Evaluating the use of germinated zoospores for the identification of effectors from Plasmopara viticola, the causal agent of grapevine downy mildew

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Grapevine downy mildew caused by *Plasmopara viticola* is one of the most important diseases affecting *Vitis spp*. The current strategy of control relies on the use of chemical fungicides. An alternative to the use of fungicides is the use of downy mildew resistant varieties, which is cost-effective and environment friendly. The identification of pathogen effectors as putative avirulence genes is a necessary step to understand the biology of the interaction as well as to choose the most efficient combination of resistance genes in a strategy of pyramiding. Based on knowledge from other Oomycetes, *P. viticola* effectors can be identified using a candidate gene strategy based on data mining of genomic resources. Public genomic resources of *P. viticola* are very limited, not to say inexistent. A recent search at NCBI/EMBL databases produced 79 *P. viticola* entries (10 ESTs and 69 core nucleotides), the majority sequences of mitochondrial or ribosomal origin. As an obligate biotrophe, *P. viticola* can only grow on living tissues and the pathogen biomass in the invasive stages of infection is quite low compared to the plant biomass. Nevertheless, zoospores are easily obtained by washing off sporangia from infected leaves; furthermore, the first stages of pathogen development (growth of germinative tubes and vesicle formation) can be reproduced in vitro. To explore the suitability of such material for the identification of pathogen effectors, we created a cDNA library from in vitro germinated spores and obtained 1500 ESTs. Preliminary sequence analysis revealed the presence of 58 ESTs from genes putatively involved on pathogenicity. Detailed sequence analysis of the ESTs as well as the expression profile of candidate effector genes will be presented.