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Search for factors potentially involved in the rapid shift in *Watermelon mosaic virus* (WMV) populations in south-eastern France

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Watermelon mosaic virus (WMV, *Potyvirus*) has been first reported in France 35 years ago, and it is now the most prevalent virus in cucurbit crops. WMV has a relatively wide host range –including several weeds– and is non-persistently transmitted by more than 35 aphid species. In 2000, new strains (referred as ‘emerging’ (EM) strains) were detected in south-eastern France. EM strains are generally more severe and phylogenetically distinct from those previously reported in France (referred as ‘classic’ (CL) strains). EM strains are divided in four phylogenetic subgroups. Since 2000, EM strains have been progressively replacing CL strains in cucurbit crops in south-eastern France. In order to look for factors that may explain this rapid change in virus populations, properties such as host range, symptomatology in susceptible hosts and aphid transmissibility were investigated for a set of 26 WMV isolates including isolates from the 3 phylogenetic groups and CL-EM or EM-EM recombinant isolates. A modelling approach, based on a 3-year observation of the spatio-temporal spread of EM and CL WMV strains in zucchini squash fields at Montfavet suggested that a dissymmetrical partial cross-protection between EM and CL strains could be a major factor in the population shifts that are observed. This hypothesis will be discussed in the light of the results of the biological tests.