

Characterization of *pyrus virus A* (PyVA), a novel velarivirus identified in pear trees

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Pome fruit viruses associated with economically important pome fruit diseases on commercial cultivars have been thoroughly studied. Nevertheless, beyond commercial cultivars there is a significant genetic diversity preserved in collections of genetic resources. During a large-scale virome survey of pear trees (*Pyrus* L.) from the germplasm collection at the CRA-W (Gembloux, Belgium), the genome of a novel velarivirus, tentatively named *Pyrus virus A* (PyVA), was sequenced in several asymptomatic trees. This poster presents the novel virus and its characterization according to the revised framework for the characterization and risk analysis of newly discovered plant viruses and viroids, shown on the left side (Figure 1).

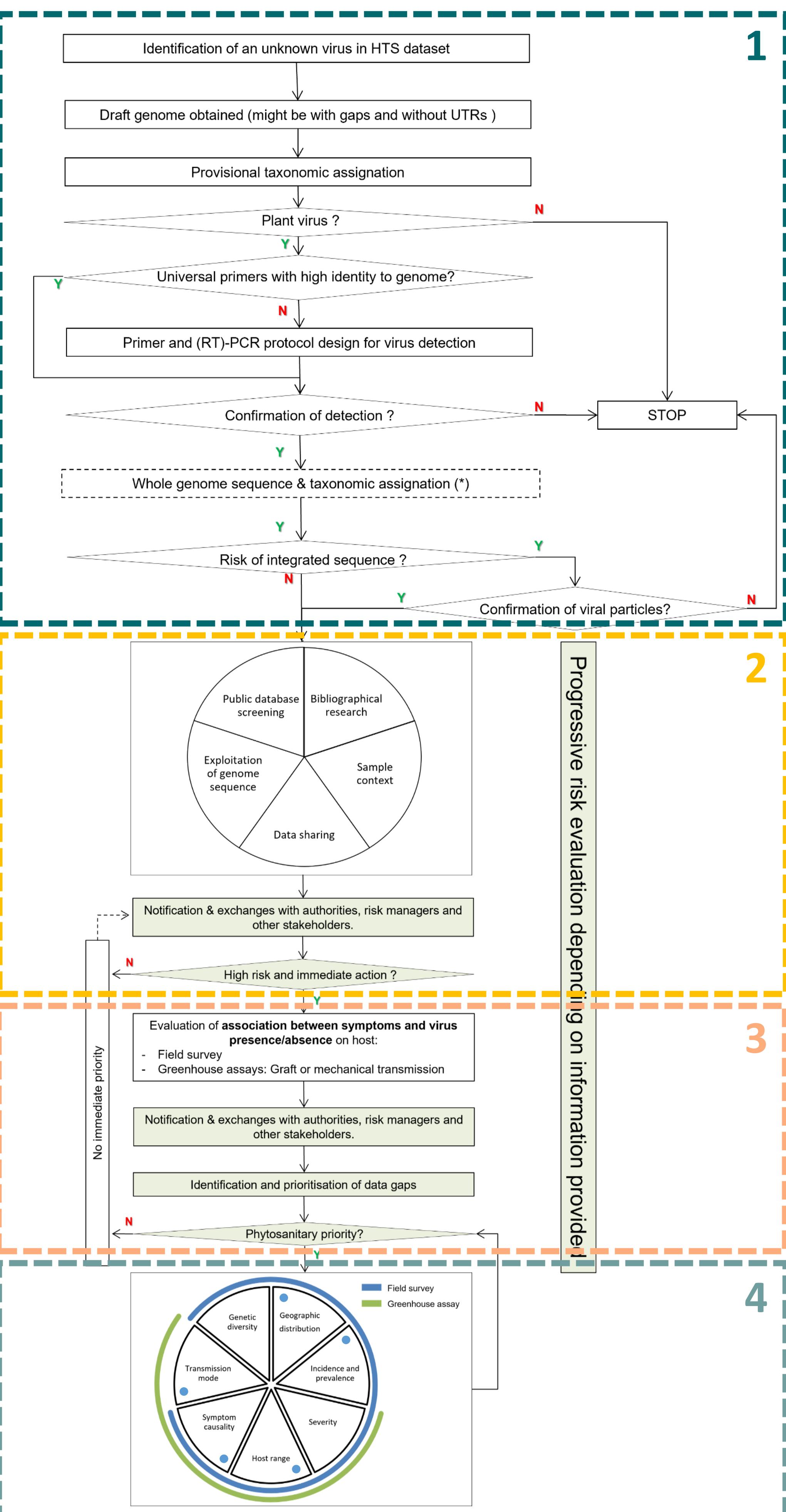


Figure 1. Proposed framework following the discovery of a novel virus or viroid. Y means positive response (yes) and N means negative response (no). Multi-stakeholders are involved in green-highlighted actions, and researchers in white-highlighted actions [1]. The titles of each box are: 1. Detection test, confirmation of detection and genome sequence; 2. Contextual information gathering and complementary analyses with the genome sequence; 3. Small- and large-scale survey; and 4. Completion of knowledge and data gaps. Dots in box 4 highlight the knowledge gaps under study.

