In a previous comparative transcriptome analysis, several genes involved in resistance to *Plasmopara viticola*, the grapevine downy mildew agent, have been identified in Mgaloblishvili, a Georgian cultivar of *Vitis vinifera*. Genes related to the synthesis of antimicrobial enzymes and compounds such as terpenes (*e.g.* valencene synthase and a cytochrome P450) were among the most frequently upregulated. The same transcriptome analysis highlighted a gene encoding for an LOB domain-containing (LBD) protein, *VvLBDp1*, putatively involved in susceptibility to *P. viticola* in the Pinot noir *V. vinifera* cultivar.

In this study, the knowledge achieved on the resistance/susceptibility features of *V. vinifera* was further deepened and exploited to set up the basis for the development of alternative means for the control of downy mildew. On the one hand, the analysis of volatile organic compound (VOC) profiles of leaf through solid-phase microextraction gas chromatography–mass spectrometry and the expression of six terpene synthases (TPSs) allowed to identify four terpenes (farnesene, nerolidol, ocimene and valencene) that, in leaf-disc assays, caused a significant reduction (53–100%) in downy mildew severity compared to the untreated control. On the other hand, the knockdown of *VvLBDp1* in Pinot noir through RNA interference (RNAi) triggered by exogenous double-stranded RNA (dsRNA) led to significant reductions in the disease severity in the experimental inoculations carried out seven days after the dsRNA treatment. Together, these results demonstrate the potential of natural bioactive molecules produced by grapevine and RNAi in silencing susceptibility factors in grapevine as innovative means for the downy mildew control.

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Targeting *Penicillium expansum* transporters with high affinity small molecules for reducing patulin production

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Fruits and vegetables represent an important component of a healthy diet. However, almost a third of all food crops could be annually lost because of fungal pathogens. Furthermore, the increase in resistance phenomena in fungi pushed the search of new molecules for controlling infections and related mycotoxins. Some of the newly proposed small molecules target fungal proteins with transporter ability. However, most of mycotoxin-producing fungi, as patulin-producer *Penicillium expansum*, have few proteins with a solved structure to be used for identifying new inhibitors. Computational approaches for protein function analyses might help in overcoming the problem, by building 3D homology models to be used in virtual screening of chemical libraries. In the present investigation, on the basis of generated 3D comparative models, it was possible to highlight approved drugs/natural compounds/chemicals able to inhibit GMC oxidoreductase and organic acid mitochondrial transporters to control *P. expansum* growth and patulin production. In particular, 1,2,3-BTA and tannic acid, predicted to inhibit mitochondrial transporters, and meticrane and 6-hydroxycoumarin, predicted to inhibit GMC oxidoreductase, proved to be effective *in vitro* and/or *in vivo*. A mixture of the identified molecules could be used as disinfecting treatment in fruit washing water and storage rooms to prevent fungal infection and mycotoxin accumulation. Finally, the presented study might be extended to the identification of high affinity small molecules of species-specific protein targets of other pathogenic fungi for preventing pre- and postharvest losses as well as for reducing the contamination by mycotoxins in fruit and vegetables.

Alfalfa mosaic virus induces accumulation of defence-related metabolites in *Nicotiana tabacum*

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Plants reaction to abiotic and biotic stresses is often related to the production of several molecules including secondary