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The « PRSV cluster » of cucurbit-infecting potyviruses: how many species, and what is their evolutionary and biological meaning?

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Cucurbits are affected by more than 60 different virus species worldwide, and new viruses are described every year. Among potyviruses, representing about 20% of all known plant viruses, at least 12 species infect cucurbits and 3 of them are among their most devastating pathogens worldwide. Even though the star-like phylogeny of potyviruses as a whole suggests an initial radiation in the genus, probably at the dawn of agriculture, several "clusters" of closely related viruses have been described. Viruses within a cluster usually share 70 to 80% sequence similarity in the coat protein coding region, so that species demarcation is not always clear-cut. Besides, they have more or less overlapping host ranges, and are in some cases controlled by the same resistance genes or gene clusters. This is the case for viruses in the "papaya ringspot virus" (PRSV) cluster. Using biological, serological and molecular data, five species have now been defined. With the exception of PRSV, their host range is mostly restricted to cucurbits and they seem to have a limited geographic distribution and/or low prevalence. Partial sequences available suggest that there are additional distinct species in the cluster.

A potyvirus isolate collected during a survey performed in Sudan in 2003 was characterized biologically and molecularly and it appears to belong to a distinct species in the PRSV cluster, tentatively named Sudan watermelon mosaic virus (SuWMV). Screening of 158 isolates collected in Sudan between 1992 and 2012 revealed the presence of SuWMV at a low frequency in 1999 and 2012, showing that the virus is maintained in the country even though it does not seem to induce important epidemics so far, and it may emerge in cucurbit crops under more favorable circumstances.

The impact of molecular threshold on species delimitation, as well as the evolutionary meaning of the diversity and geographic structure in the PRSV cluster and the behavior of melon resistance genes towards the different species will be discussed.