A novel virus is associated with the ringspot disease in Common oak (Quercus robur L.)

Marius Rehanek, Susanne von Bargen, Martina Bandte, Carmen Büttner

Humboldt-Universität zu Berlin, Albrecht Daniel Thaer-Institut für Agrar- und Gartenbauwissenschaften, Fachgebiet Phytomedizin, Lentzeallee 55/57, D-14195 Berlin, phytomedizin@agrar.hu-berlin.de

Abstract

Exploring the virome of deciduous tree species becomes more and more prominent and sheds light into the complex world of pathogens in woody plants. High-throughput sequencing technology (NGS) is a powerful tool to discover previously unidentified plant viruses. Applying such an approach to a diseased Common oak (Quercus robur) from a seed production stand in Fellinghausen, Germany led to the discovery of such a new virus. Sequence analyses revealed closest relationship to emaraviruses, a yet unassigned genus of viruses with a segmented single stranded RNA genome. Each genome segment encodes a single open reading frame in negative orientation; RNA1 consists the replicase, RNA2 a glycoprotein precursor, RNA3 the viral nucleocapsid protein, and RNA4 the putative movement protein of approximately 42 kDa (Mielke-Ehret and Mühlbach 2012). Some members of the genus contain up to four additional genomic RNAs encoding additional proteins of unknown function. The affected oak tree expressed chlorotic ringspots and mottle of leaves since several years. Specific RT-PCRs were established targeting the different identified genome segments of the putative novel emaravirus. They were applied to study the association of the virus with observed symptoms and to confirm the four putative viral RNAs in diseased oaks. Leaves from oak trees (n = 163) were sampled from sites in different European countries including a seed collection stand, park and forest trees. Virus detection was closely correlated with Common oaks exhibiting characteristic chlorotic ringspot symptoms while it was neither detectable in leaf material collected from trees without viruslike symptoms nor in Quercus spp. showing regular chlorotic patterns or partial chloroses of leaves. Showing a frequent infection of oaks in different locations indicates that it is widespread in oak populations in Germany, southern Sweden and Norway.

Reference

Mielke-Ehret N, Mühlbach HP. Emaravirus: A Novel Genus of Multipartite, Negative Strand RNA Plant Viruses. Viruses 4, 1515-1536.