

## MOLECULAR ASPECTS OF GRAPEVINE-PATHOGENIC FUNGI INTERACTIONS

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### 1. INTRODUCTION

Grapevine is a major and highly valuable fruit crop with roughly 2.25 mil ha grown worldwide in 2007 (source: U.S. Food and Agriculture Organization). Unfortunately, most of the premium cultivars used for winemaking, including the widely used European *Vitis vinifera* cultivars, are highly susceptible to several pathogenic microorganisms including fungi, oomycetes, bacteria, phytoplasma and viruses. In the past 15 years, the understanding of grapevine-pathogen interactions has entered the molecular era and will most certainly constitute a basis for future improvement of grapevine disease tolerance. After a brief presentation of the main fungal- or oomycete-induced diseases, this chapter aims to give an overview of some aspects of grapevine-pathogenic fungi or oomycete interactions, at the molecular level. It includes an overview of resistance gene analogs, elicitors that induce defense reactions in grapevine, signaling pathways and gene activation.

### 2. MAIN GRAPEVINE FUNGAL OR OOMYCETE-INDUCED DISEASES

#### 2.1. *Foliage and berry diseases*

##### 2.1.1. Powdery mildew

Powdery mildew, caused by the ascomycete *Uncinula necator* (syn.

*Erysiphe necator*), an obligate biotrophic parasite of grapevine, is considered to be one of the most important fungal diseases in viticulture worldwide. Symptoms appear as grayish powdery or dusty patches of fungus growth on the upper side of the leaves and on other green parts of the vines, leading to a decrease in photosynthetic activity. In infected clusters, berries turn hard, brown, are smaller than uninfected ones, and may split open. Besides direct loss of yield, infected berries fail to properly mature and significantly alter wine quality (Calonnec et al. 2004). Almost no *V. vinifera* cultivar is immune to *U. necator*, but other grapevine species such as *Vitis labrusca*, *Vitis aestivalis* or *Vitis berlandieri* as well as *Muscadinia rotundifolia* possess various levels of resistance (Mullins et al. 1992).

### 2.1.2. Downy mildew

Downy mildew is caused by the oomycete *Plasmopara viticola*, also an obligate biotrophic parasite of grapevine. It still is one of the most destructive grapevine diseases in Europe and in the eastern half of the United States. Downy mildew affects the leaves, fruit, and shoots of grapevines. First symptoms occur as yellowish oily lesions on the leaf upper surfaces; they rapidly give rise to white, felt-like “downy” fungal mass on the corresponding lower sides of the leaves. Infected berries first appear grayish then turn “downy” during pathogen sporulation. Yield losses occur through death of leaf tissue, low-quality fruit, and weakened young shoots.

### 2.1.3. Grey mould

Grey mould is the third major fungal disease affecting grapevine foliage and berries, particularly severe in areas where wet weather occurs between véraison and harvest. It is due to the broad host-range necrotrophic ascomycete *Botrytis cinerea*, which causes necrotic spots on leaves, total or partial destruction of the bunches before flowering and later on, rotting of berry clusters. Besides losses of fruit yield, infection of berries by *B. cinerea* also deteriorates wine quality by inducing the appearance of mushroom earthy off-odors (La Guerche et al. 2006).

Grey mould, powdery and downy mildews are controlled at the vineyard mostly by chemical spraying, sterol demethylation inhibitors or quinone outside inhibiting fungicides. However, besides negative environmental impacts, pathogens develop resistances towards these pesticides (Délye et al. 1997, Leroux et al. 1998, Chen et al. 2007).

## 2.2. Wood decay diseases

### 2.2.1. *Eutypa* dieback

*Eutypa* dieback is a wood decay disease caused by the ascomycete *Eutypa lata*. Symptoms do not usually appear until vines are at least six years old. Shoot symptoms are most evident during the beginning of the spring, with shoot arising from infected trunks being stunted with small chlorotic leaves (Moller and Kasimatis 1978). Berries fail to develop or develop very poorly, inducing yield losses ranging from 30 to 60% on highly susceptible cultivars (Munkvold and Marois 1994). *Eutypa* dieback shoot symptoms are always accompanied by a canker, which often appears V-shaped in a cross-section of the perennial wood. Cankers progress toward the trunk, killing the distal portions of the vine, and eventually, the entire vine may die in an average period of 10 years after the initial infection (Pascoe 1999). Currently, there is no cure for *Eutypa* dieback.

### 2.2.2. Esca

Esca, a.k.a. ‘apoplexy’ or ‘lack measles’ is a complex trunk disease involving at least five fungi, *Fomitiporia punctata*, *Stereum hirsutum*, *Phaeoacremonium aleophilum*, *Phaeoconiella chlamydospora*, and *E. lata*, that obstruct the vascular system (Larignon and Dubos 1997). It affects both young and older vines. Cross section in infected trunks shows a central soft, white necrosis (touchwood), surrounded by a brownish hard zone. Esca develops slowly in the grapevine until the plant exhibits a sudden apoplectic decline, eventually killing the vine within a few days. No chemical is currently available to control esca.

