

SafeGrape - Genomic of the grapevine - pathogen interactions: Botrytis cinerea virulence factors & molecular mechanisms of induced resistance

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▶ To cite this version:

Benoît Poinssot, Jani-Petri Kelloniemi, Zsuzsanna Antal, Christophe Bruel, Agnes Cimerman, et al.. SafeGrape - Genomic of the grapevine - pathogen interactions: Botrytis cinerea virulence factors & molecular mechanisms of induced resistance. Plant Genomics Seminary, Apr 2012, Pont-Royal-en-Provence, France. hal-02806243

HAL Id: hal-02806243 https://hal.inrae.fr/hal-02806243

Submitted on 6 Jun 2020

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"SafeGrape"

Genomics of the grapevine - pathogen interactions:

Botrytis cinerea virulence factors &

Molecular mechanisms of induced resistance









On the Vitis side:



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On the Botrytis side:





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UMR 5240, LyonMathias Choquer & Co

Fungal diseases in viticulture

- Grapevine is a major crop for French agriculture: 10.1 billion € (2011), 3% of the cultivated surface
- Vitis vinifera susceptible to many diseases including:



Grey mouldBotrytis cinerea

- Necrotroph
- Ascomycete



Downy mildewPlasmopara viticola

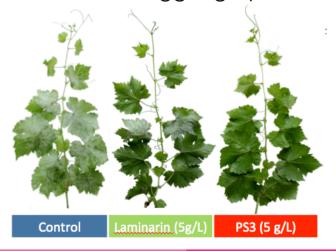
- Biotroph
- Oomycete
- Half of the fungicides used in France sprayed in vineyards but they should be reduced by 50% by 2018 (Grenelle de l'environnement).

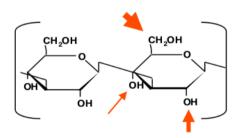
Extending our knowledge on the infection process is necessary to reduce applications of chemicals, but also to develop alternative strategies:

- Obtaining resistant cultivars (NB: no resistance gene for B. cinerea)
- Elicitation of plant immunity by biomolecules ...

PAMP – triggered immunity (PTI) in grapevine

- Several PAMP (Pathogen Associated Molecular Pattern) have been identified in grapevine:
- **Ex: Laminarin (Lam):** Linear β -1,3-glucan polymer (Laminaria digitata) induces a low resistance against B. cinerea and P. viticola by triggering grapevine defense responses (Calcium, MAPK, ROS, PR2 ...)
- Interestingly, chemical modification of this PAMP can improve its efficacy:
 Sulfated Laminarin (PS3) induces a stronger resistance against P. viticola
 but did not trigger grapevine defense responses as laminarin do.





What are the mechanisms involved?

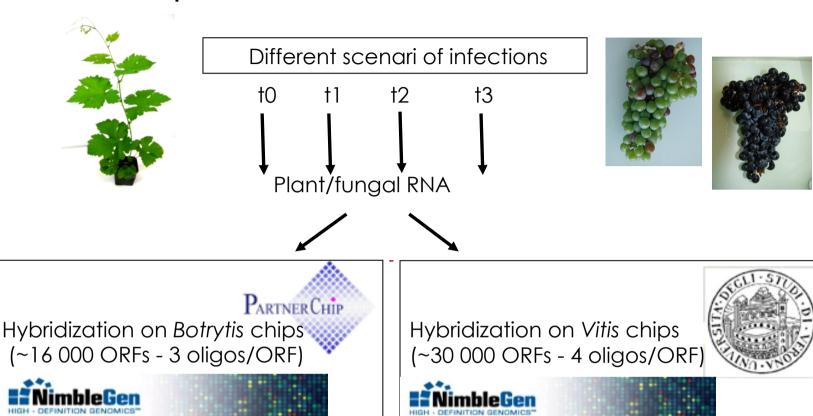


Molecular mechanisms of the interactions between grapevine and its major pathogens

The development of alternative ways to protect the grapevine from pathogens requires a better knowledge of the infection process and the mechanisms of defences. In this context, the aims of our project were:

- To identify the pathways involved in induced resistance ...
 - against different pathogens (B. cinerea versus P. viticola)
 - in different organs (leaves, veraison and mature berries)
- To elucidate the mode of action of sulfated laminarin (PS3)
- To characterise B. cinerea genes involved ...
 - in infection structures development
 - in the successful infection of berries

