Infection of *Ulmus laevis* (Pall.) with an unknown putative viral agent

Anne-Mareen Eisold, Markus Rott, Martina Bandte, Carmen Büttner

Humboldt-Universität zu Berlin, Department of plant and animal sciences, Division Phytomedicine

phytomedizin@agrar.hu-berlin.de

Plant viruses occur in herbaceous and woody plants worldwide such as in trees of forests and urban green and are known to cause severe yield losses. Visible symptoms of a virus infection comprise from chlorotic ringspots, mottling, necroses, deformation of leaves and sprouts. As a result plants suffer from a reduction of photosynthesis capacity, growth depression, dieback and a strong susceptibility to other stress factors. Due to the lack of curative measures, one of the most important management tools is to provide healthy plants and seeds for planting and prevent virus transmission within the stand. Prerequisite for understanding the spread of infectious viruses and for epidemiologic prognoses is the characterization and identification of the pathogen. Elms are known to be affected by viruses such as *Elm mosaic virus* (EMV), *Elm mottle mosaic virus* (EMoV), *Cherry leaf roll virus* (CLRV), *Tomato bushy stunt virus* (TBSV) and *Tomato ringspot virus* (ToRSV) based on visual and serological studies.

Within the study a 150 years old population of European white elm (*Ulmus laevis* Pall.) of 30 trees in the park of Caputh near Berlin with assumed virus symptoms were frequently monitored over 13 years. 15 elms were selected developing distinct leaf symptoms such as chlorotic ringspots, necroses and dieback, suggesting a virus as causal agent. Investigations on characterization and identification of a putative viral pathogen in these trees are initiated. Leave samples were tested towards so far known viruses, none could be detected. The mechanical transmission of the agent was confirmed by transmission experiments with *Chenopodium quinoa* as well as by grafting tests. Applying molecular biology methods such as reverse transcriptase polymerase chain reaction (RT-PCR), analysis of double stranded

RNA (dsRNA) and virus purification sequence information of the pathogen shall lead to identification of the causal agent. The putative viral sequence will be confirmed by comparison with virus sequences available in the NCBI (National Center for Biotechnology Information) database.