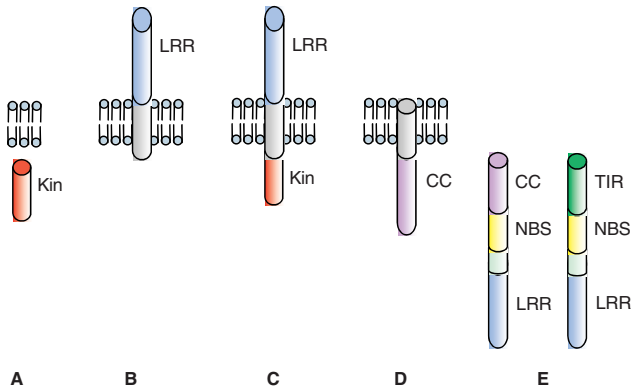
## 3. GRAPEVINE RESISTANCE GENES ANALOGS

The European grape *V. vinifera*, which accounts for about 90% of world-wide grape production for wine making, shows very low disease resistance. On the other hand, wild American species, such as *Muscadinia rotundifolia*, are resistant to various pathogens, including *U. necator* (powdery mildew), *P. viticola* (downy mildew) or *Xylella fastidiosa* (Pierce’s disease; Olmo 1986). Enhancing the resistance of cultivated grapevine to diseases therefore constitutes a major goal for breeders (Bisson et al. 2002).

### 3.1. *R-genes and the plant immune system*

In the past decade, our understanding of the molecular basis of plant disease resistance has increased steadily. Plants lack the adaptive immune system, which is the privilege of the vertebrates. To detect and successfully ward off pathogens, plants rely solely on innate immunity of each cell and on systemic signals emanating from infected sites (Dangl and Jones 2001). It is now widely admitted that the plant immune system uses two distinct defense systems (Chisholm et al. 2006). A first line of defense uses transmembrane pattern recognition receptors to recognize slowly evolving pathogen-associated molecular patterns (PAMPs), such as bacterial flagellin, lipopolysaccharide or fungal/oomycete cellulose binding elicitor proteins to activate basal defenses (Ausubel 2005). Pathogens, however, have evolved to acquire mechanisms that help them to by-pass PAMP-triggered immunity. Plants struck back by setting up a second line of defense that relies on proteins which recognize pathogen effectors or modifications of their cellular targets, a mechanism called effector-triggered immunity. Both PAMP- and effector-triggered immunity rely on the so-called resistance genes (*R-genes*).

*R-genes* can be grouped into 5 classes (Ellis et al. 2000, Dangl and Jones 2001) encoding for: (i) cytoplasmic serine/threonine kinases such as the *Pto* gene in tomato (Fig. 1A); (ii) extracellular leucine-rich repeats (LRRs) proteins anchored to a transmembrane domain, as exemplified by the tomato *Cf-9* gene



**Fig. 1.** Schematic representation of the *R-genes* products. (A) Intracellular *Pto*-like serine/threonine kinases (Kin). (B) *Cf-9*-like trans-membrane-anchored Leucine-Rich repeats (LRR). (C) *Xa21*-like proteins with an intracellular serine/threonine kinase domain and an extracellular LRR domain. (D) *RPW8* protein with a transmembrane-anchored coiled-coil (CC) domain. (E) Intracellular NBS-LRR proteins with an LRR domain in their C-terminus, a nucleotide binding site (NBS) and either a toll/interleucine-1 receptor (TIR) or a CC domain in their N-terminus. Adapted from Dangl and Jones (2001), with permission.

(Fig. 1B); (iii) receptor-like kinases (RLKs) with an extracellular LRR and an intracellular serine/threonine kinase (i.e. the rice gene *Xa21*, Fig. 1C), (iv) proteins with an N-terminal transmembrane anchor and a cytoplasmic coiled-coil (CC) domain encoded by the *Arabidopsis* *RPW8* (Resistance to Powdery Mildew 8, Fig. 1D) genes; and (v) proteins with a nucleotide binding site (NBS), and a LRR domain in their C-terminus (NBS-LRR proteins, Fig. 1E). That later class of *R*-genes can be sub-divided in two sub-classes based on their N-terminal domain (Bai et al. 2002), which can either be a toll/interleukine-1 receptor (TIR-NBS-LRR, specific to dicotyledonous species) or a coiled-coil domain (CC-NBS-LRR, present in all angiosperms).

### 3.2. *R*-genes in grapevine

*NBS-LRR* genes are the most largely represented *R*-genes in plant genomes, as exemplified by the 149 genes found in the *Arabidopsis* genome (Meyers et al. 2003), or the 480 in the rice genome (Zhou et al. 2004). Grapevine is no exception and in a survey of the grape cv Pinot Noir draft genome Velasco et al. (2007) detected 233 genes encoding for proteins containing both NBS and LRR domains (InterPro IPR001611 and IPR002182, respectively). Among them, 84 genes belong to the CC-NBS-LRR subfamily while the TIR-NBS-LRR subfamily includes 37 genes. Additionally, 112 truncated NBS-LRR encoding genes are also present in the grape genome.

