Endogenous Dionyvirus sequences are widespread in plant genomes

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Endogenous sequences from members of the *Caulimoviridae* and *Geminiviridae* families have been identified in the genome of several plant species [1, 2]. They are thought to result from illegitimate recombination events and are generally replication-defective. However, some caulimovirid sequences of tobacco, petunia and banana are capable of causing infection.

We performed in silico analyses on nucleotide sequences from plant genome databases and reconstituted 11 full length and potentially infectious viral genomes from endogenous viral sequences embedded in the genomes of monocotyledonous and dicotyledonous plant species. Sequence comparisons show that the corresponding viruses belong to a new genus in the family Caulimoviridae, tentatively named Dionyvirus. Mapping of endogenous Dionyvirus sequences was achieved in the fully sequenced genomes of grape, poplar, peach and rice, allowing for the first time the study of the distribution pattern of endogenous viral sequences at the host plant genome scale. Using the TEannot pipeline from the REPET package [3], we sensitively detected virus fragments and were able to join them to recover fragmented virus sequences. Full length and partial virus sequences were found in all four genomes, evenly distributed along chromosomes; they appear to be repeated throughout the whole genome. Allelic variations of endogenous Dionyvirus sequences were also characterized in grape, using the complete sequences of a near-homozygous line and a highly heterozygous genotype, PN40024 and Pinot Noir clone ENTAV115 respectively. Dionyvirus-specific primers were designed and used for a PCR-based large scale screening of plant germplasm. It showed that endogenous Dionyvirus sequences belonging to distinct viral species are widespread among plants of temperate, tropical and arctic origins, and that endogenization of viral sequences is therefore a common phenomenon in plants. siRNAs homologous to endogenous Dionyvirus species were identified in grape, peach, soybean and orange, providing evidence that the expression of such endogenous sequences is tightly

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regulated and/or might trigger RNAi-based antiviral defence.

References

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