Transcriptomic view of the interaction



ANAIS*: Analysis of Nimblegen Arrays Interface

Gene KO in B. cinerea

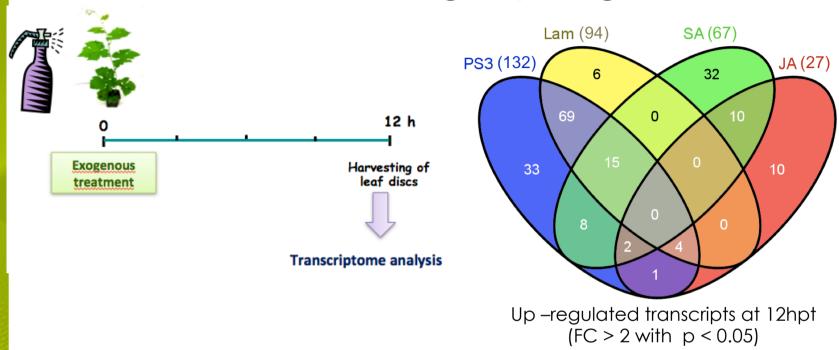
Gene silencing in V. vinifera

Coll. Plateforme Transformation vigne



* Simon & Biot, 2010

PS3 induced grape genes

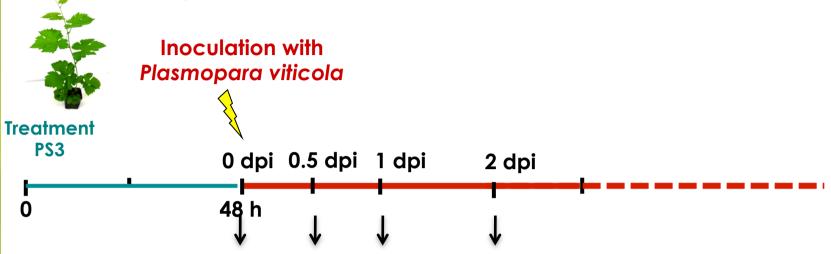


- The two β-glucans (PS3 and Lam) share only a part of their transcriptome
- PS3 does not up-regulate SA-marker genes (NRX1, WRKY40, PR-2) or JA-marker genes (13-LOXA, FAH Lyase, JAZ1, AOC1)
- PS3 up-regulates genes involved in response to biotic and abiotic stresses, in glycolysis ...

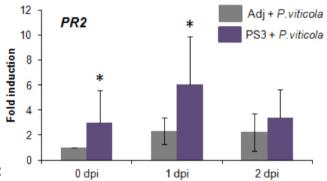
Does PS3 prime grapevine defense reactions during the infection?



PS3 primes defense reactions



- Arrays data showed that PS3 primes a faster induction of SA-marker genes (PR1, PR2, PR5, NRX1...) and PRR genes (PAMP perception)
- Faster production of SA confirmed by metabolomics
- Origin of SA currently tested (phenypropanoic versus isochorismate pathway)
- NB: **PS3** also induce a faster activation of defence genes against *B. cinerea*.

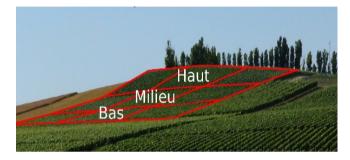




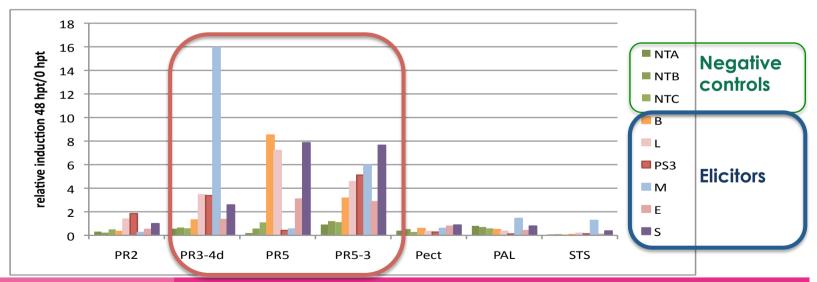
And in vineyards?



- 7 PS3-induced genes were tested in vineyards (2011):
- Green berries treated with different elicitors including PS3 (and S: non protective)
- Q-RT-PCR 0 and 48hpt (preliminary results):
 3 genes seem to be good indicators of the berry elicitation state (no indicator of the resistance state: induction by S)



Possible "decision tools" for chemical treatments?