A complete inventory of defense-related RLKs genes is not easy to make, because these proteins are also implicated in a wide range of developmentally-related signalling pathways (Shiu and Bleecker 2001). Nevertheless, 53 genes encoding putative RLKs have been identified in grapevine (Di Gaspero and Cipriani 2003), eight of them being closely related to the Pto cytosolic protein from tomato and 3 to the products of the *R*-genes *Xa21* from rice and its *Arabidopsis* homolog *FLS2*.

To date, no true homolog of the *Arabidopsis* *RPW8* resistance genes have been identified in grapevine. Two genes, however, *VRP1-1* and *VRP1-2* (for *Vitis* Resistance to *Plasmopara* 1-1 and 1-2) encode CC-NBS-LRR with a *RPW8* domain in their N-termini (Kortekamp et al. 2008). Such chimeric resistance proteins could link the pathogen effector-triggered (gene-for-gene) responses attributed to NBS-LRR proteins with the basal general resistance responses credited to *RPW8* proteins (Xiao et al. 2005, Wang et al. 2007). Interestingly, *VRP1-1* and *VRP1-2* sequences show nucleotide polymorphism that led to amino acid substitutions at several positions when compared in the downy mildew resistant *Vitis* accession Regent and the susceptible Pinot noir (Kortekamp et al. 2008), making them potentially interesting to breed resistance.

### **3.3. Cluster of *R*-genes map to chromosomal region of grapevine genetic disease resistance**

*R*-genes, particularly the NBS-LRR class, are arranged in clusters in plant genomes, a physical disposition that generates sequence variation and gene family expansion at a high rate, a point that is crucial to generate new resistance specificities (Bergelson et al. 2001, Meyers et al. 2003, Zhou et al. 2004). In grapevine, *TIR-NBS-LRR* gene clusters are preferentially located on linkage group (LG) 18, *CC-NBS-LRR* gene clusters on LG 9 and 14 and truncated *NBS-LRR* on LG 12 and 13 (Velasco et al. 2007, Moroldo et al. 2008). *RLKs* are more evenly dispersed in the grape genome, with LG 14 scoring the highest number of *RLK* coding genes (Moroldo et al. 2008).

In agreement with the role of *R*-genes in plant innate immunity, several clusters of *NBS* genes map to chromosomal regions where genetic resistance to bacterial, fungal or oomycete-induced diseases were previously assigned (Di Gaspero et al. 2007, Velasco et al. 2007). The *Run1* locus (Resistant to *Uncinula necator* 1), originating from *M. rotundifolia* (Pauquet et al. 2001), which confers resistance to powdery mildew, has a counterpart in the *Vitis* genome physically located on LG 12, in a region which contains several copies of *R*-genes (Barker et al. 2005). Additional loci for powdery mildew resistance have been reported on LG 15 and 14 in *Vitis* hybrids (Dalbo et al. 2001, Fischer et al. 2004). In the same region of LG 14, a primary locus for resistance to Pierce's disease causal agent, *Xylella fastidiosa*, was identified in the wild grape *Vitis arizonica* (Krivanek et al. 2006). Quantitative trait loci for downy mildew resistance have been mapped with SSR markers to the distal part of LG 18 (Fischer et al. 2004), and in the middle of LG 7 (Grando et al. 2003) in *Vitis* resistant accessions, nearby regions where *NBS-LRR* genes are clustered. Another major determinant responsible for resistance to *P. viticola* has been identified on LG 12 (Merdinoglu et al. 2003). In conjunction with the knowledge of the grape genome sequence, the availability of linkage maps based on transferable molecular markers (reviewed by Doligez et al. 2006) will constitute valuable tools for pathogen resistance breeding in premium *Vitis* cultivars.

## **4. ELICITORS ACTIVE ON GRAPEVINE**

Several molecules coming from microorganisms, plants or algae have been characterized as elicitors. These molecules, which encompass lipids, oligosaccharides and proteins, trigger defense responses in plants, such as the hypersensitive response (HR), the localized acquired resistance (LAR) or the systemic acquired resistance (SAR). Besides, some molecules coming from non-

pathogenic microorganisms potentiate ISR (Induced Systemic Resistance) in plants, leading to tolerance against many pathogens. These signal molecules, often recognized by a receptor (see *R*-genes, § 3), offer several possible applications as natural inducers of defense and tolerance in plants.

#### **4.1. Oligosaccharide elicitors**

Several elicitors such as  $\beta$ -1,3-glucans or  $\alpha$ -1,4-oligogalacturonides are known to be active in many plant species. In grapevine some oligosaccharides appear to be efficient, like  $\beta$ -1,4-cellobextrins (Aziz et al. 2007), cyclodextrins (Morales et al. 1998, Bru et al. 2006), laminarin extracted from algae (Aziz et al. 2003) and induce tolerance against *B. cinerea* or *P. viticola*. Sulfated glucans like  $\beta$ -1,3-glucan sulfate enhance tolerance to *P. viticola* (Trouvelot et al. 2008). In addition, two novel oligosaccharidic elicitors were purified from *B. cinerea*. These molecules, obtained from crude mycelium cell wall extracts and culture filtrate preparations, were named Botrycin and Cinerein, respectively (Repka et al. 2001a, Repka 2002, 2006). In all cases, treatment with these elicitors triggered the classical PR (Pathogenesis Related) proteins accumulation, reactive oxygen species (ROS) production, as well as  $\text{Ca}^{2+}$ , jasmonic acid (JA) and salicylic acid (SA) signalling pathways.

