Towards the characterization of a Quantitative Resistance to Downy Mildew in cultivated Sunflower, *Helianthus annuus*

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Quantitative resistance to sunflower Downy Mildew caused by the oomycete *Plasmopara halstedii* was studied on a population of recombinant inbred lines (RIL) and on a F4 population, not carrying efficient major resistance gene, in fields naturally infested by one race of the pathogen (703 or 710) and in growth chamber (710). The major quantitative trait locus (QTL) localized on linkage group 10 explains almost 40% of variation, and is not linked to any of the known race-specific resistance genes called *Pl* genes. This QTL support interval is currently 1.5 cM long. We constructed and screened a BAC library of the RIL parent (XRQ) having the QTL with the closest genetic markers in order to build a BAC contig in the QTL region, a first step towards the positional cloning strategy. The polymorphic BAC ends are currently being used as new genetic markers on the RIL and F4 population. The evaluation of the resistant phenotypes of such recombinant plants may help restricting the QTL support interval. In order to characterize the expressed genes during the interaction from both partners, plant and oomycete, we performed a cDNA sequencing approach of infected sunflower plantlets using the 454® sequencing method. A database was created and used to identify 60 new *P. halstedii* sequences. Sequence polymorphism between races of *P.halstedii* was searched to identify new markers. Putative effectors having RXLR or Crinkler domains were also characterized.