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**OP-56: Do recombinants appearing in natural populations of watermelon mosaic virus represent new agronomic threats?**

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*Watermelon mosaic virus* (WMV, *Potyvirus*) is very common in France where it has been present for at least 40 years. Since the early 2000s, new "emerging" (EM) strains of WMV, highly divergent molecularly from the "classic" (CL) strains present before and probably originating from recent introductions, were detected in southeastern France. Since both types of strains did not appear to be present in the same geographic locations before, this situation constituted a unique opportunity to study the frequency of appearance and the potential spread of recombinants in the few years following the introduction of the new strains. Analyzing isolates from experimental plots in Montfavet (Southeastern France) as well as from epidemiological surveys performed from 2004 to 2008 all around France (about 2000 WMV isolates) revealed at least 7 independent recombination events, either between CL and EM strains or between different EM subgroups. Most recombinants were found in a few plants from the same field, but, with one notable exception, did not seem to spread or be maintained locally for several years. Mixed infections of CL and EM isolates were also performed in experimental conditions in order to compare the frequency and nature of recombination events to those of natural situation. The fitness of natural recombinants relative to potential "parental" strains was also tested in controlled conditions. The epidemiological and evolutionary consequences of recombination in WMV populations will be discussed. This work represents one of the first estimation for the frequency of appearance of recombinants in natural populations of a plant RNA virus.
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