

Promoter analysis of pathogen inducible genes of grapevine

Tina Moser¹, Patrick Merz², Jochen Bogs², Eva Zyprian¹

¹Julius Kühn-Institut, Institute for Grapevine Breeding

²Dienstleistungszentrum ländlicher Raum Rheinpfalz

tina.moser@jki.bund.de

Vitis vinifera ssp. vinifera is an important fruit species in Europe but it is susceptible to Powdery and Downy Mildew caused by *Erysiphe necator* and *Plasmopara viticola*. Both Pathogens were introduced from North America in the 19th century. Since then it is necessary to treat the plants with high amounts of fungicides which causes high costs and is environmentally unfriendly. These measures can be reduced by breeding and use of resistant grapevines. Modern breeding is supported by the use of molecular markers. The development of resistance-correlated markers could be strongly improved by the understanding of the mechanism of pathogen defense. To

get an idea which genes are involved in the mechanism of pathogen defense differential gene expression studies (qRT-PCR) were done in previous work. Some candidate genes like specific transcription factors, PR5 and PR10 were found to be differentially upregulated in resistant plants after the attack of *Erysiphe necator*. In the actual project the promoters of the genes were cloned from a resistant and a susceptible grapevine. They were sequenced and analyzed *in silico*. In further work the transcriptional regulation will be analyzed in transient expression systems and heterologous systems with the help of reporter genes.