Identification of the protein interaction domain of the putative movement protein of *Cherry leaf roll virus* (CLRV)

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The putative movement protein (MP) of *Cherry leaf roll virus* (CLRV) is encoded by RNA2 upstream of the coat protein (CP) coding region. Yeast-two hybrid (YTH) studies revealed dimerization of the viral MP and CP, as well as the specific interaction of both proteins. Additionally, specific binding of the CLRV-MP to a plant protein (At-4/1) which localizes to plasmodesmata was demonstrated. These protein-protein interactions may play a substantial role in tubule-guided cell-to-cell transport of the virus within its host plant.

Therefore, we aimed to identify the peptide sequence of the CLRV-MP responsible for dimerization, binding to CLRV-CP as well as to the host factor At-4/1 and constructed 5 different N- and C-terminal deletions of the MP of the rhubarb strain CLRV-E395 (385 aa, 42 kDa). Investigating MP-deletion constructs in YTH revealed that the region between aa 46 and 80 of the putative MP of CLRV is most important to facilitate dimerization of CLRV-MP-E395 as well as binding to CLRV-CP and At-4/1. The 45 first aa of the N terminus (construct ΔN1) could be deleted without a negative effect on homo- or heterodimerization of the CLRV-MP. On the contrary when the first N terminal 80 aa of the putative MP of CLRV were deleted (construct ΔN2) protein binding was completely abolished. Also, when the last 142 aa of the C-terminal region of the CLRV-MP are missing (constructs ΔN1-C1 and ΔC1) dimerization and interaction with other proteins is hampered. However, the first 80 aa of the N terminus (construct ΔC2) showed enhanced binding to other interaction partners when compared with the full length constructs. These findings support our hypothesis that the coiled-coil structure predicted for aa 54-71 of the CLRV-MP is a functional domain essential for protein binding.