#### **4.2. Lipid elicitors**

If several lipid molecules are known to act as elicitors in plants, in grapevine the main lipidic elicitor described up to now is the ergosterol molecule. This sterol, which is typical of fungi, was described as an inducer of a specific set of defense-related genes in tobacco and associated signal transduction pathways (Kasparovsky et al. 2004, Lochman and Mikes 2006, Rossard et al. 2006). Some PR-proteins (PR-14) and enzymes of the stilbene biosynthesis pathway are highly induced in grapevine by ergosterol treatment, most probably through the activation of WRKY trans-activator factors (Gomès et al. 2003, Laquitaine et al. 2006, Marchive et al. 2007). The putative specific receptors of ergosterol remain to be identified.

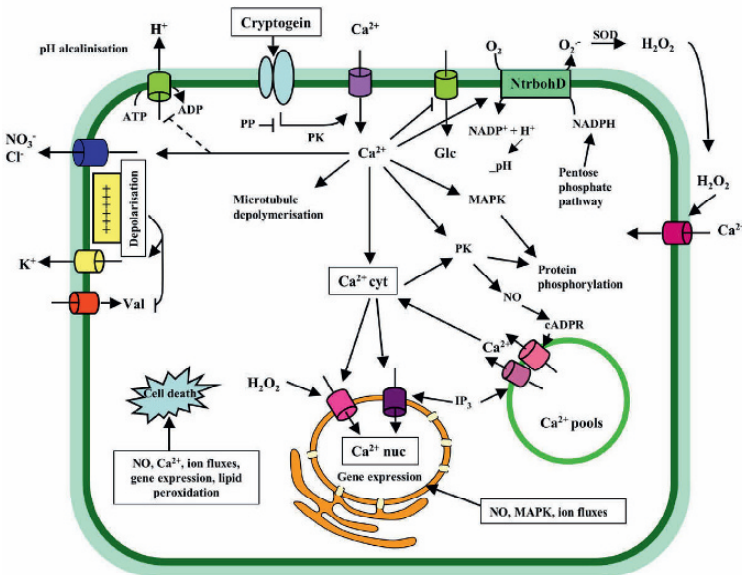
#### **4.3. Proteinaceous elicitors**

In terms of proteinaceous elicitors, two major lines of work have emerged these last years. Poinssot et al. (2003) described an endo-polygalacturonase secreted in the culture medium of *B. cinerea*, which is able to trigger full-scale early defense reactions in grapevine cell suspension cultures. Apparently, elici-

tor effect is not due to the enzyme activity. More recently, it was demonstrated that oligandrin, an elicitor of *Pithium oligandrum*, enhances *Vitis* tolerance towards *B. cinerea* (Mohamed et al. 2006). These results are of interest because elicitors were previously described to be active on tobacco but not on other plants (Ponchet et al. 1999). The fact that an elicitor could induce protection against fungal pathogens without HR response, but with modifications of the redox status of the cells, is indeed a very innovative concept.

### 5. EARLY CELLULAR EVENTS IN DEFENSE REACTIONS

Numerous studies of early plant defense reactions have been made in the last ten years. In Fig. 2 the principal steps, keys of the knowledge about this signal transduction pathway, are summarized. In model plants such as tobacco or *Arabidopsis* all these steps including perception, calcium flux activation, ROS synthesis, MAPKs (mitogen-activated protein kinases) or phosphatases activation are well characterized. In grapevine, the amount of information available, regarding early events of defense reactions, was less developed until recently (Busam et al. 1997, Jacobs et al. 1999). In the past few years, several publications aimed to decipher defense-related early signalling events in grape-



**Fig. 2.** Early cellular events triggered by pathogen recognition, as exemplified by the case of the signalling cascades induced on tobacco cells by cryptogein, an elicitor from *Phytophthora cryptogea*. Reprinted from Garcia-Brugger et al. (2006), with permission.



vine using model cell suspension cultures or entire plants (Repka 2006, Vandelle et al. 2006).

As described in paragraph 4, many elicitors have been characterized and some putative receptors identified in the Pinot Noir genome sequence. After the classical step of pathogen (or elicitor) perception, most of the crucial signalling events have been identified in grapevine. It seems that  $\text{Ca}^{2+}$  influx is the first event occurring after elicitation, by modulation of plasmamembrane  $\text{Ca}^{2+}$  channels. Later on,  $\text{NO}^{\bullet}$  is synthesized and mobilizes internal stores of  $\text{Ca}^{2+}$ . Then come ROS ( $\text{O}_2^{\bullet-}$ ,  $\text{H}_2\text{O}_2$ ) production, MAPK and phosphatase activities that have also been evidenced in elicited plants.

