Molecular basics of seed transmissibility of Cherry leaf roll virus (CLRV)

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The plant pathogen *Cherry leaf roll virus* (CLRV) is a worldwide spread Nepovirus that infects a wide range of herbaceous and woody hosts. The virus is reported to spread in nature mainly vertically by seed, but also horizontally by pollen. Although transmission through seed is a critical epidemic feature of approximately one fifth of the plant viruses (Maule & Wang, 1996), the underlying mechanisms of seed infection are not specified. In 2009 it was reported that seed transmission is also possible in *Arabidopsis thaliana* plants (Rumbou *et al.*). The serological and phylogenetic different isolates CLRV-E395 from rhubarb and CLRV-E603 from elderberry were found to a) infect *A. thaliana* plants, b) spread systemically and c) be transmitted through seed in this host. Therefore the model system *A. thaliana*-CLRV is suggested to be suitable for investigating virus-plant interactions involved in meristem invasion and seed transmission.

To identify plant and viral genes we intent to screen a cDNA expression library derived from *A. thaliana* applying the Gal4-yeast two-hybrid system (YTHS, Clontech) to study protein-protein interactions. The Gal4-YTHS permits the investigation of protein interactions under physiological conditions in the eukaryotic background of the Yeast *Saccharomyces cerevisiae* (Guo et al., 2008). The viral coat protein (CP, 512 aa, 54 kDa) and the putative movement protein (MP, 385 aa, 42 kDa) of the isolates CLRV-E395 and CLRV-E603 are applied as bait proteins for the YTHS-based screen of interacting proteins. The *A. thaliana* cDNA library was constructed from a callus cell culture of *A. thaliana* cv. Columbia fused to the GAL4-activation domain (Nemeth *et al.*, 1998). Thereby the cDNAs represent the expression pattern of undifferentiated cells similarly found in meristematic tissues of vegetative and generative organs. This study is aimed to investigate the virus invasion into these plant tissues.

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