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Geographic distribution and evolution of Cucurbitaceae and Solanaceae viruses in the French Mediterranean basin

Eric Verdin, Catherine Wipf-Scheibel, Pauline Millot, Karine Berthier, Grégory Girardot, Patrick Gognalons, Judith Hirsch, Benoit Moury, Karine Nozeran, Sylvain Piry, Alexandra Schoeny, and Cécile Desbiez

Pathologie Végétale, INRA, Montfavet, France
(cecile.desbiez@inra.fr)

Emerging plant viral diseases represent a significant burden to plant health, and their highest impact in Mediterranean agriculture is on vegetables grown under intensive horticultural practices. The emergence of a new viral disease results from a complex interaction among several factors, including ecological changes of host and vector populations, and genetic changes due to the introduction of new crop varieties and the evolution of the viruses and/or vectors. In order to better understand virus evolution and emergence, viruses and aphid vectors were mapped in Cucurbitaceae/Solanaceae crops and reservoirs in the French Mediterranean area, and virus diversity, evolution and population structure were studied through molecular epidemiology and spatial genetics approaches. Surveys were performed in summer 2016 and 2017, representing a total of 1619 crop samples, 351 weed reservoirs and 1121 aphids. The plant samples were analyzed using serological and molecular diagnostic tools, including next generation sequencing (NGS). The viral species and their frequency in crops were quite similar to those of surveys conducted ten years ago in the same areas. Contrary to other Mediterranean countries, aphid-transmitted viruses remain the most prevalent problems in France whereas whitefly-transmitted ones have not yet emerged. However, NGS analysis of viral evolution revealed the appearance of viral variants undescribed until now, especially for watermelon mosaic virus (WMV) in cucurbits, or variants not present in France before, as for cucumber mosaic virus (CMV) in solanaceous crops. Deep sequencing results also revealed complex virus populations within individual plants. The low spatial structuration of viral variability suggested frequent long-distance exchanges between viral populations even for non-persistently transmitted viruses.

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