# Deep sequencing of siRNAs for detection of known and unknown viral genomes in ornamental plants

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# DEEP SEQUENCING OF siRNAs FOR DETECTION OF KNOWN AND UNKNOWN VIRAL GENOMES IN ORNAMENTAL PLANTS

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## BACKGROUND and OBJECTIVES

Among horticultural crops, ornamental plants represent the most diversified sector in terms of genetic diversity (species, cultivars) and markets (cut flowers, plants in pots or for gardens, bulbs, shrubs). In France, the value of imported ornamental plants is 14 times greater than the value of the corresponding exports. These plants can harbor viruses that could cause serious damage in more economically important species, in particular vegetable and fruit crops, and thus present a potential source of new viral diseases. Serological and molecular diagnostic tools are effective for detection of known viruses, but considering the ever increasing number of ornamental species, their rapid turnover, and the scope of their trade worldwide, it is critical to develop means to also detect plant viruses that are not current targets of sanitary surveillance in a manner as exhaustive as possible. Further, viruses under quarantine restriction are of particular concern. In this study, we present a novel strategy for detecting known and unknown viruses of various genome types, including viroids, in a diverse panel of ornamental plants.

## MATERIALS and METHODS

First, we compared several strategies for simplifying the preparation and pooling of samples in order to minimize costs before Illumina Miseq deep sequencing of 21-24 nt siRNAs. We then analyzed 55 field samples representing 39 ornamental species of diverse origins (French and imported). The siRNAs were sequenced in 5x5 matrices of pools of 5 samples, and the reads assembled *de novo* into contigs.

## RESULTS

Assembly of the sequencing reads into contigs allowed the identification of viruses of various genome types (positive and negative ssRNA viruses, dsRNA viruses, dsDNA viruses), as well as viroids and viral sequences integrated in the host genome (EPRVs). Of the genomes observed, some were nearly identical to known viruses, but many had only moderate to weak sequence identity with known viral genomes. These potentially new viruses include badnaviruses, begomoviruses, caulimoviruses, ilarviruses, nepoviruses, partitiviruses, tymoviruses and several potyviruses. For many of the virus-positive samples, the sequencing data were confirmed by molecular amplification of the expected viral sequences.

## CONCLUSIONS

These analyses contribute to our understanding of the potential importance of ornamental plants as sources of emerging viruses in Europe, and more globally cast a new light on the respective contributions of crops, wild plants and ornamentals to plant virus epidemiology.

# Building bridges between disciplines for sustainable management of plant virus diseases


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## Programme and Abstracts