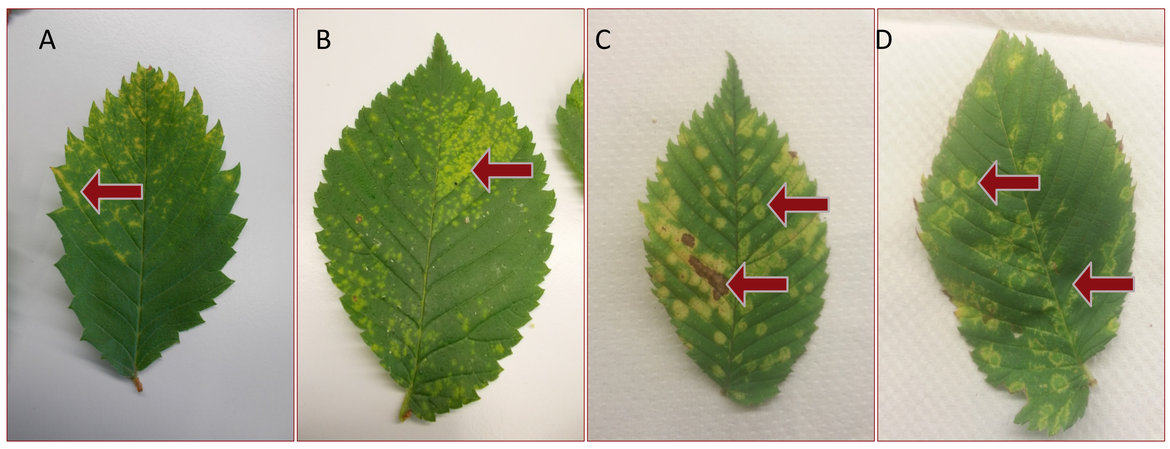

Fig. 1 virusspecific symptoms on elm leaves from the experimental garden
A – veinclearing B – mottle
C – chlorotic ringspots, necroses D – chlorotic ringspots, proliferation

