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► **To cite this version:**

Chiraz Jridi, Sarah Leon, Jean Luc Macia, Michel Yvon, Rémy Froissart. Specialization of a phytovirus to its environment: experimental evidence for a cost of adaptation. 12. Rencontres de Virologie Végétale (RVV), Jan 2009, Aussois, France. hal-02756803

HAL Id: hal-02756803

<https://hal.inrae.fr/hal-02756803>

Submitted on 3 Jun 2020

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Specialization of a phytovirus to its environment: experimental evidence for a cost of adaptation

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Studying patterns and genetic basis of adaptation is crucial to understand viral emergence and to anticipate suitable strategies of control. In this work, we propose to detect adaptive mutations in different environments (constant and variable) and to evaluate their phenotypic expression (measured by evaluation of fitness and virulence) in different environments.

We designed an experimental evolution of *Cauliflower mosaic virus* by transmitting viral populations from plant to plant in either two homogeneous environments (*Arabidopsis thaliana* or *Nicotiana bigelovii*) or a variable environment (alternation of both species). For each of these three treatments, 10 independent viral populations were evolved in parallel. After five and ten passages (approx. 150 and 300 viral generations, respectively), we sequenced complete genome length of consensus viral populations and look for mutations appearing at the same locus in more than two independent populations. These parallel mutations have a high probability to be a signature(s) of adaptive changes.

Genomic data revealed that parallel mutations appeared differentially depending on environmental contexts: (i) most of them were accumulating in constant environments; (ii) none were common to several environments. Evaluation of phenotypic effects of viral evolution in different environment gave the evidence for a cost of adaptation and suggest a positive correlation between virulence and virus accumulation. These genomic and phenotypic results will be discussed in light of evolution of specialist/generalist strategies.