A second class of signalling compounds (JA, SA and ethylene) are produced as endogenous signalling molecules and elicit pathogen protection process. Finally, a pool of defense genes gets activated, including PR proteins encoding genes, as well as phenylpropanoid and stilbene biosynthesis genes (Repka 2006, Vandelle et al. 2006). A particular class of PR-proteins is induced, the lipid transfer proteins (LTP, PR-14). These secreted proteins are able to bind JA, at least *in vitro* and trigger protection against *B. cinerea* (Girault et al. 2008). LTP-JA complexes could be one element of SAR signalling, leading to global protection of the plant against pathogens (Grant and Lamb 2006).

In conclusion, it seems that grapevine species possess all the signalling elements to respond to a pathogen attack. Nevertheless, it is clear that there are some differences between wild grapevine species and the European *V. vinifera*. For example, some *R* genes are absent from *V. vinifera* (*Run1*) and could explain the sensitivity of premium cultivars to pathogenic fungi (Barker et al. 2005).

## 6. GRAPEVINE PR-PROTEIN GENES

As already mentioned, one of the major steps in plant defense reactions is the synthesis of a particular class of proteins classically termed as 'PR' proteins. These proteins were distributed in 1999 in 11 classes. Recently, Van Loon et al. (2006) published a broader classification with 17 classes. The PR-proteins are defined as proteins that are not expressed in plants without pathogen interaction or largely induced during infection. For a protein to be classified as a PR-protein, it is necessary that its induction is described for two different plant/pathogen systems in two different laboratories. Not all the PR-proteins classes have been described in grapevine so far.

A putative sequence of a *V. vinifera* PR-1 protein was identified and cloned by Bertsch et al. (2003). The expression kinetics of a *PR-1* defense-related gene is strongly dependent on the nature of elicitor used (Repka 2001b). Comparison of *PR-1* expression in grapevine cell cultures after inoculation with

a host and a non-host pathogen revealed a high *PR-1* expression rate 3 weeks post-inoculation in *V. vinifera* cv Riesling and *Vitis riparia* cv Gloire de Montpellier, even if pathogens development was not blocked. Thus, the role of *PR-1* expression in impeding the downy mildew pathogen remains equivocal. It seems that expression of *PR-1* genes is a general stress response in some grapevine culture systems (Wielgoss and Kortekamp 2006). Three PR-1-like proteins were found to accumulate in grapevine leaves after infection by *U. necator*. Expression of these proteins was also induced by elicitor treatments in grapevine cell suspension culture (Repka et al. 2000).

The PR-2, -3, -4 and -5 classes are better documented in grapevine. In a susceptible *V. vinifera* cv, such as Riesling, inoculated with *Pseudoperonospora cubensis* (downy mildew of cucumber), a non-host pathogen in grapevine,  $\beta$ -1,3-glucanases (PR-2) and chitinases (PR-3 and -4) are largely accumulated in comparison with a host situation (*P. viticola*). Following treatment with *P. cubensis*, sporulation intensity was significantly reduced in Riesling after subsequent inoculation with *P. viticola* (Kortekamp 2006). Several PR-proteins are expressed in berries at maturity and liquid chromatography-mass spectrometry analysis of grape juice revealed the presence of several PR-3 and PR-5 (thaumatin-like) isoforms with different molecular masses, as a function of the varieties (Hayasaka et al. 2001).

*U. necator*, the causal agent of grapevine powdery mildew, induces expression of chitinases and  $\beta$ -1,3-glucanases in leaves and berries in various grapevine cultivars, including susceptible ones. Indeed, Jacobs et al. (1999) showed that the hydrolytic activity was directly related to the severity of infection at the pathogen location. PR-2, -3 and -5 were also observed in infected berries at pre-véraison stage and were highly induced by ethephon treatment. These results demonstrate a paradox: even if these classes of PR-proteins are expressed during pathogen invasion this does not offer complete protection against *U. necator*. Probably, some other more specific proteins are necessary. Alternatively, the key of the protection might be more determined by the presence or the absence of *R*-genes (resistance genes).

Furthermore, the diversity of PR proteins expressed decreases during grape maturation (Monteiro et al. 2007) and could explain the enhanced susceptibility of the berries during the last stages of ripening. Accordingly, it was demonstrated that constitutive expression in transgenic *V. vinifera* of thaumatin-like protein protects grapevine plants against anthracnose (Jaysankar et al. 2003). These plants, however, were not protected against other fungi. In addition, induction of chitinase genes in *V. vinifera* depends on the infecting pathogen, but also the type of chitinase is different in a compatible or incompatible interaction (Robert et al. 2002). The selective expression of specific chitinases might be a reliable indicator of the SAR response in *V. vinifera* (Busam et al. 1997).

A grapevine class 10 PR-protein was cloned from *V. vinifera* leaves infiltrated with the incompatible bacterial pathogen *Pseudomonas syringae* pv Pisi (Robert et al. 2001). To our knowledge, it is the only example of *PR-10* gene characterized in grapevine. The accumulation of the corresponding mRNA was observed from 3 to 96 h post-inoculation and was followed by the accumulation, between 24 and, at least, 96 h after inoculation, of the encoded polypeptide, detected by immunoblotting.

