Analysis of the movement protein coding region of *Cherry leaf roll virus* (CLRV)

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ABSTRACT

Cherry leaf roll virus (CLRV) is a worldwide distributed plant virus infecting a wide range of woody and herbaceous hosts (Büttner et al. 2011). The isometric, bipartite virus consists of 2 single stranded RNA genome segments, each encoding a large open reading frame. The putative movement protein (MP) as well as the coat protein (CP) is encoded by RNA2 (von Bargen et al. 2012). MP and CP are involved in tubule-guided cell-to-cell movement of CLRV particles, thus enabling systemic infection of host tissue. This includes the invasion of gametophytes which is a prerequisite for effective virus dispersal via pollen and seed. Both gene products are expressed as part of polyprotein 2 (P2) which is postranslationally processed into its functional subunits by the viral proteinase encoded on RNA1. We analyzed the cleavage sites utilized to release the putative MP and the CP from the P2 in order to further characterize the mature peptides. Protein-protein interaction analyses revealed dimerization of the viral MP and CP, as well as the specific interaction of both proteins. Specific binding of the CLRV-MP to a plant protein (At-4/1) which can be associated with plasmodesmata was demonstrated. The regions within the putative MP responsible for dimerization and specific binding of other proteins were determined by analysis of deletion mutants.

References

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