Experimental setup

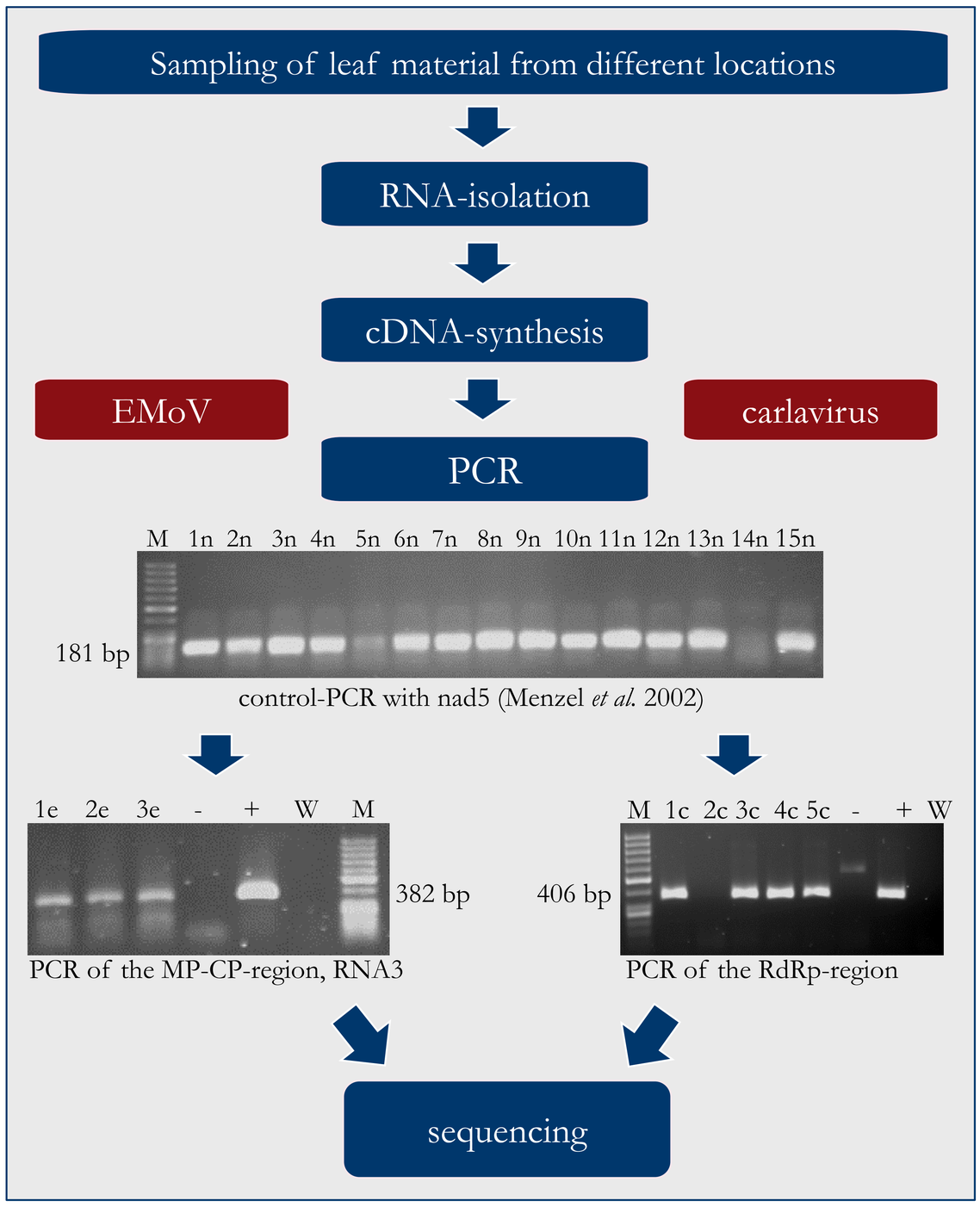

Fig 2: Overview of applied methods for virus detection with examples of results. Separation of PCR products by gel electrophoresis (denomination of PCR samples: n = nad5, e = EMoV, c = Carlavirus)

Results

Testing of leafmaterial of 103 elm trees from different locations (Tab. 1) by RT-PCR for EMoV and putative carlavirus infection (Fig. 2)

- 64 samples positive for put. Carlavirus → 62.0 %
- 8 samples positive for EMoV → 7.8 %
- 3 asymptomatic trees positive → 2.9 %
- 3 samples positive for both viruses → 2.9 %

→ The majority of symptomatic trees was infected by the putative carlavirus (66.7 %) while EMoV was not detectable.

Table 1: Overview of virus detection in elm trees from different locations

location	Virus-supected symptoms	No. of trees	EMoV positive	„carla“ positive	both positive
Berlin	chloroses, necroses, clearing	25	4	15	2
	no symptoms	3	1	0	0
Experimental garden	chloroses, ringspots, clearing, necroses,	34	0	29	0
	no symptome	3	0	2	0
Brandenburg	chloroses, proliferation of leaves	30	3	15	1
	no symptoms	1	0	0	0
Other locations northern Germany	chloroses, clearing	6	0	3	0
	no symptoms	0	0	0	0
total		**103**	**8**	**64**	**3**

Conclusions

Elm mottle virus was detectable in 8 elm trees from 2 different locations which was confirmed by Sanger-sequencing of PCR products followed by database search (blastn). Sequence identity of samples were between 98.6 and 100 % on nucleotide level.

PCR using specific primers designed for the detection of the novel **tentative carlavirus** confirmed 66.7% of samples showing virus-suspected symptoms to be infectd by the virus.. The virus could be detected in samples independent of the type of symptoms and location of the trees.

Some elms without visiible leaf symptoms were demonstrated to be infected by EMoV and the putative carlavirus. Furthermore, 3 trees from 2 different locations were mixed infected by both viruses. In several trees showing virus-like symptoms neither of the two viruses were detectable by RT-PCR suggesting that additional viruses may be involved in the observed disease.

This study provides first hints towards the impact of a putative carlavirus in the observed disease of Ulmus laevis.

References

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