The story of the PR-14 family is more complicated. These proteins (Lipid Transfer Proteins) were shown to be involved in several physiological processes. It is now quite clear that some isoforms are clearly involved in defense reaction signalling process (Maldonado et al. 2002, Blein et al. 2002, Grant and Lamb 2006). Several isoforms of LTP have been described in grapevine (Coutos-Thévenot et al. 1993). Some of them were induced by fungal elicitor treatments (Gomès et al. 2003). Ergosterol-induced protection of grape against *B. cinerea* relies on the expression of a type I lipid transfer protein, which is mediated by a WRKY trans-activating protein (Laquitaine et al. 2006). In addition, Girault et al. (2008) demonstrated that some grapevine LTP were able to bind JA, and that exogenous application of a LTP-JA complex induces protection of grapevine towards infection by *B. cinerea*. All LTPs, however, are not defense-related. Other isoforms seem to be involved in other physiological process, like somatic embryo development and epidermal layer formation. Accordingly, over-expression of the *VvLTP1* gene interferes with somatic embryo development in grapevine and abolishes the bilateral symmetry of embryos (François et al. 2008).

The last classes of PR-proteins that have been described in grapevine are the germin and germin-like proteins (PR-15 and -16). Recently, 7 members of the grapevine germin-like multigenic family were cloned in *V. vinifera* (Godfrey et al. 2007). Among them, one gene, *VvGLP3* (*V. vinifera* germin-like 3), have no basal expression level and is strongly induced by powdery mildew infection. Another member of the family, *VvGLP7*, responds to both *P. viticola* and *B. cinerea* infection. Some germin-like proteins exhibit oxalate oxidase or superoxide dismutase activities, but their exact role in plant defense reactions is far from being elucidated.

According to the literature, PR-6, -7, -8, -9, -11, -12, and -13, have not been described in grapevine yet. Nevertheless, using the sequences of the first member of each class to be published (Van Loon et al. 2006), a BLAST analysis indicate the presence of putative homolog genes in the Pinot noir genome (<http://www.genoscope.cns.fr/externe/GenomeBrowser/Vitis/>) for all these PR-protein classes, with the noticeable exception of PR-13 (thionins). Table 1 summarizes the BLAST results, by presenting for each PR-protein class the first

**Table 1.** Putative homolog genes for PR-6, 7, 8, 9, 11, 12 and 13 in the Pinot noir genome. For each PR-protein class, the grapevine genome database was probed with the sequence a typical member, as described by Van loon et al. (2006).

PR-protein class	Typical member	Properties	Putative grape homolog genes*	Linkage group
6	Tomato inhibitor I	Proteinase inhibitors	GSVIVT00020160001	5
			GSVIVT00020161001	5
			GSVIVT00029370001	13
7	Tomato P <sub>69</sub>	Endoproteases	GSVIVT00001054001	2
			GSVIVT00001055001	2
			GSVIVT00001051001	2
			GSVIVT00001053001	2
			GSVIVT00001034001	2
			GSVIVT00001056001	2
8	Cucumber chitinase	Type III Chitinases	GSVIVT00006464001	Unknown
			GSVIVT00026961001	15
			GSVIVT00026949001	15
			GSVIVT00026950001	15
			GSVIVT00006463001	Unknown
			GSVIVT00020672001	14
9	Tobacco lignin-forming peroxidase	Peroxidase	GSVIVT00024722001	6
			GSVIVT00025396001	8
			GSVIVT00024724001	6
			GSVIVT00024717001	6
			GSVIVT00037460001	8
			GSVIVP00018771001	12
11	Parsley PR-1	Ribonuclease-like	GSVIVP00012304001	Unknown
			GSVIVP00012300001	Unknown
			GSVIVP00012296001	Unknown
			GSVIVP00005601001	Unknown
			GSVIVP00005604001	Unknown
			GSVIVP00005606001	Unknown
12	Radish Rs-AFP3	Defensins	GSVIVT00035146001	1
			GSVIVT00014577001	18
			GSVIVT00002075001	19
13	<i>Arabidopsis</i> THI2.1	Thionins	None detected	

\* Putative grape PR-proteins transcripts are designated by their Genoscope annotation number (<http://www.genoscope.cns.fr/externe/GenomeBrowser/Vitis/>).

6 transcripts detected in the database (only 3 were detected for PR-12, defensins). Such an analysis is of course far from being exhaustive and is just intended to point the need of additional studies in the future to better characterize PR-protein families in grapevine.

