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Brown stripe in *Botryosphaeria dieback*: differential responses of three grapevine cultivars

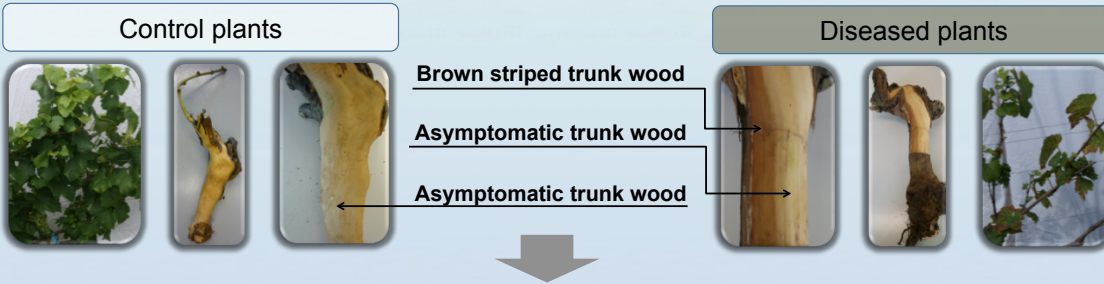
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Background and aim of the work

Botryosphaeria dieback, involving several xylem-inhabiting fungi of the *Botryosphaeriaceae*, is among the grapevine trunk diseases that represent a threat for viticulture worldwide due to the decreased production of affected plants and their premature death. *Botryosphaeria dieback* is characterized by a typical wood discoloration called "brown stripe" ⁽¹⁾. Herein, a proteome comparison of the brown striped wood from *Botryosphaeria dieback*-affected standing vines cultivar 'Chardonnay', 'Gewurztraminer' and 'Mourvèdre' was performed. These 3 cultivars were selected since cv. 'Chardonnay' is less susceptible than cv. 'Gewurztraminer' and cv. 'Mourvèdre' to *Botryosphaeria dieback* and esca disease. The transcript analysis for 15 targeted genes and the quantification of both total phenolics and specific stilbenes were also performed.

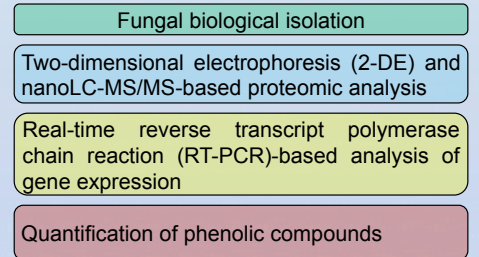
Materials and Methods



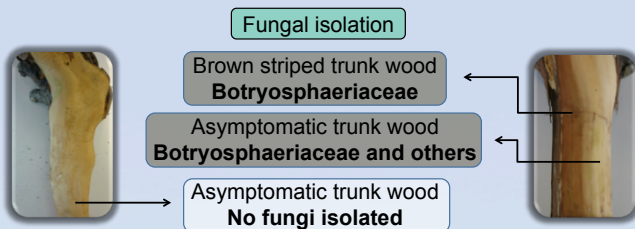
Brown stripe appears as a superficial, longitudinal orange/brown stripe just beneath the bark. Unlike other grapevine trunk disease-related wood discolorations, brown stripe is not detectable before the vegetative season ⁽¹⁾. Furthermore, brown stripe is always associated with foliar symptoms ⁽²⁾.

Plant material and related groups of samples.

Cultivar/rootstock	Vineyard age and location	Sample group		
		Control plants	Diseased plants	
		Asymptomatic wood	Asymptomatic wood	Brown striped wood
Chardonnay/41B	27 years – Avize (Epernay) - France	ACC	ADC	BDC
Gewurztraminer/16-49C	24 years – Rouffach (Colmar) - France	ACG	ADG	BDG
Mourvèdre/3309	15 years – Rodilhan (Nîmes) - France	ACM	ADM	BDM



Results and Discussion



The high rate of *Botryosphaeriaceae* biological isolation from the brown stripe confirms the association of this symptom with *Botryosphaeria dieback* agents. In response to these pathogens and/or their toxic metabolites, our results show the abundance of PR proteins (PR-2, PR-5 and PR-17) and members of the antioxidant system (GST5, cysPEROX) in the brown striped wood of the three cultivars. Additionally, total phenolics and some specific stilbenes were more accumulated in the brown striped wood.

Major changes in protein expression, gene expression and phenolic compound accumulation compared to the related controls.

Sample group	Analysis		
	Proteomic analysis	Gene expression analysis	Phenolic compounds
Chardonnay	ADC	no important changes observed	↑ <i>HSPCP</i>
	BDC	↓ primary metabolism	↑ <i>trans-resveratrol</i>
Gewurztraminer	ADG	↑ <i>endoglu</i>	↑ <i>POX4</i>
	BDG		↑ defense
Mourvèdre	ADM	↑ primary metabolism	↑ <i>trans-vitisin A</i>
	BDM		↓ <i>HSPCP</i>
			↑ <i>trans-ε-viniferin</i>
			↑ <i>trans-piceatannol</i>
			↑ <i>trans-ε-viniferin</i>
			↑ <i>trans-piceids</i>

Strongest differences among the three cultivars concerned especially proteins of the primary metabolism, which looked to be particularly impaired in 'Chardonnay' (BDC). In 'Gewurztraminer' (BDG), the glycolysis and citrate cycle pathways seemed to be over regulated while a deficiency of the antioxidant system and an over regulation of some amino acid metabolism appeared to occur in Mourvèdre (BDM). The different susceptibility of the three cultivars could be explained, at least in part, by the diverse expression of various proteins involved in defense, stress tolerance and metabolism. Validation of these findings using complementary approaches could be carried out in the future.

References

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