

Dynamics of Flavescence dorée in the canton of Vaud

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A Phytoplasma-associated disease

Flavescence dorée (FD) is an epidemic grapevine disease caused by the pathogen '*Candidatus Phytoplasma vitis*', a wall-less, non-cultivable bacterium. It has been detected in the canton of Vaud since 2015.

As a quarantine disease, a specific control protocol is mandatory. It includes the uprooting of infected vine stocks, or even of the whole plot above a certain contamination threshold, and the establishment of a control perimeter and the application of insecticides. This causes severe economic losses.

In this work we aim to determine the source of the FD epidemic and how it is spreading in the canton of Vaud

Genotyping : determination of gene version

DNA samples from infected grapevines between 2015 and 2016, analyzed as part of the compulsory control and the regional monitoring from two sites, were sequenced.

Four genes, which are known to be a source of variability between strains of FDp, were chosen to determine FDp genetic profile in canton of Vaud : map, dnaK, vmpA and malG.

Table I : FDp genotypes from Tour-de-Peilz and Blonay outbreaks

	Genotypes			
	2015		2016	
Sites	Tour-de-Peilz	Blonay	Tour-de-Peilz	Blonay
Genes				
map	M54	M54	M54	M54
dnaK	dnaK1	dnaK1	dnaK1	dnaK1
vmpA	vmpA1-B	vmpA1-B	vmpA1-B	vmpA1-B
malG	malG3	malG1/G3	malG3	malG1/G3

Results

- FDp strains in the different samples are genetically close and the variability is only observed in the **malG** gene.
- The spatial separation of the malG gene genotypes, into two sites that develop over time, suggests distinct disease introduction for the initial infection.
- First results from 2015 and 2016 samples show an initial infection from **planting material**.
- Outbreaks are developing, suggesting the action of insect vectors whose identity is not yet determined.

Conclusions

The FD epidemic in the canton of Vaud has a dynamic on two different scales :

- On the scale of the canton of Vaud, the dissemination of FD is clonal via plant material
- On the scale of the plot, dissemination is vectorial via insect vectors

A complex disease cycle

Despite the uprooting of infected vine plants and pesticide treatments, the epidemic continues to develop.

FD can emerge from different reservoirs from the landscape or be established by infected grapevines. The spread of the disease is mediated by insect vectors.

In the case of contamination from wild plants, there is genome variability between Flavescence dorée phytoplasma (FDp) strains. In comparison, for a contamination by planting material there is almost no variability. Gene analyses can therefore help to determine the causes of the FD epidemic.

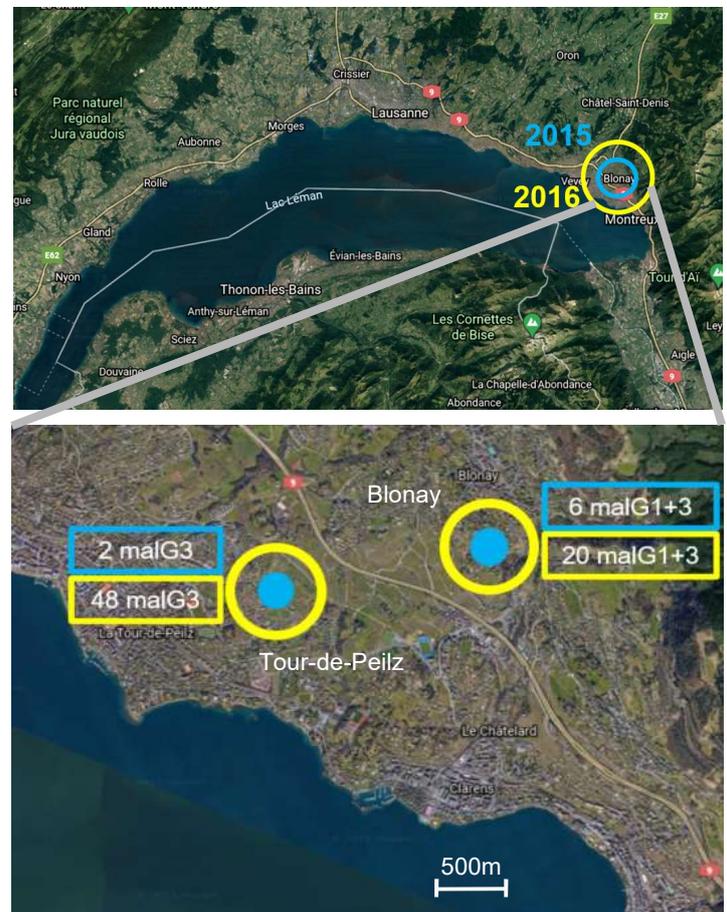


Figure 1 : Map with FD infection sites in canton of Vaud and the malG type distribution between Tour-de-Peilz and Blonay for 2015 and 2016

Perspectives

- Samples from 2017 to 2020 will undergo the same analysis as those from 2015 and 2016 to determine how the FD dynamic is evolving.
- An in-depth study of insects is considered in order to highlight all the possible vectors involved in the epidemic.