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Genetic Determinism and Evolutionary Reconstruction of a Host Jump in a Plant Virus

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In spite of their widespread occurrence, only few host jumps by plant viruses have been evidenced and the molecular bases of even fewer have been determined. A combination of three independent approaches, 1) experimental evolution followed by reverse genetics analysis, 2) positive selection analysis, and 3) locus-by-locus analysis of molecular variance (AMOVA) allowed reconstructing the *Potato virus Y* (PVY; genus Potyvirus, family Potyviridae) jump to pepper (*Capsicum annuum*), probably from other solanaceous plants. Synthetic chimeras between infectious cDNA clones of two PVY isolates with contrasted levels of adaptation to *C. annuum* showed that the P3 and, to a lower extent, the CI cistron played important roles in infectivity toward *C. annuum*. The three analytical approaches pinpointed a single nonsynonymous substitution in the P3 and P3N-PIPO cistrons that evolved several times independently and conferred adaptation to *C. annuum*. In addition to increasing our knowledge of host jumps in plant viruses, this study illustrates also the efficiency of locus-by-locus AMOVA and combined approaches to identify adaptive mutations in the genome of RNA viruses.

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