

## **Transcriptome analysis of grapevine powdery mildew to elucidate the molecular basis of resistance to metrafenone**

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### **Abstract Text:**

Grapevine powdery mildew, caused by *Erysiphe necator*, is a serious disease widespread in all grape growing areas. The pathogen can infect all green parts of the plant, causing the major economic damage on bunches. Metrafenone is a valuable fungicide used in the powdery mildew disease management since 2006 especially in rotation with other chemistries on grapevine and cereals. Its exact mechanism of action is still not known, but based on cross-resistance studies it is different from other fungicides used in powdery mildew management. Early studies on barley and wheat powdery mildews suggest that it may interfere with hyphal morphogenesis, polarised hyphal growth and the establishment and maintenance of cell polarity.

Obtaining RNA of a good quality and sufficient quantity from obligate plant pathogens like powdery mildews can be problematic especially due to their tight adherence to the host plant epidermis and low mycelium availability at early developmental stages. Here, we searched for the best methodology for tissue collection and the RNA extraction with the aim to perform RNA transcriptome analysis to compare the expression of *E. necator* strains sensitive and resistant to metrafenone, identified previously by our research group. The data of gene expression from these different treatments will be compared to identify possible biosynthetic pathways/enzymatic targets involved in the interaction with metrafenone.