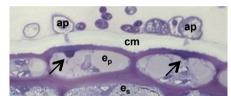


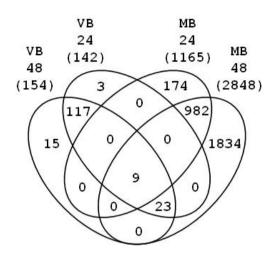
What happens when Botrytis infects berries?

Veraison berries (VB)







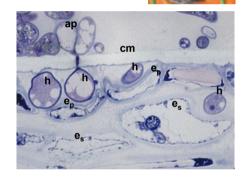


Up-regulated genes at 24 and 48 hpi (FC > 2 with p < 0.05)

Harvest berries (HB)





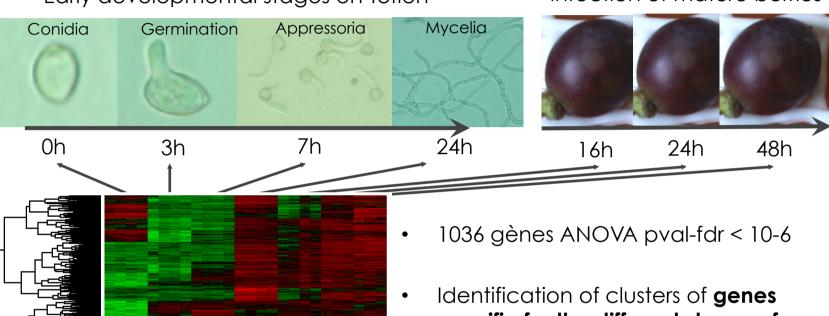


- B. cinerea infection is successful on mature berries but not at the veraison stage
- Transcriptomics revealed very different reactions from the host.

What happens on the grey side?



Infection of mature berries



- Identification of clusters of genes specific for the different stages of infection structure development
- Identification of genes that are upregulated in planta





Botrytis genes up-regulated in berries



Fungal genes up-regulated during the early stages of berries infection showed an enrichment in biological processes related to necrotrophy:

- Cell wall degrading enzymes
- Production of secondary metabolites including phytotoxins (botrydial and botcinic acid), unknown terpens and polyketides, and ABA!
- Transmembrane transport: ABC, MFS-type sugar and amino acids transporters
- Oxydative stress response

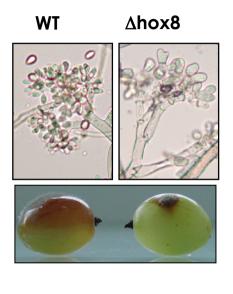
Additionnaly, some genes coding for components of signalisation (e.g. transcription factors) were highly up-regulated during the infection.

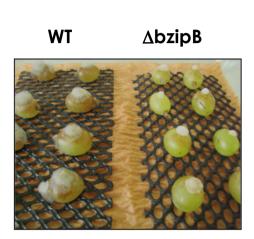
About 20 KO mutants constructed so far to validate these functions ...

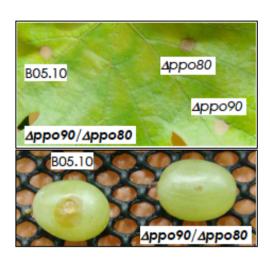




Regulation of fungal development and necrotrophy







- The homeodomain HOX8 (Arabesque) and BzipB transcription factors are both involved in conidiation and necrotrophic growth.
- **Fungal oxylipins** synthetized by *PPO80* and *PPO90* dioxygenases are also necessary (NB: fungal <u>AND</u> plant oxylipins regulate conidiation and mycotoxins production in *Aspergillus* ...)
- Further transcriptomics analyses are planned to identify the downstream target genes ... and investigate the regulation of phytotoxic secondary metabolites.





Main inputs

Large set of grape and B. cinerea transcriptomics data: 1st complete view of the interaction

MAMP- and priming-induced resistances:

- Induced pathway depends on the pathogen but also on the grape organ
- PS3 allows a faster activation of these pathways ("priming")
- During berries maturation, there is a shift in the response pathway.
- Silencing of candidate PRR genes ... (Coll. INRA Colmar)
- Validation of markers of the elicitation state in vineyards ... (Coll. Comité Champagne)

<u>Fungal virulence factors:</u> mutagenesis of about 20 genes highlights the important roles of

- Secondary metabolism: phytotoxins, ABA
- Key regulators of fungal development and virulence: transcription factors, kinase, oxylipins

Possible crosstalks? Oxylipins? ABA?









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Adaptation et Pathogénie