## 7. GRAPEVINE PHYTOALEXINS BIOSYNTHESIS AND METABOLISM

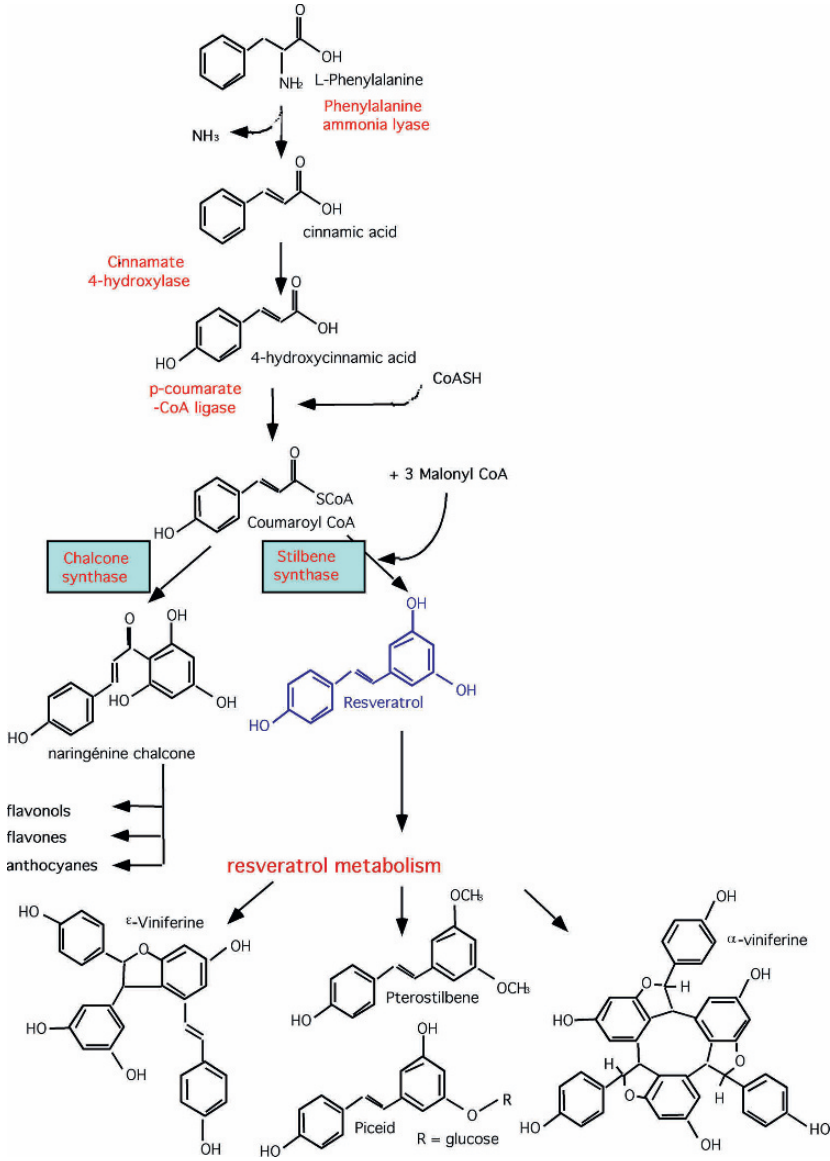
### 7.1. *Stilbene synthase genes*

The knowledge of grapevine phytoalexin metabolism (Fig. 3) has increased vastly in the past decade. In woody plants, the classical phenylpropanoid pathway is split at the coumaroyl-CoA step by the stilbene synthase activity, which synthesizes resveratrol by condensation of 3-malonyl-CoA with one molecule of coumaroyl-CoA (Langcake and Pryce 1976, Langcake and Pryce 1977, Pont and Pezet 1990, Pezet and Pont 1995). This enzyme activity belongs to a multigenic family and has been already characterized by Wiese et al. (1994).

The first genes coding a *Vitis* stilbene synthase (*VST*) was cloned by Melchior and Kindl (1990), and afterwards several other genes were characterized (Richter et al. 2005). The recent publication of the grapevine Pinot Noir genome revealed the presence of 21 putative stilbene synthase genes, essentially on LG 10 and 16 (Velasco et al. 2007). This number fits nicely with a recent stilbene synthase gene expression analysis in infected grapes leaves (Richter et al. 2005). Stilbene synthases exhibit a high degree of homology with chalcone synthase and are known to be induced by several stimuli, including UV light, which is the major abiotic inducer (Adrian et al. 2000, Bonomelli et al. 2004).

Stilbene synthase genes are down-regulated during grape berry ripening, due to a competition between stilbene and chalcone synthase activities; that latter enzyme being activated after véraison for anthocyan and flavonoid accumulation in pellicula. A large group of biotic inducers are able to promote stilbene synthase expression and microorganisms were shown to have a direct effect on resveratrol accumulation. *B. cinerea* is the most common fungus able to act on phenylpropanoid pathway (Liswidowati et al. 1991, Bais et al. 2000, Keller et al. 2003). The level of the response, however, depends largely on the cultivar (Gabler et al. 2003), and it is possible to class the level of tolerance of cultivars in the field in regard to the capacity to accumulate resveratrol after UV light induction, as summarized in the Table 2 (Coutos-Thevenot et al. 2001).

Several other fungi were found to induce resveratrol production. *Aspergillus* induces expression of *VST* genes (Jean-Denis et al. 2006) and more problematic pathogens like three of the fungi associated with Esca, promote stilbene production (Bruno and Sparapano 2006a, 2006b). Bacteria-like *Pseudomonas*



**Fig 3.** Biosynthesis pathway of grapevine stilbenes. Reprinted from Coutos-Thevenot et al. (2001) with permission.

*syringae* pv Pisi seem also to act as inducers during HR of grapevine (Robert et al. 2001). Various studies have demonstrated the ability of purified elicitors to induce VST gene activation or resveratrol synthesis. Ergosterol, a specific sterol of fungi and a non-specific elicitor, is highly efficient (Laquitaine et al.

