OP-50: Molecular epidemiology of Watermelon mosaic virus in France and evolution of viral populations

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Watermelon mosaic virus (WMV, Potyvirus) is known in France for more than 30 years, and is the most frequently detected virus in cucurbit crops. WMV has a larger host range than most potyviruses. In natural conditions, it infects many common weeds that represent potential virus reservoirs, and may allow local WMV isolates to persist in the environment in the absence of cucurbit crops. The agronomic impact of WMV in France remained limited for a long time, particularly on zucchini squash, since the virus induced only mild symptoms on leaves without any damages on fruits. Since 1999, more severe symptoms of leaf and fruit deformation, resulting in important agronomic losses, have been associated with WMV in zucchini squash crops. A molecular study revealed that only one group of strains was observed in France before 1999, whereas since 1999 a second group, highly divergent at the molecular level, was also detected. We performed epidemiological surveys from 2004 to 2007 in order to study the variability of WMV and its geographic structure. Within the “emerging” group, four molecular subgroups were defined unambiguously. Our results revealed a strong geographic structure of the classical and emerging isolates: whereas the classical isolates are found wherever WMV is present, the emerging ones are restricted so far to South-Eastern France. Besides, a structure was also observed at a lower scale between the subgroups of emerging isolates. In South-Eastern France, both types of strains are present, sometimes in the same field or the same plant, what raises the question of the interactions between classical and emerging isolates (competition between isolates, population replacements, and risk for emergence of recombinants with unknown biological properties…). This situation remained rather stable between 2004 and 2006, although the proportion of emerging isolates tended to increase. Our results suggest that the emerging strains spread only slowly from their site(s) of introduction but may progressively replace local strains.