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Effectome Abstract

Title: RNA-Seq study of host resistance and isolate aggressiveness on gene expression in *Phytophthora capsici*

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Oomycetes are a threat to many plant species important for food, wood and ornamentals. The Oomycete *Phytophthora capsici* attacks various plant species of agronomic interest, including pepper strongly impacted by the resulting root-rot disease. A few partially resistant pepper genitors were described. The released *P. capsici* genome and a RNA-Seq study delivered information on the pathogen transcriptome. To identify the molecular basis of pathogenicity, we aim to characterize by a RNA-seq analysis the gene expression of *P. capsici* according to the host accession, the isolate aggressiveness and the time-course after inoculation. Two pepper accessions differing in their resistance level were inoculated with two *P. capsici* isolates differing in their aggressiveness, separately. Tissues containing the pathogen were collected at 24 and 72 hours after inoculation. Three independent replicates were done for the 8 conditions giving 24 biological samples. For each sample, total RNA was extracted and sequenced by the Illumina technology. Between 27 and 60 million paired-reads per sample were produced. Between 73.8 and 80.1 % of the total paired-reads mapped, with 0.004 to 6.010 % to the reference *P. capsici* gene models and 93.9 to 99.9 % to the pepper transcriptome contigs. We observed a correlation between the number of mapped paired-reads of *P. capsici* and the level of host resistance or isolate aggressiveness. The mapping of the paired-reads on a library of 1475 *P. capsici* effectors revealed differentially expressed RxLR effectors. The underway statistical study of those data would identify the genes expressed in the various conditions and the differentially expressed effectors between host accessions, isolates and time-course after inoculation.

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