

Emaraviruses in woody hosts - how far can you count?

Susanne von Barga¹, Marius Rehanek¹, Jenny Roßbach¹, Thierry Candresse², Hans-Peter Mühlbach³, Artemis Rumbou¹, Michael Kube⁴, Martina Bandte¹, Carmen Büttner¹

¹ *Humboldt-Universität zu Berlin, Division Phytomedicine, Lentzeallee 55/57, 14195 Berlin, Germany*

² *UMR 1332 BFP, INRA, Univ Bordeaux, 33882 Villenave d'Ornon, France*

³ *University of Hamburg, Biocenter Klein Flottbek, Ohnhorststraße 18, 22609 Hamburg, Germany*

⁴ *Johann Heinrich von Thünen-Institute, Institute of Forest Genetics, Eberswalder Chaussee 3a, 15377 Waldsiedersdorf, Germany*

ABSTRACT

European mountain ash ringspot-associated virus (EMARaV) is the type member of the genus *Emaravirus* comprising plant viruses with a segmented ss(-)RNA genome mainly infecting woody hosts. Emaraviruses consists of at least four conserved monocistronic genome segments within the enveloped spherical particle, encoding the replicase (RNA1), a glycoprotein precursor (RNA2), the viral nucleocapsid protein (RNA3), and a movement protein (MP, RNA4). Some members of the genus contain up to four additional genomic RNA molecules encoding proteins of unknown function. Until now, no genome segment has been identified in EMARaV encoding a 42 kDa protein which is orthologous to the functionally characterized MPs of related emaraviruses. Viruses within the genus are transmitted by eriophyid gall mites and have a narrow host range usually restricted to few related species. Recently, new tentative emaraviruses have been described, which are associated with diseases for instance in redbud and kiwifruit, by application of high-throughput sequencing techniques (di Bello et al. 2016, Zheng et al. 2016). Here, we report novel putative emaraviruses affecting different broad-leaved tree species with chlorotic ringspots, veinbanding, mosaic, mottle and/or leaf deformation. Viral sequences were retrieved from contigs assembled from raw data of a standard-paired end 100 library generated by a metagenomic approach with random hexamers or applying generic primers during the preparation of cDNA-libraries for illumina RNASeq. Preliminary analyses of results provide first insight into the genome organization of four putative new emaraviruses discovered in important deciduous tree species of the European forest and urban green space.

References:

Di Bello PL, Laney AG, Druciarek T, Ho T, Gergerich RC, Keller KE, Martin RR, Tzanetakis IE 2016. A novel emaravirus is associated with redbud yellow ringspot disease. *Virus Research* 222, 41–47.

Zheng Y, Navarro B, Wang G, Wang Y, Yang Z, Xu W, Zhu C, Wang L, Di Serio F, Hong N 2016. Actinidia chlorotic ringspot-associated virus: a novel emaravirus infecting kiwifruit plants. *Molecular Plant Pathology* doi:10.1111/mpp.1242.