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DOWN-REGULATION OF TRASCRIPTIONAL ACTIVITY IN GRAPEVINE FOLLOWING *PLASMOPARA VITICOLA* INFECTION

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Plasmopara viticola is an obligate biotrophic pathogen that obtains its nutritional resources from grape living cells through haustoria. The haustorium-host cell interface is thought to involve a largely unknown, extensive molecular traffick. A comprehensive analysis of transcriptional changes associated to the infection process of *P. viticola* in susceptible grapevine (cv. Riesling) has been undertaken by cDNA-AFLP, with the aim to identify differentially expressed genes from the plant and from the pathogen, in infected leaves at the oil spot stage.

RNA was extracted from leaves of *in vitro* grape plants either infected with *P. viticola* or healthy, as well as from sporangia. Amplifications with 128 primer combinations allowed visualization of about 7000 transcripts, with 1700 differentially expressed fragments characterizing the interaction. Most of them are predicted to be of plant origin with 75% of them down-regulated. However, a small percentage of *Plasmopara* genes are also expected to be identified. Differentially expressed fragments of cDNA have been successfully sequenced. After homology search in databases, all transcripts are being classified into functional categories. Selected genes, possibly involved in signal transduction, will be the object of further investigations. Additionally, about 2700 cDNA fragments from sporangia have been identified, that are going to represent a possible wide integration of the presently scarce knowledge on expressed *P. viticola* sequences.