Endogenous caulimovirid sequences are widespread in plant genomes

Andrew D.W. Geering ¹, Nathalie Choisne ², Silvia Vezzulli ³, Tanya Sharahskin ⁴;Riccardo Velasco ³, Hadi Quesneville ² & Pierre-Yves Teycheney ⁵

Endogenous sequences from members of the *Caulimoviridae* and *Geminiviridae* families have been identified in the genome of several plant species. 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 Brassicaceae, Euphorbiacae, Fabacae, Myrtaceae, Poaceae, Rutaceae, Saliaceae and Vitaceae 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 two fully sequenced grape genomes, allowing for the first time the study of the distribution pattern of endogenous viral sequences at the host plant genome scale. Dionyvirus-specific primers were designed and used for a PCR-based large scale screening of plant germplasm. It showed that endogenous Dionyvirus sequences are widespread among plants of temperate, tropical and arctic origins, and belong to distinct viral species. Endogenous Dionyvirus sequences belonging to distinct viral species were also identified in single host plants, showing that endogenization of viral sequences is a common phenomenon in plants. Our work shed new lights on plant/virus molecular interactions. The potential contributions of endogenous viral sequences to normal plant functions and to plant and virus evolution will be discussed.

¹ Queensland Primary Industries and Fisheries, 80 Meiers Road, Indooroopilly, QLD 4068, Australia

² INRA, Centre de recherche de Versailles, Route de Saint Cyr, 78026 Versailles Cedex, France

³ IASMA Research and Innovation Centre, Fondazione Edmund Mach, Genomics and Crop Biology Area, Via E. Mach 1, 38010 San Michele a/Adige (TN), Italy

⁴ Queensland University of Technology, School of Natural Resource Sciences, Brisbane, QLD 4001, Australia

⁵ CIRAD-Bios, UPR75, Station de Neufchâteau, Sainte-Marie, F-97130 Capesterre Belle-Eau, Guadeloupe, France