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## Virome of cross-protected grapevines under natural conditions: what else is in there?

Julie Kubina, Jean-Michel Hily, Pierre Mustin, Claude Gertz, Gérard Demangeat, Anne Sicard, Olivier Lemaire, Emmanuelle Vigne

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title	<b>Virome of cross-protected grapevines under natural conditions: what else is in there?</b>
list of authors. <u>Presenting author</u> underlined	Julie Kubina <sup>1*</sup> , Jean-Michel Hily <sup>1,2</sup> , Pierre Mustin <sup>1</sup> , Claude Gertz <sup>1</sup> , Gérard Demangeat <sup>1</sup> , Anne Sicard <sup>1</sup> , Olivier Lemaire <sup>1</sup> , and <u>Emmanuelle Vigne</u> <sup>1</sup>
author's addresses	<sup>1</sup> Université de Strasbourg, INRAE Grand Est-Colmar, SVQV UMR-A 1131, 68000 Colmar, France <sup>2</sup> IFV, 30240 Le Grau-Du-Roi, France *current adress: Université de Strasbourg Institut de biologie moléculaire des plantes (IBMP, CNRS) 12, rue du Général Zimmer, 67000 Strasbourg, France
e-mail of the presenting author	<a href="mailto:emmanuelle.vigne@inrae.fr">emmanuelle.vigne@inrae.fr</a>

Grapevine (*Vitis* spp.), one of the most grown fruit crops worldwide, was domesticated ca. 6000 BCE. It is generally assumed that viruses, that were probably part of the ecosystem at that time, were widely spread by vegetative propagation, grafting, transplantation of vines and extensive exchange of *Vitis* germplasm on a global scale (Reynolds, 2017). To date, with at least 101 viruses identified, grapevine hosts the largest number of viruses among cultivated crops, each plant being infected by several viral species (Fuchs, 2023). Some ubiquitous viruses have little or no negative biological impact on the vines: they are considered as the background virome (Saldarelli et al., 2017). Others may be responsible for detrimental diseases and in particular grapevine fanleaf virus (GFLV) is depicted as one of the most severe viruses causing fanleaf degeneration which engendered serious economic losses (Andret-Link et al., 2004). Naturally transmitted by *Xiphinema index*, an ectoparasitic nematode, this virus is endemic in France and is present in about 2/3 of the vineyard (Demangeat et al., 2005). As there are currently no effective methods for combating this virus, winegrowers are left with no solution. In this context, mild strain cross-protection (MSCP) could be an alternative for the management of this disease (Pechinger et al., 2019). MSCP is based on the inoculation of a plant with a mild viral isolate to protect crops from subsequent infection by closely related severe isolates. The effectiveness and sustainability of this biocontrol method is mainly based on the genetic and phenotypic stability of the primary isolate and its ability to counteract challenger isolates present in the area of use.

In this study, the efficacy of MSCP against fanleaf degeneration was assessed by monitoring 1,950 primary-infected vines with mild GFLV isolates (originated from Burgundy region in France) that were implanted in the same viticultural region in a diseased commercial plot exhibiting severe symptoms before uprooting. After 14 years, 81% of the vines displayed mild symptoms with good fruit production aptitudes. In order to determine if superinfection occurred, the infectious status of about 200 vines showing contrasted phenotypes were determined using high-throughput sequencing technologies (total RNA and amplicon sequencing). After phylogenetic analysis, more than 70% of the GFLV sequences grouped into the same clades as those of the primary isolates, indicating low level of superinfection and stability of the mild isolates. Our results will be discussed with the aim at developing MSCP as a workable approach to prevent fanleaf degeneration while taking into account the complex virome of grapevines in vineyards.

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