2006). The endo-polygalacturonase BcPG1 produced by *B. cinerea* induces *VST1* mRNA accumulation 4 hours after treatment of grapevine cell suspension and is more active than oligogalacturonate elicitors (Poinssot et al. 2003). Several other molecules are also effective inducers of resveratrol production in grapevine (Borie et al. 2004, Laura et al. 2007), like oligogalacturonates (Aziz et al. 2004),  $\beta$ -1-3 glucane sulfate (Trouvelot et al. 2008), as well as chemicals like aluminium chloride (Adrian et al. 1996) or benzothiazole (Iriti et al. 2004, see also Chapter 12 in this book). Even if its mechanism of action is not well understood, resveratrol inhibits the growth of several fungi or oomycetes. Microbiologic tests revealed a good effect on *Botrytis* and *Eutypa lata* mycelium growth (Adrian et al. 1997, Coutos-Thevenot et al. 2001), *P. viticola* (Pezet et al. 2004) and *Venturia inaequalis* growth (Schulze et al. 2005). If resveratrol is active, its metabolites like pterostilbene (methylated form) and viniferins (oligomer metabolites) seem to be much more efficient (Pezet et al. 2004). On the other hand, the glycosylated form (piceid) seems to be less active and could be a soluble storage form (Pezet et al. 2004). It is suspected that enzymes, like methyl transferases and oxidases, could be involved in these mechanisms.

**Table 2.** Effects of *Botrytis* infection or UV treatment on resveratrol accumulation by various grapevine cultivars. Data are means of four independent experiments  $\pm$  standard error. Nd: not detected. Reprinted from Coutos-Thévenot et al. (2001), with permission.

Variety / cultivars	Control (not induced)	<i>Botrytis</i> Resveratrol ( $\mu\text{g}\cdot\text{g}^{-1}$ DW)	UV light Resveratrol ( $\mu\text{g}\cdot\text{g}^{-1}$ DW)
Rupestris	nd	nd	350 ( $\pm$ 115)
41B Rootstock	nd	112 ( $\pm$ 30)	240 ( $\pm$ 120)
Ugni blanc 479	nd	86 ( $\pm$ 45)	210 ( $\pm$ 74)
Pinot Noir 386	nd	103 ( $\pm$ 31)	87 ( $\pm$ 49)
Folle blanche	nd	101 ( $\pm$ 16)	38 ( $\pm$ 11)

## 7.2. Hormones and signalling

Signalling pathways involved in stilbenes accumulation in grapevine are less clear-cut. It seems that stilbene synthase activation is probably due to a cross-talk between several pathways. The role of JA and methyl-JA are well documented with a very efficient induction ( Zhang et al. 2002, Curtin et al. 2003, Larronde et al. 2003, Repka et al. 2004, Tassoni et al. 2005, Vezzulli et al. 2007), but the one of SA is less understood. It seems that SA acts on the phenylpropanoid pathway by inducing phenylalanine ammonia lyase and stilbene synthase genes expression (Chen et al. 2006, Wen et al. 2005, Wen et al.

2008). Ethylene also appears to be involved (Grimmig et al. 2002).

### 7.3. Use in transgenic plants

After the first evidence that tobacco plants, which do not naturally produce stilbenes, become tolerant to *B. cinerea* when transformed with *p35S-VST1* chimeric gene (Hain et al. 1993), the idea of generating transgenic grapevine that over-express stilbene synthase rapidly gained ground. The 41B rootstock was transformed with the *PR10* promoter, which is highly inducible by *B. cinerea* infection, fused to the *VST1* coding sequence. Some transgenic clones showed a high level of *in vitro* tolerance to *Botrytis* and could be also tolerant to *E. lata* (Coutos-Thévenot et al. 2001). More recently, these results were confirmed by several groups on various plant species, like grapevine (Fan et al. 2008), hop (Schwekendiek et al. 2007), oilseed rape (Husken et al. 2005), papaya (Zhu et al. 2004), poplar (Giorcelli et al. 2004) and apple (Szankowski et al. 2003). These examples prove the importance of stilbenes in plant defense mechanisms and open many future applications. Moreover, treatment of post-harvested fruits with resveratrol improves their resistance for conservation (Urena et al. 2003).

## 8. CONCLUSIONS

In the last 15 years, our understanding of molecular aspects of grapevine-fungi interactions has increased largely. The recent publication of the Pinot Noir genome will undoubtedly be a valuable tool for future studies. However, a fair deal of work remains to be done, to precisely decipher and finely characterize the different steps of the pathogen detection by the plant and the subsequent activation and establishment of defense reactions.

This applies, for example, to the characterization of the not yet described, but present in the grapevine genome, PR-protein families; or to the comparative studies of the genetic diversity of resistance genes and other defense-related genes, in the various cultivated and wild grapevines. The global outcome of the knowledge of grapevine defense reaction studies at the molecular level has already started to be integrated to breeding experiments, either through genetic transformation or through marker-assisted selection. It is reasonably safe to bet that this tendency will increase in the future.

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