Emaraviruses – an emerging genus with novel plant viruses affecting broadleaved tree species in Europe

Susanne von Bargen¹, Marius Rehanek¹, Max Tischendorf¹, Jenny Roßbach¹, Rim Al Kubrusli¹, Maria Landgraf¹, Thierry Candresse², Chantal Faure², Armelle Marais-Colombel², Katia Gindro³, Jean-Sébastien Reynard³, 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 Forschungsanstalt Agroscope Changins-Wädenswil, Route de Duillier 50, Case Postale1012, 1260 Nyon 1, Switzerland

ABSTRACT

The genus Emaravirus (Fimoviridae, Bunyavirales) comprises plant viruses with a segmented ss(-)RNA genome which are transmitted by eriophyid gall mites. Emaraviruses consists of at least five monocistronic genome segments within the enveloped spherical particle, encoding the replicase (RNA1), a glycoprotein precursor (RNA2), the viral nucleocapsid protein (RNA3), a movement protein (MP, RNA4), and a RNA5 encoding a small protein of 22-27 kDa with unknown function. Some members of the genus contain up to three additional genomic RNAs. Viruses within the genus have a narrow host range usually restricted to few related species. Most of them cause diseases in economically and ecologically important woody plants. Recently, new emaraviruses which are associated with diseases for instance in redbud, kiwifruit, and blackberry were discovered. These findings demonstrated that application of latest diagnostic techniques in plant virology such as next generation sequencing promotes the identification of novel members of this genus. Here, we report novel putative emaraviruses affecting different broad-leaved tree species exhibiting chlorotic ringspots, veinbanding, mosaic, mottle and/or leaf deformation. The viromes of Common oak (Quercus robur), European ash (Fraxinus excelsior), Eurasian aspen (Populus tremula), and sycamore maple (Acer pseudoplatanus) exhibiting virus-suspected symptoms were determined by highthroughput sequencing (NGS, RNA-Seq, Illumina). Analyses of NGS-generated sequence contigs identified plant viruses showing highest sequence identities to members of the genus emaravirus. Confirmation of NGS results by RT-PCR based specific detection allowed the association with observed symptoms and analysis of geographic distribution of these identified viruses. This study provides evidence that tentative novel emaraviruses are widespread in Europe and are associated with diseases of important deciduous tree species observed for a long time.