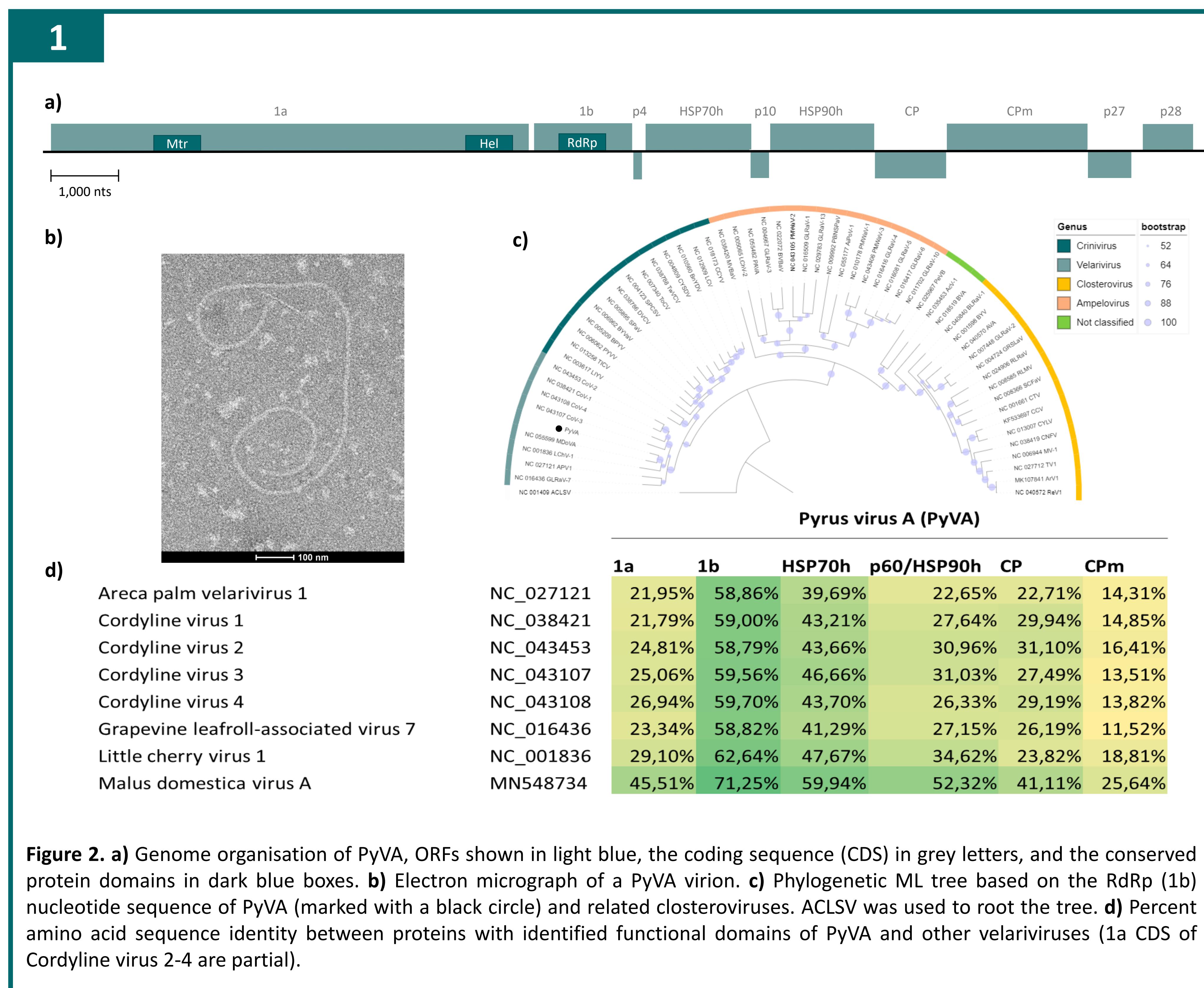


Figure 2. a) Genome organisation of PyVA, ORFs shown in light blue, the coding sequence (CDS) in grey letters, and the conserved protein domains in dark blue boxes. b) Electron micrograph of a PyVA virion. c) Phylogenetic ML tree based on the RdRp (1b) nucleotide sequence of PyVA (marked with a black circle) and related closteroviruses. ACLSV was used to root the tree. d) Percent amino acid sequence identity between proteins with identified functional domains of PyVA and other velariviruses (1a CDS of Cordyline virus 2-4 are partial).

3 Field survey (no symptoms observed):		
	HTS	RT-PCR
Belgium (Apple)	0/105	nt
Belgium (Pear)	5/114 (4%)	1/27 (3%)
France (wild)	0/16	nt
Switzerland (Pear)	nt	0/10
Slovenia (Pear)	nt	0/14

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- Velariviruses infect primarily woody hosts, in which no apparent symptoms are induced, and are not known to be seed and mechanically transmitted [2]. Areca palm velarivirus 1 (APV1) can be transmitted by mealybugs [3].
- Accession n° 626 was used for electron microscopy as PyVA was the only virus detected. No apparent symptoms could be observed in the tree during spring and summer 2021 and 2022 (Figure 3).



Figure 3. Tree accession n° 626.

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- Buds from tree accession n° 626 (CRA-W) were grafted onto various pear indicators to study the effects of the virus on the host. In addition, buds will be grafted onto commercially important pear cultivars.
- In order to complete the full characterization, a study of potential vectors is the next step (i.e., mealybugs from the genus *Pseudococcus*).



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