A new potyvirus virulence determinant: the CI C-terminus modulates pathogenicity of Lettuce mosaic virus in lettuce

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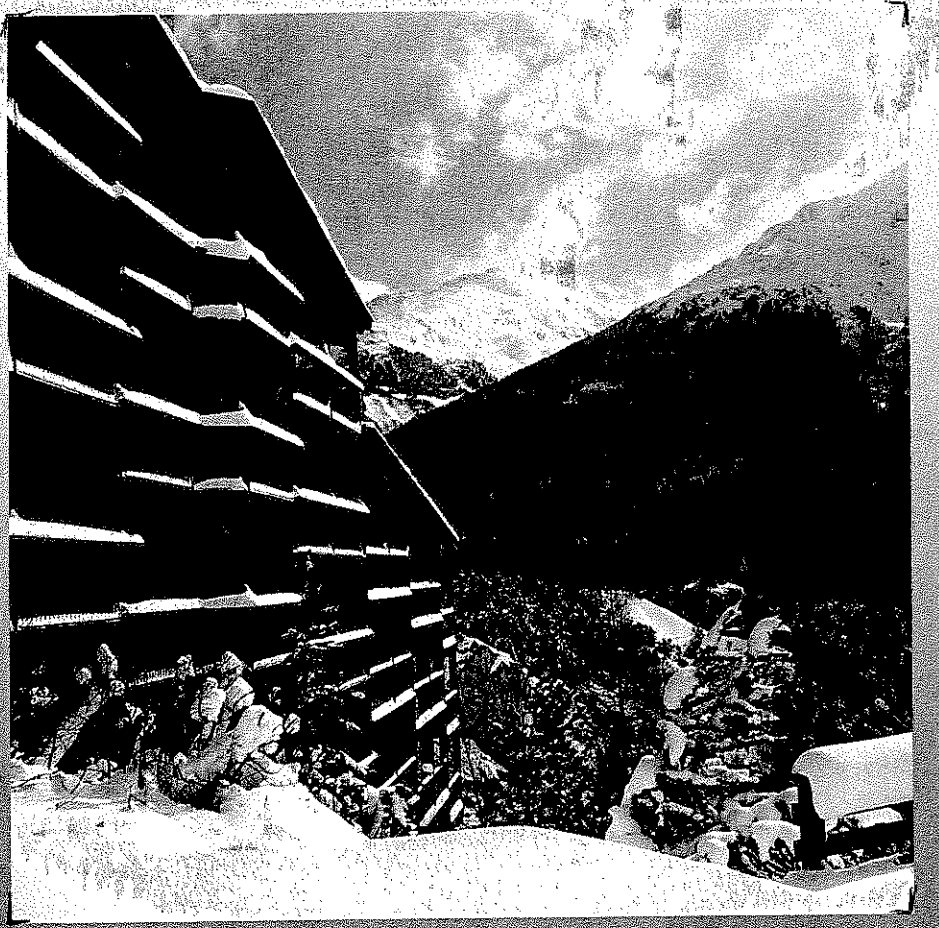

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A new potyvirus virulence determinant: the CI C-terminus modulates pathogenicity of *Lettuce mosaic virus* in lettuce.

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In recent years, components of the eukaryotic translation initiation complex were identified as essential determinants in the outcome of RNA virus infections, including potyviruses. In particular, recessive allelic genes *mo1*^{1} and *mo1*^{2} in lettuce, currently used to protect lettuce crops against *Lettuce mosaic virus* (LMV), were shown to correspond to mutant alleles of the gene encoding eIF4E (2, 3). Recently, the LMV resistance-breaking determinants were analyzed and shown to map not only to the VPg encoding region (identified so far as the single potyvirus virulence determinant) but also to the C-terminus of the CI helicase, providing the first example of a potyvirus CI acting as a determinant for eIF4E-mediated recessive resistance breaking (1). By performing *in vitro* and *in vivo* interaction assays, a complex interaction network between the LMV CI and other factors, such as the viral VPg and the plant eIF4E was revealed. Furthermore, through a global survey of the biological and molecular diversity of LMV isolates, we showed that propagation of several non-lettuce isolates of LMV in *mo1*^{1} plants is accompanied by a gain in pathogenicity correlated with the accumulation of mutations in the C-terminus of the CI. The contribution of those CI mutations to the viral fitness in susceptible and resistance lettuce and to *mo1* alleles-breaking is currently being evaluated.

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