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Genome organization of a novel emaravirus in Common oak (*Quercus robur* L.)

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Abstract

The emergent group of emaraviruses becomes more and more prominent. It contains several classified and unclassified members of different hosts ranging from important ornamental and economical plants like rowans, roses and fig to several deciduous trees. All these viruses have a segmented genome of a core of four monocistronic RNAs in common. The RNA1 encodes the RNA-depending RNA-Polymerase, the RNA2 encodes a glycoproteinpresursor, the RNA3 encodes the nucleocapsidprotein and the RNA4 encodes the supposed movement protein. Beyond this core components further number of genome segments varies greatly between different members of the genus. For some members eight fragments in total could be identified. However, their function in the viral life cycle remains to be determined. Here, a new putative member of emaraviruses was identified in a diseased Common oak in a nursery in Fellinghausen (Northern Westfalia). It was tentatively named Common oak ringspot-associated virus (CORaV) and shown to be widely spread in Germany, Sweden and Norway. High throughput sequencing and application of full length PCR according to Di Bello et al. (2015) allowed the determination of the genome structure of CORaV. Results support the relationship of the virus to members of the genus emaravirus.

References

Di Bello PL, Ho T, Tzanetakis IE. The evolution of emaraviruses is becoming more complex: seven segments identified in the causal agent of Rose rosette disease. Virus Research 210, 241–244.