

# First candidate genes in the resistance locus *Ren3* against grapevine powdery mildew (*Erysiphe necator*)

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One of the most devastating fungal diseases in European grapevine *Vitis vinifera* L., is powdery mildew. This disease which is caused by the pathogen *Erysiphe necator* leads to enormous annual losses of yield if no counteractions such as the excessive use of fungicides are taken. The pathogen was introduced to Europe around 1845 from America and has spread over nearly all grapevine growing regions worldwide.

American wild *Vitis* species have obtained a natural resistance to *E. necator* due to co-evolution and are preferred resources for grapevine resistance breeding. Up to now there are several loci known originating from these wild *Vitis* species which confer resistance to powdery mildew. One of these is *Ren3* which was first detected in the cultivar 'Regent' by FISCHER et al. (2004).

The project analyzing this resistance locus includes the creation of a physical map of *Ren3* by assembling BAC clone sequences together with next generation sequencing data obtained from cultivars carrying *Ren3*. This physical map will be the basis for

the identification of candidate genes which confer resistance to powdery mildew.

To elucidate the function of candidate genes found in *Ren3*, differential gene expression has to be evaluated by performing qRT-PCR. This could confirm a possible interaction in the assumed resistance mechanisms.

Candidate genes which show differential expression upon infection with *E. necator* have to be transferred into susceptible grapevine cultivars to further confirm their involvement in the resistance to powdery mildew.

In order to get a better understanding of the attack of *E. necator* and the defense of grapevine microscopic studies have to be performed comparatively with resistant and susceptible grapevine cultivars. This will shed light on the different plant reactions and hopefully help to understand the mechanisms of resistance.

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