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Cross-adaptation of endive necrotic mosaic potyvirus to different species of the Asteraceae is due to VPg mutations with pleiotropic effects

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Cross-adaptation occurs when adaptation to a novel environment, for example a novel host species, drives also an adaptation to another environment to which the organism was not exposed and that did not act as a selection factor. In natural conditions, endive necrotic mosaic virus (ENMV) is mostly confined to wild salsify (*Tragopogon pratensis*) and infects occasionally lettuce (*Lactuca sativa*) crops. To investigate the capacity of viruses to infect novel host species and the associated mechanisms, we performed an experimental evolution of ENMV in five species of the family Asteraceae (*L. sativa*, *T. pratensis*, *Calendula arvensis*, *Zinnia elegans* or *Cichorium endivia*).

Increase in viral pathogenicity was observed in *C. arvensis* and *Z. elegans* only and cross-adaptations between *C. arvensis* and *Z. elegans* were also noticed. Parallel nonsynonymous substitutions were observed at different nucleotide positions in the VPg cistron of the adapted ENMV populations, and were candidates for the observed pathogenicity changes. Some of these were shared between *C. arvensis*- and *Z. elegans*-evolved populations, and could explain the cross-adaptations.

Using a reverse genetics approach with an infectious cDNA clone of ENMV, we validated that several of these mutations were sufficient to confer adaptation to *C. arvensis*, *Z. elegans* or both. This result indicates that the molecular mechanisms involved in host jumps of ENMV, i.e. adaptation to novel species, can be similar to those involved in resistance breakdown for other potyviruses, i.e. adaptation to novel genotypes carrying resistance genes within a species, since they involve the same viral protein and, partly, the same protein domains.

Using a larger set of species of the Asteraceae, we are now testing the hypothesis that such cross-adaptations occur preferentially at the within-tribe level in this botanical family.